

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 10, 2005, 17:30:38 ; Search time 218 Seconds
(without alignments)
8961.504 Million cell updates/sec
Title: US-10-029-020-14
Perfect score: 14887
Sequence: 1 MDVKERKPYRSLRRDAER.....ELSDSANNIHFMRQSEWGR 2769

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | |
|------------|---------|-------------|--------|--------------------|
| Result No. | Score | Query Match | Length | Description |
| 1 | 14529 | 97.6 | 2771 | Q9WTS7 MOUSE |
| 2 | 14269 | 95.8 | 2825 | O70465 MOUSE |
| 3 | 12033.5 | 80.8 | 2824 | Q9W7R3 brachydanio |
| 4 | 10227 | 68.7 | 2715 | Q9WTS6 MOUSE |
| 5 | 10095.5 | 67.8 | 2500 | Q4RFP1 TETNG |
| 6 | 9968 | 67.0 | 2192 | O804R1 brachydanio |
| 7 | 9642 | 64.8 | 2705 | Q9W6V6 gallus gall |
| 8 | 9636 | 64.7 | 2765 | Q9NBW7 MOUSE |
| 9 | 9620.5 | 64.6 | 2764 | Q9NBW8 MOUSE |
| 10 | 9616.5 | 64.6 | 2802 | Q9DERS CHICK |
| 11 | 9610.5 | 64.6 | 2764 | Q9WTS5 MOUSE |
| 12 | 9607 | 64.5 | 2731 | Q9WTS4 MOUSE |
| 13 | 9601 | 64.5 | 2765 | Q9RLK2 RAT |
| 14 | 9584 | 64.4 | 2725 | Q9JZ17 HUMAN |
| 15 | 9501 | 63.8 | 2725 | Q9UKZ4 HUMAN |
| 16 | 9303 | 62.5 | 2590 | Q9W7R4 brachydanio |
| 17 | 9145 | 61.4 | 2346 | Q9JLC1 MOUSE |
| 18 | 8059.5 | 54.1 | 2142 | Q9ULJ2 HUMAN |
| 19 | 8025.5 | 53.9 | 2742 | Q4SZV7 TETNG |
| 20 | 7826.5 | 52.6 | 2319 | Q4RT87 TETNG |
| 21 | 7340 | 49.3 | 1399 | Q6N022 HUMAN |
| 22 | 7179 | 48.2 | 2086 | Q4S403 TETNG |
| 23 | 7063 | 47.4 | 1828 | Q80TD2 MOUSE |
| 24 | 6774 | 45.5 | 1769 | Q9P273 HUMAN |
| 25 | 6189 | 41.6 | 1198 | Q80TF5 MOUSE |
| 26 | 5638 | 37.9 | 1086 | Q9P2P4 homo sapien |
| 27 | 5614 | 37.7 | 1071 | Q7Z3C7 HUMAN |
| 28 | 4670.5 | 31.4 | 1405 | Q4SZV6 TETNG |
| 29 | 4528.5 | 30.4 | 1465 | Q4RTA7 TETNG |
| 30 | 3979.5 | 26.7 | 1045 | Q9NVJ1 HUMAN |
| 31 | 3918.5 | 26.3 | 2594 | Q7QK12 anopheles g |

RESULT 1

Q9WTS7 MOUSE

ID Q5WTS7 MOUSE PRELIMINARY; PRT; 2771 AA.

AC Q9WTS7;

DT 01-NOV-1999 (Tremblrel. 12, Created)

DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Ten-m4.

GN Name=Odz4; Synonyms=ten-m4;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Balb/c; TISSUE=Brain;

RA Ohashi T., Zhou X., Feng K., Richter B., Moergelin M., Perez M.T.,

Su W., Chiquet-Ehrismann R., Rauch U., Faessler R.;

"Mouse Ten-m/Odz is a new family of dimeric type II transmembrane

proteins expressed in many tissues.";

RL J. Cell Biol. 0:0-0(1999).

DR EMBL; AB025413; BAA77399.1; -; mRNA.

DR HSP; P16109; IFSB.

DR MGI; MGI:2447063; Odz4.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR001258; NHL.

DR InterPro; IPR009471; Ten_N.

DR InterPro; IPR006530; YD.

DR Pfam; PF01436; NHL; 6.

DR Pfam; PF05593; RNS_repeat; 5.

DR Pfam; PF06484; Ten_N; 1.

DR SMART; SM00181; EGF; 7.

DR TIGRPFAMS; TIGR01643; YD repeat 2x; 5.

DR PROSITE; PS00022; EGF_1; UNKNOWN_8.

DR PROSITE; PS01186; EGF_2; 7.

DR PROSITE; PS50026; EGF_3; 5.

SQ SEQUENCE 2771 AA; 308499 MW; 1492E1EE1A0DBF0C CRC64;

Query Match

97.6%; Score 14529; DB 2; Length 2771;

Best Local Similarity 97.0%; Pred. No. 0;

Matches 2688; Conservative 40; Mismatches 41; Indels 2; Gaps 1;

Qy 1 MDVKERKPYRSLRRDAERYTSSADSEEGKAPQKYSSETLKAYDQDARLAYGSRV 60

Db 1 MDVKERKPYRSLRRDAERYTSSADSEEGKAPQKYSSETLKAYDQDARLAYGSRV 60

Qy 61 KDIVPQAEAEFCRTGANFTLRELGLVETPPHGLTYRTDGLPCGYSMGSGSADMEAD 120

Db 61 KDMVPQAEAEFCRTGANFTLRELGLVETPPHGLTYRTDGLPCGYSMGSGSADMEAD 120

Qy 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTETDHPGQLQNHLRTPP 180

Db 121 TVLSPEHPVRLMGRSTRGRSCLSRANSNLTLTDTHEWETDHPSSLQNHPLRTPP 180
Qy 181 PPLSHAHTPNQHAASINSNRGNFTPRSNPSPAPTDHSLGEPGAGQAPHAQENWL 240
Db 181 PPLPHAHTPNQHAASINSNRGNFTPRSNPSPAPTDHSLGEPGAGQAPHAQENWL 240
Qy 241 LNSNIPLETRNLKGFPGFTGLTQDNLIEMDILGASHRDGAYSOGHFLFKPGGTSPLFCCTS 300
Db 241 LNSNIPLETRNLKGFPGFTGLTQDNLIEMDILSASRHDGAYSOGHFLFKPGGTSPLFCCTS 300
Qy 301 PGYPLTSSVYSPPRPLPRSTFARPAFNLKPKSKYCNWKCAALSAIVISATLVILLAYF 360
Db 301 PGYPLTSSVYSPPRPLPRSTFARPAFNLKPKSKYCNWKCAALSAIVISATLVILLAYF 360
Qy 361 VAMHLFGLNWLQPMEG--QMYEITEDTASSWPVPTDVSYPGSGTGLETDPDKGKGTE 418
Db 361 VAMHLFGLNWLQPMEGQMYEITEDTASSWPVPTDVSYPGSGTGLETDPDKGKGAAE 420
Qy 419 GKPSSFFPEDSFIDSGEIDVGRASOKIPPGTFWRSQVFIIDHPVHLKFNVSGLKAAIVGI 478
Db 421 GKPSSLFPEDSFIDSGEIDVGRASOKIPPGTFWRSQVFIIDHPVHLKFNVSGLKAAIVGI 480
Qy 479 YGRKGLPPSHTOFDVVELLDGRRLLTOEARSLEGTPROSRGTVPPSSSHETGFIQYLDGI 538
Db 481 YGRKGLPPSHTOFDVVELLDGRRLLTOEARSLEGTPROSRGTVPPSSSHETGFIQYLDGI 540
Qy 539 WHLAFYNDGKESEVVSFLTTAIESVDNCPNCGNGDCISGTCFGLFGLPDCGRASCP 598
Db 541 WHLAFYNDGKESEVVSFLTTAIESVDNCPNCGNGDCISGTCFGLFGLPDCGRASCP 600
Qy 599 VJCSNGQYMKGRCLCHSGWKABCDVPTNQCIDVACSNHGTCTINGTCICNPGYGESCE 658
Db 601 VJCSNGQYMKGRCLCHSGWKABCDVPTNQCIDVACSNHGTCTINGTCICNPGYGESCE 660
Qy 659 EYDCMDPTCSRGVCGVGRGCHFCVWGNGTNCETPRATCLDQCSGHGTFLPDTGLCSDPS 718
Db 661 EYDCMDPTCSRGVCGVGRGCHFCVWGNGTNCETPRATCLDQCSGHGTFLPDTGLCNDPS 720
Qy 719 WTGHDCSIBICAADCGHGVCGVGTCTCRCEBGMWGAACDQACHPCAEBHGTCTRDGKCECS 778
Db 721 WTGHDCSIBICAADCGHGVCGVGTCTCRCEBGMWGAACDQACHPCAEBHGTCTRDGKCECS 780
Qy 779 PGWNGEHCCTIAHYLDRAWKVGCPGLCNGNGRCTLDLNGWHVCOLGWRGAGCOTSMETAC 838
Db 781 PGWNGEHCCTIAHYLDRAWKVGCPGLCNGNGRCTLDLNGWHVCOLGWRGAGCOTSMETGC 840
Qy 839 GDSKONDGGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIOBTQVVPVQQNLHGSFYDRI 898
Db 841 GDSKONDGGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIOBTQVVPVQQNLNPFYDRI 900
Qy 899 KFLVGRDSTHIIIPGENPFDGHA CVIRGQVMTSDGTPLVGVNISFVNPNPLFGYTTISRODQ 958
Db 901 KFLVGRDSTHIIIPGENPFDGHA CVIRGQVMTSDGTPLVGVNISFVNPNPLFGYTTISRODQ 960
Qy 959 SFDLVNTNGISIIILPERAPPFTQOHTLWLPMDRPFVMTETIMRHEENETPSCDLSNFAR 1018
Db 961 SFDLVNTNGISIIILPERAPPFTQOHTLWLPMDRPFVMTETIMRHEENETPSCDLSNFAR 1020
Qy 1019 PNPVVSPLTSPASSCAEKGPIVPEIOALQBEISISGCKMRLSYLSSTPGVKSVLRIS 1078
Db 1021 PNPVVSPLTSPASSCAEKGPIVPEIOALQBEIVTAGCKMRLSYLSSTPGVKSVLRIS 1080
Qy 1079 LTHPTIIPFNLMKVLMAVEGBLFRKWFAPAAAPDLSYFPIWDKTDVYNQKVFGLSEAFVSV 1138
Db 1081 LTHPTIIPFNLMKVLMAVEGBLFRKWFAPAAAPDLSYFPIWDKTDVYNQKVFGLSEAFVSV 1140
Qy 1139 GYEYESCPDIIWEKRTTVLQGEVIDASKLGWSLDKXHALNTQSGILHKHGENQFVSQ 1198
Db 1141 GYEYESCPDIIWEKRTTVLQGEVIDASKLGWSLDKXHALNTQSGILHKHGENQFVSQ 1200
Qy 1199 QPPIVGSIMNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDVFNIRIPFSG 1258

Db 1201 QPPIVGSIMNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDVFNIRIPFSG 1260
Qy 1259 NVTNILERNKDFRHSHPAHKYYLATDPMGSAVFLSDNSNRRVFKIKSTVVVXDLVKNS 1318
Db 1261 NVTNILERNKDFRHSHPAHKYYLATDPMGSAVFLSDNSNRRVFKIKSTVVVXDLVKNS 1320
Qy 1319 EVVAGTGQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGII 1378
Db 1321 EVVAGTGQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGII 1380
Qy 1379 STLGSNDLTSARPLSCDSVMDISQVRLWPTDLAINPMDNSLYVLDNNVVLQISENHQV 1438
Db 1381 STLGSNDLTSARPLSCDSVMDISQVRLWPTDLAINPMDNSLYVLDNNVVLQISENHQV 1440
Qy 1439 RIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYTAETDEKKINRIQVT 1498
Db 1441 RIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYTAETDEKKINRIQVT 1500
Qy 1499 TSGEISLVAGAPSGCDCKNDANCDGSGDDGYAKDAKLNTPSSLAVCADGELYVADLGN 1558
Db 1501 TSGEISLVAGAPSGCDCKNDANCDGSGDDGYAKDAKLNTPSSLAVCADGELYVADLGN 1560
Qy 1559 RIRFIRKNKPFNTQNMVELSSPIDQELYLPTDTGKHLYTOSLPTGDIYNYFTYTGDDGI 1618
Db 1561 RIRFIRKNKPFNTQNMVELSSPIDQELYLPTDTGKHLYTOSLPTGDIYNYFTYTGDDGI 1620
Qy 1619 TLIIDNNGMNVNRDSTGMPLWLVVDPGVVYVMTGMTNSALKSVTTQGHELAMMTYHGN 1678
Db 1621 THIIDNNGMNVNRDSTGMPLWLVVDPGVVYVMTGMTNSALKSVTTQGHELAMMTYHGN 1680
Qy 1679 SGLLATKSNENGWTTFFEYDSFGRLTNVTPTFGQVSSFRSDTSSSVHVQVETSSKDDVTI 1738
Db 1681 SGLLATKSNENGWTTFFEYDSFGRLTNVTPTFGQVSSFRSDTSSSVHVQVETSSKDDVTI 1740
Qy 1739 TTNLASAGAFYTLQDQVRNSYYTGADGSLRLLLANGMEVALQTPHLLAGTWNPTVGR 1798
Db 1741 TTNLASAGAFYTLQDQVRNSYYTGADGSLRLLLANGMEVALQTPHLLAGTWNPTVGR 1800
Qy 1799 NVTLPIDNGLNLEWQRKEQARGQVTVFGRRLRVHNRNLLSLDFDTRTRTEKIYDDRHK 1858
Db 1801 NVTLPIDNGLNLEWQRKEQARGQVTVFGRRLRVHNRNLLSLDFDTRTRTEKIYDDRHK 1860
Qy 1859 FTLRILYDQAGRPSLWSPSSRLNGVNYTSPGGYIAGIQGIMSERMEBYDQAGRITSRIF 1918
Db 1861 FTLRILYDQAGRPSLWSPSSRLNGVNYTSPGGYIAGIQGIMSERMEBYDQAGRITSRIF 1920
Qy 1919 ADGKTWSYTYLEKSMVLLHLSQRYIFEFDKNDRLSSVTMPNVARQTLTETRSVGYRNI 1978
Db 1921 ADGKTWSYTYLEKSMVLLHLSQRYIFEFDKNDRLSSVTMPNVARQTLTETRSVGYRNI 1980
Qy 1979 YQPPEGNASVTDFTEDGHLAHTFVLTGRBVIYKGLSKLAETLYDTTKVSPYDETA 2038
Db 1981 YQPPEGNASVTDFTEDGHLAHTFVLTGRBVIYKGLSKLAETLYDTTKVSPYDETA 2040
Qy 2039 GMLKTIINQNEGFCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNDNSFRVTSNQAVI 2098
Db 2041 GMLKTIINQNEGFCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNDNSFRVTSNQAVI 2100
Qy 2099 NETPLPIDLYRVDVSGKTEFGKFGVIYDINOIITTAVMTHTKHFDAYGRMKEVQYBI 2158
Db 2101 NETPLPIDLYRVDVSGKTEFGKFGVIYDINOIITTAVMTHTKHFDAYGRMKEVQYBI 2160
Qy 2159 FRSLMYWNTVQYDNMGRVVKELKVGPNATTRYSEYDADQLOQTVSINDKPLWRYSD 2218
Db 2161 FRSLMYWNTVQYDNMGRVVKELKVGPNATTRYSEYDADQLOQTVSINDKPLWRYSD 2220
Qy 2219 LINGNLHLLSPGNSARLTPLRYDIRITRLGDVQYKMDDEDFLQRGGDIFBYSNAGLLI 2278
Db 2221 LINGNLHLLSPGNSARLTPLRYDIRITRLGDVQYKMDDEDFLQRGGDIFBYSNAGLLI 2280
Qy 2279 KAYNPAGSWSVRVYDGLGRRVSSKSSHHLQFFYADLTNPDKVTHLYNHSSEITSY 2338
Db 2281 KAYNPAGSWSVRVYDGLGRRVSSKSSHHLQFFYADLTNPDKVTHLYNHSSEITSY 2340

QY 2339 YDLQCHLFAMELSSGDEFFIACDNIGTIPAVFSGTGLMIKQILYATAYGEIYMDTNPNFOI 2398
Db 2341 YDLQCHLFAMELSSGDEFFIACDNIGTIPAVFSGTGLMIKQILYATAYGEIYMDTNPNFOI 2400
QY 2399 IIGYHGLYDPLTKLVHMGRRDYDVLGRWTSPPDHELKHLSSNNVMPFNLYMPKNNPI 2458
Db 2401 IIGYHGLYDPLTKLVHMGRRDYDVLGRWTSPPDHELKHLSSNNVMPFNLYMPKNNPI 2460
QY 2459 SNSQDIKCFMTDVSNNWLLTTFQFQHNVIIPGYPKDMDAMEPSYELIHTOMKTQEWDSKS 2518
Db 2461 SNSQDIKCFMTDVSNNWLLTTFQFQHNVIIPGYPKDMDAMEPSYELIHTOMKTQEWDSKS 2520
QY 2519 ILGVQCEVQKQKAFVTLERFDQLYSTISCCQAPTKKTFASSGSGVFGKGVKFAKDKGR 2578
Db 2521 ILGVQCEVQKQKAFVTLERFDQLYSTISCCQAPTKKTFASSGSGVFGKGVKFAKDKGR 2580
QY 2579 VTTDIIISVANEDGRRAAILNNAHYLENLHFTIDGVDTHTYFVKPSPSEGDLAILGLSGGR 2638
Db 2581 VTTDIIISVANEDGRRAAILNNAHYLENLHFTIDGVDTHTYFVKPSPSEGDLAILGLSGGR 2640
QY 2639 RTLENGVNVTVSQINTVINGRTRYTDIQLQYGAALCNTRYGTYLDEKARVLELARORA 2698
Db 2641 RTLENGVNVTVSQINTVINGRTRYTDIQLQYRALCNTRYGTYLDEKARVLELARORA 2700
QY 2699 VROAWAREQORLREGEGLRAWTEGEKQOVLSTGRVOGYDGFVVISVEQYPELSDSANNI 2758
Db 2701 VROAWAREQORLREGEGLRAWTEGEKQOVLSTGRVOGYDGFVVISVEQYPELSDSANNI 2760
QY 2759 HFMROSEMGR 2769
Db 2761 HFMROSEMGR 2771

RESULT 2

ID 070465 MOUSE PRELIMINARY; PRT; 2825 AA.
AC 070465,
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE DOC4.
GN Name=Od24; Synonyms=Doc4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NIH/Swiss;
RX MEDLINE=98315054; PubMed=9649432; DOI=10.1093/emboj/17.13.3619;
RA Wang X.-Z., Kuroda M., Sok J., Batchvarova N., Kimmel R., Chung P.,
RA Zinszner H., Ron D.,
RT "Identification of novel stress-induced genes downstream of chop.";
RL EMBO J. 17:3619-3630(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NIH/Swiss;
RA Wang X.-Z., Ron D.,
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF059485; AAC31807.1; -, mRNA.
DR PIR, T14271; T14271.
DR HSSP, P16109; 1FSB.
DR Ensembl; ENSMUSG00000048078; Mus musculus.
DR MGI; MGI:2447063; Od24.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR009471; Ten N.
DR InterPro; IPR006530; YD-
Pfam; PF01436; NHL; 6.

DR Pfam; PF05593; RHS_repeat; 5.
DR Pfam; PF06484; Ten N; 1.
DR SMART; SM00181; EGF; 7.
DR TIGRFAMs; TIGR01643; YD_repeat_2x; 5.
DR PROSITE; PS00022; EGF_1; UNKNOWN_8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 4.
SQ SEQUENCE 2825 AA; 313485 MW; A120D98080886032 CRC64;

Query Match 95.8%; Score 14269; DB 2; Length 2825;

Best Local Similarity 93.4%; Pred. No. 0;
Matches 2654; Conservative 47; Mismatches 52; Indels 88; Gaps 4;

QY 1 MDVKERKPYRSLRRRDAERRYSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
Db 1 MDVKERKPYRSLRRRDAERRYSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
QY 61 KDIVPOAEAEFCRTGANFTLRELGLBEVTPPHGTLVYRTDGLPQCGYSMGASDADHEAD 120
Db 61 KDMVPOAEAEFCRTGNFTLRELGLGEMTPPHGTLVYRTDGLPQCGYSMGASDADHEAD 120
QY 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTET----- 164
Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETGAPLHCSSASSTPIEQ 180
QY 165 -----DHPGGL 170
Db 181 SPSPPPPPANESQRRLLGNVQAQPTDSDSEEFVPSNPLVKSGSASLGAANDHPSSL 240
QY 171 QNHARLRTPPPLSHAHATPNQHHAAASINLNNGFTPRSNPNPSAPTSHISGEPAGGAQ 230
Db 241 QNHPLRLTDPPLPHAHATPNQHHAAASINLNNGFTPRSNPNPSAPTSHISGEPAGGAQ 300
QY 231 EPAHAQENLLNSNI PLETENLCKQPLGTLQNLLEMDILGASRHDGAYSDGHFLKPG 290
Db 301 EPHAQDNVNLNSKI PVETENLCKQPLGTLQNLLEMDILGASRHDGAYSDGHFLKPG 360
QY 291 GTSPLFCTTSPGYPLTSSVYSPPRPLPRSTFARPAFNLKPKSKYCNWKAALSAIVIS 350
Db 361 GTSPLFCTTSPGYPLTSSVYSPPRPLPRSTFARPAFNLKPKSKYCNWKAALSAIVIS 420
QY 351 ATLVIILAYFVAMHFLGNLHLPMEG--QMYEITEDTASSWPVPTDVSLYPSGCTGLET 408
Db 421 ATLVIILAYFVAMHFLGNLHLPMEGQMYEITEDTASSWPVPTDVSLYPSGCTGLET 480
QY 409 PDRKGKTTTGKPSSEFPEDSFIDSGEIDVGRASQKI PPGTFWRSOVFIDHPVHLKFNV 468
Db 481 PDRKGKGAEGKPSSEFPEDSFIDSGEIDVGRASQKI PPGTFWRSOVFIDHPVHLKFNV 540
QY 469 SLGKAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQEARSLGCTPRQSRGTVPSSSHET 528
Db 541 SLGKAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQEARSLGCTPRQSRGTVPSSSHET 600
QY 529 GFQYLDSDGIWHLAFYNDGKESVVSFLTTAIESVDNCPNCYNGNGDCISGTCFCFLGFL 588
Db 601 GFQYLDSDGIWHLAFYNDGKESVVSFLTTAIESVDNCPNCYNGNGDCISGTCFCFLGFL 660
QY 589 GPDGGRASCPLVCSGNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCTTGTCIC 648
Db 661 GPDGGRASCPLVCSGNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCTTGTCIC 720
QY 649 NPGYKGSCEVDCMDPTCSGRGVGVGECHCFVGMGGTNCETPRATCLQCSGHGFLP 708
Db 721 NPGYKGSCEVDCMDPTCSGRGVGVGECHCFVGMGGTNCETPRATCLQCSGHGFLP 780
QY 709 DTGLSCDPSWTGHDCSIETCAADCGGHGVGVGCTCRCEBGMGAACQDQACHPRCAEHG 768
Db 781 DTGLCNCDPSTGHDCSIETCAADCGGHGVGVGCTCRCEBGMGAACQDQACHPRCAEHG 840
QY 769 TCRDGGKCECPGWNGBHCTTAHYLDREVVKGGCGFLCNGNGRCTLDLNGHVCVCLGWRGA 828
Db 841 TCRDGGKCECPGWNGBHCTTAHYLDREVVKGGCGFLCNGNGRCTLDLNGHVCVCLGWRGT 891

| | | | |
|----|------|--|------|
| Qy | 829 | GCDTSMETACGDSKDNDDGGLVCHMDPCCLQPLICHNPCLCLGSPNPLDIIQETQVPVQ | 888 |
| Db | 892 | GCDTSMETCCGGKDNDDGGLVCHMDPCCLQPLCHVNPLCLGSPDPLDIIQETQAPVQ | 951 |
| Qy | 889 | QNLHSFYDRIKFLVGRDSTHIIIPGENPPDGGHACVIRGOVWTSOGTPLVGVNISFVNPL | 948 |
| Db | 952 | QNLNSFYDRIKFLVGRDSTHSIIPGENPDDGGHACVIRGOVWTSOGTPLVGVNISFINNPL | 1011 |
| Qy | 949 | FGYTIISRODGSFDLVNNGGISIIIRFRERAPFITQEHTLWLIPWDRFFVYMETIIMRHEBNEI | 1008 |
| Db | 1012 | FGYTIISRODGSFDLVNNGGISIIIRFRERAPFITQEHTLWLIPWDRFFVYMETIIMRHEBNEI | 1071 |
| Qy | 1009 | PSCDLSNFARPNPVVSPSLTSPASSCAEKGPVPEIQALQOEETISGCKWRLSYSSRT | 1068 |
| Db | 1072 | PSRDLSNFARPNPVVSPSLTSPASSCAEKGPVPEIQALQOEETIIVAGCKWRLSYSSRT | 1131 |
| Qy | 1069 | PGYKSVLRISLTHPTIIPFNLMKVHMAVEGRLEPRKWFAPAAAPDLSYYFIDKTDVYNQKV | 1128 |
| Db | 1132 | PGYKSVLRISLTHPTIIPFNLMKVHMAVEGRLEPRKWFAPAAAPDLSYYFIDKTDVYNQKV | 1191 |
| Qy | 1129 | FGLSEAFVSVGYEYESCPDILILWEKRTTVLQGYEIDASKLGWSLDKXHAALNTQSGILHK | 1188 |
| Db | 1192 | FGLSEAFVSVGYEYESCPDILILWEKRTAVLQGYEIDASKLGWSLDKXHAALNTQSGILHK | 1251 |
| Qy | 1189 | NGNGENQFVSQOPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDF | 1248 |
| Db | 1252 | NGNGENQFVSQOPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDF | 1311 |
| Qy | 1249 | NYIIRIIPSGNVNTHILELRNKPFRHSHPAHKYIYLATDPMGSAVFUSDNSNRVFKIKST | 1308 |
| Db | 1312 | NYIIRIIPSGNVNTHILEM:-----SHSPAHKYIYLATDPMGSAVFLSDTNSRRVFKVKST | 1364 |
| Qy | 1309 | VVVKDLVKNSEVAGTGDQCLPPDDTRCGDGGKATEATLNPRGIIIVDKFGLIYFVDGTM | 1368 |
| Db | 1365 | TVVKDLVKNSEVAGTGDQCLPPDDTRCGDGGKATEATLNPRGIIIVDKFGLIYFVDGTM | 1424 |
| Qy | 1369 | IRRIDQNGIISTLLGSNDLTSARPLSCDSYMDISQVRLEPPTDLAINPMDNSLYVLDDNV | 1428 |
| Db | 1425 | IRRYDQNGIISTLLGSNDLTSARPLSCDSYMEISQVRLEWPTDLAINPMDNSLYVLDDNV | 1484 |
| Qy | 1429 | VLOIASENHQVRIIVAGRPWHQCPGIDHFTLSKVAIHATLESATALAVSHNGVLIYAETDE | 1488 |
| Db | 1485 | VLOIASENHQVRIIVAGRPWHQCPGIDQLFUSKVAIHATLESATALAVSHNGVLIYAETDE | 1544 |
| Qy | 1489 | KKINIRIQVTTSGEISLVAGAPSGCCCKNDANCDCFSGDDGYAKDAKLANTPSSLAVCAGD | 1548 |
| Db | 1545 | KKINIRIQVTTSGEISLVAGAPSGCCCKNDANCDCFSGDDGYAKDAKLANTPSSLAVCAGD | 1604 |
| Qy | 1549 | ELYVADLGNRIIRPIRNKQFPLNTQNMVELSSPIDQELYLFDITGKHLYTQSILPTGDYLY | 1608 |
| Db | 1605 | ELYVADLGNRIIRPIRNKQFPLNTQNMVELSSPIDQELYLFDITSGKHLYTQSILPTGDYLY | 1664 |
| Qy | 1609 | NFTYTGDDGITLITDNNGNMNVRRDSTGNPLVLVDPGOVYVWVTMGTSALKSVTTQGH | 1668 |
| Db | 1665 | NFTYTGDDGITLITDNNGNMNVRRDSTGNPLVLVDPGOVYVWVTMGTSALKSVTTQGH | 1724 |
| Qy | 1669 | ELAMMTHGNSGLLATKSNENGWTTPEYDQSFQRLTNVTFPTQCVSFSRSDTSSVHVQV | 1728 |
| Db | 1725 | ELAMMTHGNSGLLATKSNENGWTTPEYDQSFQRLTNVTFPTQCVSFSRSDTSSVHVQV | 1784 |
| Qy | 1729 | ETSSKDDVTITTNLSAGAFYTLLOQVNRNSYIIGADGSIIRLLANGMEVALQTEPHLLA | 1788 |
| Db | 1785 | ETSSKDDVTITTHLSGSGAFYTLLOQVNRNSYIIGADGSIIRLLANGMEVALQTEPHLLA | 1844 |
| Qy | 1789 | GTVPNTVGKENVTLPIDINGLNLVEMRQKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTR | 1848 |
| Db | 1845 | GTVPNTVGKENVTLPIDINGLNLVEMRQKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTR | 1904 |
| Qy | 1849 | TEKIYDDHKFTLRIILYDQAGRPSLWSSBRLNGVNVTYSPGCIYAGIORGIMSERMEYD | 1908 |
| Db | 1905 | TEKIYDDHKFTLRIILYDQAGRPSLWSSBRLNGVNVTYSPGCIYAGIORGIMSERMEYD | 1964 |
| Qy | 1909 | QAGRITSRIPADGKTWSYTVLEKSMVLLHLSRQYIFEFDKNDRILSSVTMPNVARQTLBT | 1968 |

| | | | |
|--------------|--|---|---------------|
| Db | 1965 | QAGRIITSRIFADGKMWSYTYLEKSMVLHLHSORQYIFEFDPKNDRLSSVTPMNPVARQTLET | 2024 |
| Qy | 1969 | IRSVGYRNIIYQPEGNASVIODFTEDGHLHHTFYLGTCGRRVLYKYGKLSKAETLYDIT | 2028 |
| Db | 2025 | IRSVGYRNIIYQPEGNASVIODFTEDGHLHHTFYLGTCGRRVLYKYGKLSKAETLYDIT | 2084 |
| Qy | 2029 | KVSFTYDETAGMLKTLINLQNEGFTCTIRYRQIGPLIDRQIFRTEEGMVNARFDYNYDNS | 2088 |
| Db | 2085 | KVSFTYDETAGMLKTLINLQNEGFTCTIRYRQIGPLIDRQIFRTEEGMVNARFDYNYDNS | 2144 |
| Qy | 2089 | FRYTSQAVINETPLPIDLYRYDDUSGKTEQEGKFGVIYVDINOIITTAWMHTKHFDAY | 2148 |
| Db | 2145 | FRYTSQAVINETPLPIDLYRYDDUSGKTEQEGKFGVIYVDINOIITTAWMHTSHRFDAY | 2204 |
| Qy | 2149 | GRMKEVQEYIFRSLMYMTVQDNNMRGVVKELKVGYPANTTRYSEYDADGQLOQTVSIN | 2208 |
| Db | 2205 | GRMKEVQEYIFRSLMYMTVQDNNMRGVVKELKVGYPANTTRYSEYDADGQLOQTVSIN | 2264 |
| Qy | 2209 | DKPLWYSYDLNGNLHLSPGNSARLTPURYDIRIRITRLGDVQYKMDSDGFLRQGGDI | 2268 |
| Db | 2265 | DKPLWYSYDLNGNLHLSPGNSARLTPURYDIRIRITRLGDVQYKMDSDGFLRQGGDV | 2324 |
| Qy | 2269 | FEYNSAGLLIKAYNRAGSWSRYRYDGLGRRYSSKSSHHLQFFYADLTNPTKVTHLYN | 2328 |
| Db | 2325 | FEYNSAGLLIKAYNRAGSWSRYRYDGLGRRYSSKSSHHLQFFYADLTNPTKVTHLYS | 2384 |
| Qy | 2329 | HSSSEITSIYYDLQGLHFAMELSSGDEFYIACNIGTPLAVPSGTGLMIKQILYATYGEI | 2388 |
| Db | 2385 | HSSSEITSIYYDLQGLHFAMELSSGDEFYIACNIGTPLAVPSGTGLMIKQILYATYGEI | 2444 |
| Qy | 2389 | YMDTNENFOIIGYHGGLYDPLTKLVHMGRRDYDLAGRWTSPPDHSLKGLSSNVMPEN | 2448 |
| Db | 2445 | YMDTNENFOIIGYHGGLYDPLTKLVHMGRRDYDLAGRWTSPPDHSLKGLSSNVMPEN | 2504 |
| Qy | 2449 | LYMFKNKNPISNSQDIKCFMPTDVNSWLLTFGFLQHNVIIPGYPKPDMADAMEPSYELIHTQM | 2508 |
| Db | 2505 | LYMFKNKNPISNSQDIKCFMPTDVNSWLLTFGFLQHNVIIPGYPKPDMADAMEPSYELVHTQM | 2564 |
| Qy | 2509 | KTQEWDNKSIIIGVQCEVQOKLKAFTVLERPDLGSIITSCQOAPKTKKFPASSGSVFGK | 2568 |
| Db | 2565 | KTQEWDNKSIIIGVQCEVQOKLKAFTVLERPDLGSIITSCQOAPKTKKFPASSGSVFGK | 2624 |
| Qy | 2569 | GVKFALKDGRVTTDIIISVANEDGRVAAILNHAHYLENLHFTIDCGVDTHYFVKPGPSEGD | 2628 |
| Db | 2625 | GVKFALKDGRVTTDIIISVANEDGRVAAILNHAHYLENLHFTIDCGVDTHYFVKPGPSEGD | 2684 |
| Qy | 2629 | LAILGLSGRRITLNGVNVTSQINTVINGRTRRYTDIQLYGALCLNTRVYGTTLUDEKA | 2688 |
| Db | 2685 | LAILGLSGRRITLNGVNVTSQINTVINGRTRRYTDIQLYGALCLNTRVYGTTLUDEKV | 2744 |
| Qy | 2689 | RVLELARQAVRQAWAREQOORUREGEEGLRAWTEGEKQOVLSTGRVQGVDFGVTSVEQY | 2748 |
| Db | 2745 | RVLELARQAVRQAWAREQOORUREGEEGLRAWTEGEKQOVLSTGRVQGVDFGVTSVEQY | 2804 |
| Qy | 2749 | PELSDSANNIHPMRQSEMGR 2769 | |
| Db | 2805 | PELSDSANNIHPMRQSEMGR 2825 | |
| RESULT 3 | | | |
| Q9W7R3_BRARE | | | |
| ID | Q9W7R3_BRARE | PRELIMINARY; | PRT; 2824 AA. |
| AC | Q9W7R3; | | |
| DT | 01-NOV-1999 | (TREMBLrel. 12, Created) | |
| DT | 01-NOV-1999 | (TREMBLrel. 12, Last sequence update) | |
| DT | 01-WAR-2004 | (TREMBLrel. 26, Last annotation update) | |
| DT | Ten-m4 | | |
| DN | Name=od24; Synonyms=ten-m4; | | |
| OS | Brachydanio rerio (Zebrafish) | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; | | |
| OC | Cyprinidae; Danio. | | |

Db 1662 LNFYTSGEGLSSITDKNKNRVSIRRDSTGLPLMGPDGQTFWFTGTTNNALKSVAAQ 1721
Qy 1667 GHELAMWTYHGSGLLATKSNENGWTTTFEYEDSFGRLTNVPTPTQGVSSFRSDTSSVHV 1726
Db 1722 GQEIAMVTYHGSGLLATKSNEDGWSFTFEYDNYGRLTNVPTPTGRVSSYRTSDSTVRV 1781
Qy 1727 QVETSKDVTITTNLSASGAFYTLLOQOVNRNYYIGADGSLRLLLLANGMEVALTEPHL 1786
Db 1782 QTEGSKNKEDITVTNLSASGTFYTLMQDQVKNSYYIGLDSLRLLVLANGMEVSLTEPHL 1841
Qy 1787 LAGTVNPTVKGKRVNLTPIIDINGLNVEMRQKQARGQVTVFGRRLRVNRNLLSLDDFRV 1846
Db 1842 LSGTVNPTVSKKRVNLTPIIDINGLNVEMRQKQARGQVTVFGRRLRVNRNLLSLMDFRV 1901
Qy 1847 TRTEKIYDDHRKFTLRILYDQAGRPSLMSPLSRLNGVNVYSPGGYIAGIQKIGMSERME 1906
Db 1902 TRTEKIVYDDHRKFTLRILYDHAGRPTLWAPSSRLNGVNVYSPGGHIAGIQRGTMSVRME 1961
Qy 1907 YQAGRITSRIIPADGKTSYTYLEKSMVLLLSHQRYIFEFKNDRLSSVTMPNVAROTL 1966
Db 1962 YDQNGRITSKIIPADGKTSYTYLEKSMVLLLSYQRYIFEFKNDRLSSVTMPNVAROTL 2021
Qy 1967 ETIRSGVYRNYYQPEGNASVIQDFTDGHLLHTFYLGTGRVLYKYGKLSKLAETLYD 2026
Db 2022 ETIRSGYRNYYRPEGNATVLDQYSEDGLLQTHOQGTGRVLYKYGKLSRLLEIYD 2081
Qy 2027 TTKTSFTYDETAGMLKTNLQNEGFTCTIRYQIGPLIDRQIFRTEBGMVNAREFDNYD 2086
Db 2082 TTIRAFSYDESAGMLKTVGLQSEGFACTIRYQIGPLIDRQIFRTEBGMVNAREFDNYD 2141
Qy 2087 NSFRVTSQAVINETPLDILYRDDVSGKTEQFGKFGVIYDINQITTAVMTHTKHFD 2146
Db 2142 NSFRVTSQAVINETPLDILYRDDVSGKTEQFGKFGVIYDINQITTAVMTHTKHFD 2201
Qy 2147 AYGRMKEVQYEIYFRSLMYMWTYQDNMGRVVKELKVGFPYANTYRSEYEDADGQLQVVS 2206
Db 2202 AYGRMKEVQYEIYFRSLMYMWTYQDNMGRVVKELKVGFPYANTYRSEYEDADGQLQVVS 2261
Qy 2207 INDKPLMRYSYDLNGLNHLSPGNSARLTPLRYDIRITRLDGYQVKMDEDFLQRGG 2266
Db 2262 INDKPLMRYSYDLNGLNHLSPGNSARLTPLRYDIRITRLDGYQVKMDEDFLQRGN 2321
Qy 2267 DIFEVNSAGLLIKAYNRAGSNVRYDGLGRVSSKSHHLOFFFYADLTNPKVTHL 2326
Db 2322 DFEFVNSAGLLIKAYNRAGSNVRYDGLGRVSSKSHHLOFFFYADLTNPKVTHL 2381
Qy 2327 YNHSSEITSLYDLOQHLFAMELSSGDEFFYIACDNIGTPLAVFGSGTGLMIKQILYTAYG 2386
Db 2382 YNHSSEITSLYDLOQHLFAMELSSGDEFFYIACDNIGTPLAVFGSGTGLMIKQILYTAFG 2441
Qy 2387 EYIMDTNPNFQIIGVHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHMLKHLSSNNVMP 2446
Db 2442 EYVLDNPNFQIIGVHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHMLKHLSSNNVMP 2501
Qy 2447 FNLVYFKNNPNLSNODIKCFMTDYNMILLTFGFLHNVIPGYPKPDMDAMEPSYELVHT 2506
Db 2502 FNLVYFKNNPNLSNODIKCFMTDYNMILLTFGFLHNVIPGYPKPDMDAMEPSYELVHT 2561
Qy 2507 QMKTQEWNSKSLGVQCEVQKQKAFVTLERFDQLYGSTITSQQAPKTKKFPASGGSVF 2566
Db 2562 QIKTQEWNSKSLGVQCEVQKQKAFVTLERFDQLYGSTITSQQAPKTKKFPATGTSLVF 2621
Qy 2567 GKGVPALKDGRVTTDITSVANEDGRRVAAIINHAHYLENLHFTTIDGVDTHTYFVKPGPSE 2626
Db 2622 GKGVPALKDGRVTTDITSVANEDGRRVAAIINHAHYLENLHFTTIDGVDTHTYFVKPGPSE 2681
Qy 2627 GDLATILGSGGRRTLENGVNVTVSINTVNGRTRRYTDIOLQYCALCINTRYGTTLDEE 2686
Db 2682 GDLATILGSGGRRTLENGVNVTVSINTVNGRTRRYTDIOLQYCALCINTRYGTTLDEE 2741
Qy 2687 KARVLELARQAVRAQWAREQORREGBEGFRAMTEGBKQKQVLSTGRVQGYDGFVIVSE 2746

Db 2742 KVRVLELARQAVATANAHERHRLRQCEGSGRAWTDGERQOLLSSGRVQGYEGFYIVSVD 2801
Qy 2747 QYPELSDSANNIHPMRQSEMGR 2769
Db 2802 QPELTDNNINNVHWRQTEMGRR 2824
RESULT 4
ID Q9WTS6 MOUSE
AC Q9WTS6; PRELIMINARY; PRT; 2715 AA.
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ten-m3.
GN Name=Odz3; Synonym=ten-m3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=Balb/c; TISSUE=Brain;
RA Ohashi T., Zhou X., Feng K., Richter B., Moergelin M., Perez M.T.,
RA Su W., Chiquet-Ehrismann R., Rauch U., Faessler R.;
RT "Mouse Ten-m/Odz is a new family of dimeric type II transmembrane
RT proteins expressed in many tissues.";
RL EMBL; AB025412; BAA77398.1; -; mRNA.
DR HSSP; P00750; 1TPG.
DR Ensemble; ENSMUSG00000031561; Mus musculus.
DR MGI; MGI:1345183; Odz3.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR009471; Ten_N.
DR InterPro; IPR008530; YD.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF01436; NHL; 6.
DR Pfam; PF05593; RHS repeat; 6.
DR Pfam; PF06484; Ten_N; 1.
DR SMART; SM00181; EGF; 7.
DR TIGRFAMs; TIGR01643; YD_repeat_2x; 5.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 5.
SQ SEQUENCE 2715 AA; 303063 MW; 598F46A77334C2E1 CRC64;
Query Match 68.7%; Score 10227; DB 2; Length 2715;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 1864; Conservative 370; Mismatches 457; Indels 102; Gaps 19;
Qy 1 MDVKRRPYSLTR-RRDAERRYSSADSEEGKAP-QKSYSSSETLKAYDQD-ARLAYG 57
Db 1 MDVKRRPYSLTKSRREKERRYTNSSADNEECVPTQKSYSSSETLKAPDHDISRLLYG 60
Qy 58 SRVKDIYVQEAEEFCRTGANFTLRELGLBEVTPPHGTYRTDGLPQCGYSMGAGSDAM 117
Db 61 NRVKDLVHREADEVTRQGNFTLRQLGVCSATRRGVAFCAEMGLPHRGYSISAGSDAT 120
Qy 118 EADTVLSPHVRPLWGRSTRSGRSCLSRANSNLTLTDTEHEN---TETDHPGLQNH 174
Db 121 ENEAVMSPHAMRLWGRGVKSGRSCLSRANSNLTLTDTEHENRSDSESEQPSNNPQGP 180
Qy 175 RLRTPPPLPPLSHAPTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQ---- 230
Db 181 TLQPLPP--SHKQHPAQHH-PSITSLNRNSLTNRNOSPAP-----PAALPAELQTT 229
Qy 231 -EPAAHQENLLNSNITPLETRNLGKQPFGLQDNLEIMDILGASRHDGAYSDGHFLPKP 289
Db 230 PESVOLQDSVWLGSNVPLESR-----HFLFKT 256

QY 1041 IVEIQAQBEISIGCKMRLSSLSRTPGYKSVLRISLTHPTTIPFNLMKVHLMVAVEGR 1100
DB 1015 -----KTAGYKSLLRVTLTHSTIPFNLMKVHLMVAVEGR 1048
QY 1101 LFRKFAAAPDLIYYFIWDTVDYQNVQKVGFLGSAFVSUGVEYESCDPLILWEKRTTVLQ 1160
DB 1049 LFRKFWPAAPNLSDYFVWDRADYVSKVYGLSEFVSUGVEYESCPDFILWEKRAAVLQ 1108
QY 1161 YETDASKLGWSLDKHALNIQSGILHKGNGENQFVSQQPVTGSMGNGRRRSISCPSC 1220
DB 1109 YETTASKLGWTVDKHALNIQSGILHKGNGENVFISQQPVTGSMGNGRRRSISCPSC 1168
QY 1221 NGLADGNKLLAPVALTCGSDSLYVGFNYIRIPFSGNVTNILELR--NKDFRHSHSPA 1278
DB 1169 NGLADGNKLLAPVALACGSDSLYVGFNYVVRRIFTTGNVTSVLELRFCTSMFASBEH--- 1225
QY 1279 HKYLYLATDPMGSAVFLSDNSRRVFKIKSTVTVKDLV---KNSEVVA---GTGDQCLPFD 1332
DB 1226 -----LVVSVEDTSRLPLRCHSRVAVIWLCCASARGEICTFFFPFCACVCLPY- 1272
QY 1333 DTRCGDGGKATEATLNPRTGITVDKGLIYFVDGTMIRRIDQNGIISTLLGSDNLTLSARP 1392
DB 1273 ---C-----CITVDKYGVIFFVDGTMIRRIDQNGIISTLLGSDNLTLSARP 1314
QY 1393 LSCDSVMMDISQVRLEWPTDLAINPMDNSLYVLNNVVLQISENHQVRIVAGRPMHCQVPG 1452
DB 1315 LSCDAVMDISQVRLEWPTDLAVPLDNLVLDNNVVLQISENHQVRIVAGRPIHCQVPG 1374
QY 1453 IDHFLSKVAIHATLESATALAVSHNGVLVIAETDEKKINRIQVTTSGEISLVAGAPSG 1512
DB 1375 IDHFIMSKVAIHATLESANALAVSHNGTILVIAESDEKKINVRQ----- 1418
QY 1513 CDCNDANCDCFSGDDGYAKADAKLNPSSSLAVCADGELYADLGNIRIRIRKKNKPLNT 1572
DB 1419 ----- 1418
QY 1573 QNMVELSSPIDQELYLFDTTGKHLYTQSLPTGDYLVNFTYTGDDITLITDNNGNMNVNR 1632
DB 1419 QN-----EKHIITR----- 1427
QY 1633 RDSGTGMPMLWLVPDQGVYVMTGNTSALKSVTTQGHELAMVTHYHNSGLLATKSNENGWT 1692
DB 1428 ----- 1427
QY 1693 TFVEYDSFGLTNVFTPTGOVSSPRSDTSSVHVQVETSSKDDVTITNLSSASAFVTL 1752
DB 1428 -----YDSYGRLTNNVFTPTGOVSSYRTDADSVRIQTGSKENITVTNLSSASGTFTYLM 1483
QY 1753 QDOVRNSYIIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVTKRNVTLPIDNGLNLVE 1812
DB 1484 QDOVRNSYFGLDGLRLVLANGMEVSLHTEPHLLAGTIIPVTSKRNITLAIIDNGLNLVE 1543
QY 1813 WRQKEQARGQVTVFGRRLRVHNRNLSLDFRVRTTEKIYDDHRKFTLRILYDQAGRPS 1872
DB 1544 WRQKEQARGQVTVYGRRLRVHNRNLSLDFRITRTEKYVDDHRKFTLRILYDHAQRPT 1603
QY 1873 LWPSSSLNGVNVTYSGGYIAGIQRGIMSERMEYDQAGRTSRIFADGKTWSTVYLEKS 1932
DB 1604 LWPSSSLNGVNVTYSGGNGVAGIQRTGTVSRMEYDQGTGRITSQIFADGKSWTVYLEKS 1663
QY 1933 MVLLLLHSQROVIFEFDKNDRLSSVTMPNVAROTLETIRSVGYRNIIYQPPEGNASVLODF 1992
DB 1664 MVLLLYSQROVIFEFDKNDRLSSVTMPNVARHTLETSSRGYRTTYQPPEGNASVLQDY 1723
QY 1993 TEDGHLHFTYLGTRGRVIVKYKGLSKLAETLYDTTKVSFTYDRTAGMLKTIINLQNGFT 2052
DB 1724 SEEQQLLQTTYLGTRGRVIVKYKGLAKLEMLYDTRIGFYDDELTKMLKTVNLQSGFT 1783
QY 2053 CTIYRQIGPLIDRQIRFRFTEEGMVNARFDVYNVNSFRVTSMQAVINETPLDILYRDD 2112
DB 1784 CTYVRQIGPLIDRQIRFRFSEEGMVNARLDVYDVSFRVTSMQAVINETPLDILYRDD 1843
QY 2113 VSGKTEQFGKGVYIYDINQIITTAVMTHTKHFDAYGRMKVEQVEIFRSLMVMWTVQYDN 2172

DB 1844 VSGKTEQFGKGVYIYDINQIITTAVMTHTKHFDAYGRMKVEQVEIFRSLMVMWTVQYDN 1903
QY 2173 MGRVVKELKVGPPYANTTRYSEYEDADGOLQTVSINDKPLWRYSYDLNGLNHLHLLSPGNSA 2232
DB 1904 MGRVVKELKVGPPYANTTRYSEYEDADGOLQTVSINDKPLWRYSYDLNGLNHLHLLSPGNSA 1963
QY 2233 RUTPLRYDIRDIRLGRDVOYKMDGFLRQRGDIFENYAGLLIKAYNRAGSWSVYR 2292
DB 1964 RUTPLRYDNDRITRLGDVOYKMDGFLRQRGDIFENYAGLLIKAYNRAGSWSVYR 2023
QY 2293 YDGLGRVSSKSHSHLOFFYADLTNPVTHLYNHSSEITSLYDLOQHLFAMELSS 2352
DB 2024 YDGLGRVSSRSISGHLOFFYADLTNPVTHLYNHSSEITSLYDLOQHLFAMELSS 2083
QY 2353 GBEFYIACDNIGTPLAVFSGTGLMIKOILYTAIGEYIMDTNPNFQIIGYHGLYDPLTK 2412
DB 2084 GBEFYVACDNIGTPLAVFSGAGIMIKOILHTAFGEVYLDNTPSFQIIGYOGGLYPLSR 2143
QY 2413 LVHMGRRDYDLVLAGRWTSPLHKLWSSNNVFNLPNFKNNNPIISNODIKCFMTDVN 2472
DB 2144 LVHMGKRDYDLVLAGRWTTNPLEIWKRLNSKHIAFPNNYMFKNNNPLSNNEIKCYMTDVN 2203
QY 2473 SWLLTFGQLHNVIPGYPKPDMAMPSEYELHTQMTQEWDSKSLGVOCEVQOLKA 2532
DB 2204 SWLVTFGQLYVNPVPGYHKPNTESMEPSYELVTRQIKTQEWDSKSLGVOCEVQOLKA 2263
QY 2533 FVTLERFDOLYGTSTITSQOAPKTKFASGSSVFGKGVKVPALKDGRVTTDIISVANEDGR 2592
DB 2264 FVKLERFGQYLGAKSAGCQPTETKHFATWGSIFGKGVKVPALREGRVSTDIISLANEDGR 2323
QY 2593 RVAAILNHAYLENLHFTIDGVDVTHYFVKPSPGSEGLAILGLSGRRRTLENGVNVTVSQI 2652
DB 2324 RMAAVLNDAYLEHLEHFTVAGMDTHYFVKMGVPEGDLSLIGMTVGORTLETGVNVTVSQV 2383
QY 2653 NTVLNGRTRYDIQLOYGALCLNTRYGTTLDDEKARVLELAROAVRQAWAREOQRLRE 2712
DB 2384 NAVLNGRTRYDIQLOYGTLNTRYGSSVDSEKARILEMARQRAVTOAWAREOQRLRD 2443
QY 2713 GEEGLRAWTEGEKQOVLSTGRVQGVGDFVVISVEQYPELSDSANNHFMQSEMGRR 2769
DB 2444 GEEGRWTWTEGEKQOVLSTGRVQGVGDFVVISVEQYPELSDSVNNHFMQSEMGRR 2500

RESULT 6
Q804R1_BRARE PRELIMINARY; PRT: 2192 AA.
AC Q804R1;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Odd Oz/ten-m homolog 4 (Fragment).
GN Name=od24; ORFName=od24-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Babbage A.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL807754; CAD61260.1; -; Genomic_DNA.
DR HSSP; P16109; 1FSB.
DR Ensembl; ENSDARG0000006161; Danio rerio.
DR ZFIN; ZDB-GENE-990714-20; od24.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001259; NHL.
DR Pfam; PF01436; NHL; 5.
DR Pfam; PF05593; RHS_repeat; 5.

Db 1124 VHKNGENMFISQQPPVISTMGMGHQHSVSCSNCNGLNALNSKLPAPVALTSGPDGSVYI 1183

QY 1246 GDFNYTRIRFPSPGNVTNILELRKDFRSHSPAHKIYIATDPMGAVFLSDNSRVRFKI 1305

Db 1184 GDFNFVRIRFPSPGNSIGILELRNRDRHSTSPAHKIYIADVPVSESLYLSNDTNRVYKA 1243

QY 1306 KSTVVVVKIDLVKNSVAVAGTDOCLPDDTRCGDGGKATEATJNPRGIITVDKFGIIFYVD 1365

Db 1244 KSLIETKDLAKNVVDVAVAGTDOCLPDDQSHCGDGGKASEASLNSPRGIITDKRGIIFYVD 1303

QY 1366 GTMIRIDQNGIISTLLGNSDLTSAPLSCDSVMDISQVRLEWPTDLAINPMDNSLYLVD 1425

Db 1304 GTMIRKIDENGMITTIIGNSGLTSTQPLSCDSGMDITQVRLEWPTDLTWNPLDNLVYLD 1363

QY 1426 NNVLQISENHQVRIIVAGPBMCOVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAB 1485

Db 1364 NNVLQISENSRRVRIIAGPIHCQVPGIDHFLVSVKVAIHSTLESARAIASHSGIPYIRE 1423

QY 1486 TDEKINRIRQVTTSGEISLVAGAPSGCDCKNDANDCDFSGDDGVAKAKLNTPSSLAVC 1545

Db 1424 TBERKINRIRQVTTNGEISIIAGAPSDCKDPNCDPFGDGGYAKADAKLKAPSSLAVS 1483

QY 1546 AGELYVADLGNIRIRFIRKRPFLNTQNMYSLSPIQELYLFDTTGKHLYTQSLPTGD 1605

Db 1484 PDDTLVYVADLGNIRIRAVSRNKAHLSDTNMYEIASPADQELYQFTINGTHLHTLNIIRD 1543

QY 1606 YLYNFTYTGDDITLITDNGNWNVVRDSTGMPLWLVPDQGVVWTMTGNSALKSVTT 1665

Db 1544 YLYNFTYSGEGDVATITSGNGSNVHIRDTSGLPLWVVVPGGVVWYLTSSNGVLKRYVA 1603

QY 1666 QGHELAMTYHNGSLGKLLATKSNENGWTTTFEYDVSFGLRTNVTFTPGOVSSPSSDPTDSSVH 1725

Db 1604 QGYNLAMTYPGNTGLLATKSNBENGWTTTYEYDSDGHLTNATFTPGEVSSPSSDVEKLTIR 1663

QY 1726 VQVETSSKDDVTITNLSASGAFYTLQDQVNSYIYGADSLRLLLLANGMEVALQTEPH 1785

Db 1664 VELDTSNRENMTATNFSATSIYTLKQDNTQNIYRVSPDGLRVTTFASGMEITLNTPEH 1723

QY 1786 LLAGTVNPTVGRKNTVLPIDNGLNLVEMRQREKQAGQVTVFGRRLRVHNRNLLSLDPR 1845

Db 1724 ILIAGVVSPTLGCNLSLPGHNSNIIEWRQREQTGNISTFERLRRAHNRNLLSIDFDH 1783

QY 1846 VTRTEKIYDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTVSPGGYIAGIQRGIMSRM 1905

Db 1784 VTRTGKIYDHRKFTLRIMYDQTRPVLWSPISKNEVNTIYSHSLGVTYIQRGTWIEKM 1843

QY 1906 EYDQAGRITSRIIPACKTWSYTYLSEKSVLLHSQRYIFEPDKNDRLLSSVTMPNVARQT 1965

Db 1844 EYDPSGNIISRTWADGKIWSYTYLSEKSVMLLSQRRYIFEYDQSDYLLSVTMPSMVRHA 1903

QY 1966 LETIRSVGYRNIYOPPEGNASVIOFTEDGHLHTEVLGTGRRVIYKYGKLSKLAETLY 2025

Db 1904 LQTMLSVGYRNIYTPPDSGAAFIQDVTDRGALLQTLPGTGRVRYLYKYSQSRUSEILY 1963

QY 2026 DTTKVSFTYDETAGMLKTLINLQEGFTCTIRYRQIGPLIDRQIFRFTBEGMVNARFDYNY 2085

Db 1964 DTTQVTFTEESSGVKTIHLMDHGFICTIRYRQTPGLIGRQIFRFBSEGLVNARFDYSY 2023

QY 2086 DNSFRVTSQAVINETPLIDILYRYDDVSGKTEQFGKFGVIYDINQIITAVMTHTKHF 2145

Db 2024 -NNFRVTSQAVINETPLIDILYRYDDVSGRTEQFGKFSVINYDLNQVITTTVMKHTKIF 2082

QY 2146 DAYGRMKEVQYEIFRSLMYMTVQYDNMGRVVVKELKVPVANTTRYSEYVDAGLOLTV 2205

Db 2083 SANGQVIEVQYIELKSIAYWMTIQDNNGRMVVICDIRVGVDANITTRYFYEDRQLOQTV 2142

QY 2206 SINDKPLMRYSYDLNGLNLLSPGNSARLTPLRYDIRDIRTLRLGADVQKMDDEDGFLRQG 2265

Db 2143 SVNDKTQWRYSYDLNGLNLLSHGNSARLTPLRYDLDRDIRTLRLGIEQYKMDDEDGFLRQG 2202

QY 2266 GDIFPYNAGLLIKAYNRAGWSVRYRYDGLGRRVSSKSHHLLQFFYADLTPTKVTHT 2325

Db 2203 NEIFEYNSNGLNKAYNKVSGMTVQYCYDGLGRRVASKSSSLGQHLQFFYADLSNPPIRVTH 2262

QY 2326 LYNHSSSEITSLYYDLOQLHFLFAMELSSGDEFYIACDNIGTBLAVPSGTGLMIKQILYIAY 2385

Db 2263 LYNHSSSEITSLYYDLOQLHFLFAMELSSGEEYVACDNTGTPLAVPSSRGQWIKELIYTPY 2322

QY 2386 GEIYMDTNPFPQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHKLWKLSSSNVM 2445

Db 2323 GEIYQDTPNPQVIVGPHGGLYDSLTKLVHLGQRDYDVIAGRWTTPNHHIWKHLNAV-PQ 2381

QY 2446 PFNLYMFQNNNPINSODIKCFMTDVNSWLLTFQQLHNVIIPGYPKPMDAMEPSYELIH 2505

Db 2382 PFNLYSFENNYPVGRIQDVAKYTTDIGSWLELFGQLHNVLPFPKPEIEALETTYELLQ 2441

QY 2506 TOMKTOEWDSKSTILGVCQEVOKAKFVTLERFDQLYGSTIITSCQOAPKTKKASSGSV 2565

Db 2442 LQTTQEWDPKGTILGICQELQKQLRNFIQDLPMTPTRYSDGKCYEGVKQPRFAALPSV 2501

QY 2566 FGKGVKALQDGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTIDGVDRHYFKVQPS 2625

Db 2502 FGKGIKFAIKDGIWADIIGVANEDSRRIAILNNAHYLENLHFTIEGRDTHYFIKLGSL 2561

QY 2626 EGDIAILGSGRRTLENGVNVTVSQINTVLNGRTRYTDIQLQYGALCLMNTRYGTTLDE 2685

Db 2562 EEDLSLIGNTGRRILENGVNVTVSQMTSVNGRTRRFADTQLQHGALCFNVRYGTTVEE 2621

QY 2686 EKARVLELARQRAVROAWAREQOBLREGELRAWTEGEOOVLSTGRVOGYDGFVLSV 2745

Db 2622 EKNHVLVARQRAVAQAWTKEORRLQGBEGIRAWTDGKQOOLLNTRGVQGYDGFVLSV 2681

QY 2746 EOYPELSDSANNIHFMRQSEMGR 2769

Db 2682 EOYLELSDSANNIHFMRQSEIGRR 2705

RESULT 8

Q5NBW7 MOUSE PRELIMINARY; PRT; 2765 AA.

AC Q5NBW7;

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Odd Oz/ten-m homolog 2 (Drosophila).

GN Name=Odz2; ORFNames=RP23-41F14.1-002;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN (1)

RP NUCLEOTIDE SEQUENCE.

RA Holt K.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN (2)

RP NUCLEOTIDE SEQUENCE.

RA Oliver K.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN (3)

RP NUCLEOTIDE SEQUENCE.

RA Pelan S.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN (4)

RP NUCLEOTIDE SEQUENCE.

RA Matthews L.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN (5)

RP NUCLEOTIDE SEQUENCE.

RA Bird C.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL713915; CAI35945.1; -; Genomic DNA.

DR EMBL; AL713919; CAI35942.1; -; Genomic DNA.

DR EMBL; AL713956; CAI35934.1; -; Genomic DNA.

DR EMBL; BX000433; CAI35947.1; -; Genomic DNA.

DR EMBL; BX539311; CAI36038.1; -; Genomic DNA.

| | | | |
|----|------|---|---|
| | DR | EMBL; AL645912; | CAI35084.1; -; Genomic_DNA. |
| | DR | EMBL; AL645912; | CAI35945.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713956; | CAI35945.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713919; | CAI35945.1; JOINED; Genomic DNA. |
| | DR | EMBL; BX539311; | CAI35945.1; JOINED; Genomic DNA. |
| | DR | EMBL; BX000433; | CAI35945.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL645912; | CAI35942.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713915; | CAI35942.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713956; | CAI35942.1; JOINED; Genomic DNA. |
| | DR | EMBL; BX000433; | CAI35942.1; JOINED; Genomic DNA. |
| | DR | EMBL; BX539311; | CAI35942.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL645912; | CAI35947.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713915; | CAI35947.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713919; | CAI35947.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713956; | CAI35947.1; JOINED; Genomic DNA. |
| | DR | EMBL; BX539311; | CAI35947.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL645912; | CAI36038.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713915; | CAI36038.1; JOINED; Genomic DNA. |
| | DR | EMBL; BX000433; | CAI36038.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713956; | CAI36038.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713919; | CAI35084.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713956; | CAI35084.1; JOINED; Genomic DNA. |
| | DR | EMBL; BX000433; | CAI35084.1; JOINED; Genomic DNA. |
| | DR | EMBL; AL713919; | CAI35084.1; JOINED; Genomic DNA. |
| | DR | EMBL; BX539311; | CAI35084.1; JOINED; Genomic DNA. |
| | DR | InterPro; IPR000742; | EGF_2. |
| | DR | InterPro; IPR006209; | EGF-like. |
| | DR | InterPro; IPR006210; | IEGF. |
| | DR | InterPro; IPR001258; | NHL. |
| | DR | InterPro; IPR009471; | Ten_N. |
| | DR | InterPro; IPR006530; | YD. |
| | DR | Pfam; PF00008; | EGF; 3. |
| | DR | Pfam; PF01436; | NHL; 6. |
| | DR | Pfam; PF05593; | RHS_repeat; 5. |
| | DR | Pfam; PF06484; | Ten_N; 1. |
| | DR | SMART; SM00181; | EGF; 8. |
| | DR | TIGRFAMs; TIGR01643; | YD_repeat_2x; 5. |
| | DR | PROSITE; PS00022; | EGF_1; 8. |
| | DR | PROSITE; PS01186; | EGF_2; 7. |
| | DR | PROSITE; PS50026; | EGF_3; 4. |
| | SQ | SEQUENCE | 2765 AA; 306678 MW; E538D8FD0272761A3 CRC64; |
| | | Query Match | 64.7%; Score 9636; DB 2; Length 2765; |
| | | Best Local Similarity | 62.0%; Pred.No. 0; |
| | | Matches 1772; | Conservative 417; Mismatches 488; Indels 180; Gaps 27 |
| Qy | 1 | MDVKERKPYRSLTRRR-DAERRYTSSADSEEGAP-OKSYSSETLKAYDDARLAYCS | 58 |
| Dd | 1 | MDVKDNR-HRSLTRGRCCKECRYTSSLDSDCRVPTQKSYSSSETLKKAYDHDSRMHYGN | 59 |
| Qy | 59 | RVKDTVPQAEFCFRGTGANFTLRLEGLVEETPPHGLTYRTDIGLPQGYSMGAGSDADME | 118 |
| Dd | 60 | RTVDLVHRSEDEFSSRGNTFLAELGICEPS-PHRSGYCSDMGLIQGVSLTGSDADS | 118 |
| Qy | 119 | ADTVLSPEHPVRLWGRSTRSGRSCLSRRANSNLTLDTEHEHTETHDPG----- | 168 |
| Dd | 119 | TEGGWSPEHAIRLWCGIKSRSSGLSRENSALTLLTSDNENKSDDDNGRPPIPTSSSS | 178 |
| Qy | .169 | -----G.169 | |
| Dd | 179 | LPLSAQLPSSHNNPPPVSCQMPLDLSNTSHQIMTDNPDEEFSPNSYLLRACSGPQQASSG | 238 |
| Qy | 170 | LNQH---AELRTPPPPLSHANTPNQHHAAASINSINRCGNFTPRSN----BSPAPTDSLGS | 232 |
| Dd | 239 | PNNHHSQSTLRPLPP-PHNHTLGHSH--SSANSUNRNLSLNRKSIQIHAPAFND--LAT | 294 |
| Qy | 223 | BPPAGAQBPAHQONWILLINSNIPLETRNLKGCPFLGTLOONLIEMDILGASHDGAYS | 282 |

Db 1301 IYRVKSLSGAKDLAGNSEVVAGTGEQCLPFDEARCGDGKKAVDATLMSPRGIAVDKNGLM 1360
QY 1362 YFVDTGTMIRIDONGIISTLLGNDLTSRPLSCDSVMDISQVRLBWPDTDLAINPMDNSL 1421
Db 1361 YFVDATMIRKVDQNGIISTLLGNDLTAVRPLSCDSDMDVAQVRLBWPDTDLAINPMDNSL 1420
QY 1422 YVLDDNNVLQISNHOVRIVAGRPMHCQVPGIDHFLLSKVATHATESATALAVSHGV 1481
Db 1421 YVLNNVILRITENHQVSIAGRPMHCQVPGID-YLSLSKLIATHSALESASAIASHTGVL 1479
QY 1482 YIAETDEKKINRQVTTSGEISLVAGAPSGCDCKNDANCDFSGDDGYAKDAKNTSPS 1541
Db 1480 YITETDEKKINRLQVTTNGEICLLAGAADCDCKNDVNCICVSGDDAATADAILNSPSS 1539
QY 1542 LAVCAGDELYVADLGNIRIFRKNKPFNTQNMVELSPIDQELYFTTQKHLYTQSL 1601
Db 1540 LAVAPDGTIYADLGNIRIRAVSKNPKVLNAFNQYEAASPGQEYLVFNADGIHQVTVSL 1599
QY 1602 PTGDLYNFTYTGDDITLITDNGNMVNRDSTGMPLWLVPDQGVYVMTGNTNSALK 1661
Db 1600 VTGEYLYNFTYADNDVTELDNNGNSLKIRDSGMPHLLMPDNQITLITLVGNGGLK 1659
QY 1662 SVTTQGHELAMTYHONGSGLLATKSNENGTTFEYDSFGRLTNTVTFPTQGVSSFRSDTD 1721
Db 1660 AVSTQNLGLMTYDGNLTGLLATKSDETGWTTFYDYDHEGRLTNTVTRPTGVVTSLHREME 1719
QY 1722 SSVHVQVETSSK-DDVTITNLSASGAFYTLLOQVRSNYYIGADGSLRLLLANGHEVAL 1780
Db 1720 KSIITIDIENSRDDVTITNLSSEASYTVVQDQVRNSYQCNNGTLRVMYANGMAVSF 1779
QY 1781 QTEPHLLAGTVNPTGKRVNLTPIDNGNLNVEMRQEQVTFVGRRLRVHNRNLLS 1840
Db 1780 HSEPHVLACTIPTIGRCNISLPMEGLNSIEWRLRKEQIKGVTFIRGKLRVHGRNLLS 1839
QY 1841 LPDRVTRTEKIYDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVYTPGGYIAGIQRI 1900
Db 1840 IDYDRNIRTEKIYDHRKFTLRILYDQGRPELWLPSSGLAAVNVSYFPNGRLAGLQGA 1899
QY 1901 MSERMEYDQAGRITSRIFADGKTWSVYLEKSMWLLLSHQRYIEFDPKNDLSLSTVTPN 1960
Db 1900 MSERIDIDQGRIVSRMFADGKWSYSYLDKSNVLLLSQSRQYIEFYDSSRLKHLAVTWS 1959
QY 1961 VAROTLETIRSYGYRNIIYQPEGNASVIQDTEDEGLHLHTFYLGTGRVYIKYGLSKL 2020
Db 1960 VARHSMSTHTSIGYRNINYPESPASVIFDYDSDGRILKTSFLGTGRQVFKYGLSKL 2019
QY 2021 AETLYDTTKVSTYDETAGMLKTIINLQNEGFTCTTIRYQIGPLIDRQIRFRFTEEGMNAR 2080
Db 2020 SEIVYDSTAVTFGYDETTGVLMXVNLQSGGFSCTIRYKVGPLVDKQIYRFSEEGMINAR 2079
QY 2081 FOYNY-DNSFRVTSQAVINETPLDILYRYDDVSGKTEQFGKFGVIYVDINOIITTAVM 2139
Db 2080 FOYTHDNSFRATSKPVISETPLVDLYRYDEISGKVEHFGKFGVIYVDINOIITTAVM 2139
QY 2140 THTKHFDAYGRMKEVQYEIFRSLYMMTVQVDMGRVVKELKLGYPYANTTRYSEYDAD 2199
Db 2140 TUSKHFDTHGRIVEQYEMFRSLYMMTVQVDSMGRVVKELKLGYPYANTTRYDYDGD 2199
QY 2200 GOLQTVSNDKPLWYSYDLNGLNHLSPGNSARLTPLRYDIRITRLGDVQVYMDBDG 2259
Db 2200 GOLQSVAVNDRFTWYSYDLNGLNHLNPGNSARLPLRYDIRITRLGDVQVYKIDDDG 2259
QY 2260 FLQRQGGDI FEYNSAGLIIKAYNRAGMSVRYRYDGLGRRVSSKSHHLLQFFVADLTN 2319
Db 2260 YLCQSGSDI FEYNSGELLTRAYNKASGMSVQRYDGVGRBARSYKTNLGHLLQYFYSDLHN 2319
QY 2320 PTKVTHLYNHSSEITSYLDLQGLHFAVELSSGDEFYACDNTGTPLAVFSGTGLMIKQ 2379
Db 2320 PTRITHVYHNSSEITSYLDLQGLHFAVESSEGEYVAGSDNTGTPLAVFSINGLMIKQ 2379
QY 2380 ILYTAYGEIYMDTNPNFOIIGYHGLGYDPLTKLVHMGRRDYDLVLAGRWTSFDPHELWKHL 2439
Db 2380 LOYTAYGEIYDSDNPDFQMVIGFPHGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWRNV 2439

QY 2440 SSSNVMPNLYMFKNNNPISNSQDIKCPMTDVNSGWLTLTFGQLHNVIIPGYPKPDMAMBP 2499
Db 2440 GKPEA-PENLYMFKNNNPISNELDLKNVTVTVKSWLVMFGQLSNIIIPGFPRAKMYFVP 2498
QY 2500 SYELIHTQMTQEWDNKSIILGVQCEVQKQLKAFVTLERFDQLYGSTITSQQAPKTKK- 2558
Db 2499 PYELSESQAS-----ENGOLITGVQOOTTERHNOQFLAJE-----GVITKKLHASIREKA 2548
QY 2559 ---FASGSGVFGKGVKFKALDKGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVD 2615
Db 2549 GHWFATTTPIIGKIGMFAIKREGVTTGVSSJASEDSRKVASVLNAYYLDKWHYSIEGKD 2608
QY 2616 THYFVKGPSPSGDLAII LGLSGRRRTLENGVNVTVSQNTVNLNGRTRRYTDIQLQYCALCL 2675
Db 2609 THYFVKIGAADGDIIVLTGTTIGRKVLESQVNVTVSQPTLLVNGRTRRFTNIEFQYSTILL 2668
QY 2676 NTRYG---TTLDEKARVLELARAVRQAWARQQRLREGEGGLRAWTEGEKQOVLSTG 2732
Db 2669 SIRVGLTPDULDEKARVLDQARQALGTAWAKEQQKARDREGSRLRWTEGEKQOVLSTG 2728
QY 2733 RVQYDGFVVISVQYPELSDSANNIHFMRQSEMR 2769
Db 2729 RVQYEGYVYVLPVEQYPELADSSSNIQFLRQNEWGKR 2765

RESULT 9
QSNBWB MOUSE
ID QSNBWB MOUSE PRELIMINARY; PRT; 2764 AA.
AC QSNBWB;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Odd Oz/cen-m homolog 2 (Drosophila).
GN Name=Od22; ORFNames=RP23-41F14.1-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Oliver K.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Matthews L.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Bird C.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX000433; CAI35946.1; -; Genomic DNA.
DR EMBL; AL645912; CAI35083.1; -; Genomic DNA.
DR EMBL; AL713919; CAI35941.1; -; Genomic DNA.
DR EMBL; AL713915; CAI35944.1; -; Genomic DNA.
DR EMBL; AL713956; CAI35933.1; -; Genomic DNA.
DR EMBL; BX539311; CAI36037.1; -; Genomic DNA.
DR EMBL; BX000433; CAI35933.1; JOINED; Genomic DNA.
DR EMBL; BX539311; CAI35933.1; JOINED; Genomic DNA.
DR EMBL; AL645912; CAI35946.1; JOINED; Genomic DNA.
DR EMBL; AL713919; CAI35946.1; JOINED; Genomic DNA.
DR EMBL; BX539311; CAI35946.1; JOINED; Genomic DNA.
DR EMBL; AL645912; CAI36037.1; JOINED; Genomic DNA.
DR EMBL; AL713919; CAI36037.1; JOINED; Genomic DNA.

| | | | |
|----|------|--|------|
| Db | 1420 | YVLENNVILRITENHOVSIIAGRPMHCQVPGID-YLSLKLAHSALESASAIAISHTGVL | 1478 |
| Qy | 1482 | YIAETDEKINIRIQVTTSGEISLVAGAPSCDCKNDANCDCFSGDDGYAKADLNPSS | 1541 |
| Db | 1479 | YIETDEKINRLQVTTNGEICLLAGASDCCDKNVNCICYSGDDAYATDALNPS | 1538 |
| Qy | 1542 | LAVCADGELYVADLGNIRIRIFIRKKNKPLNTQNNYELSSPIDQLXYLFDTTGKHLXTQSL | 1601 |
| Db | 1539 | LAVAPDGTIYIADLGNIRIRAVSKNPKVLANFQNEYZAASPGEBQLYFVNADGIIHOYTVSL | 1598 |
| Qy | 1602 | PTGDYLYNFTYTGDDITLITDNNGNMNVRRDSTGMLWLVLVDPGQVYVWMTGNTSALK | 1661 |
| Db | 1599 | VTGEYLYNFTYSAONDVTELDNNGNSLUKRRDSSGMPRHLLMPDNOIITLVTGNGSLK | 1658 |
| Qy | 1662 | SVTTQGHELAMWTHGNSGLLATKSNENGWTTTFEYDSFGRLTNVTFPTGQVSSFRSDTD | 1721 |
| Db | 1659 | AVSTONLELGLMTYDGNLTGLLATKSDTEGWTTFYDYDHEGRLTNVTRPTGVVTLSHREME | 1718 |
| Qy | 1722 | SSVHVQVETSSK-DDVITITNLSASGAFYLLQDVNSYIYGADGSIRLLLANGMEVAL | 1780 |
| Db | 1719 | KSITIDIENSRDDDVITITNLSVEASYTVQDVNSYQLCNNGGTLRVYANGVAVSF | 1778 |
| Qy | 1781 | QTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEMRQKEQARGQVTFGRRLRVHNRNLLS | 1840 |
| Db | 1779 | HSEPHVLAGTITPTIGRCNISLPMENGLNSIEWLRKEQIKGKVTIIFGRKLRVHGRNLLS | 1838 |
| Qy | 1841 | LDPRVTRTEKIYDHRKFTLRILYDQAGRPSSLSPSSRLNGVNVTVSPGGYIAGIQGI | 1900 |
| Db | 1839 | IDYDRNTRTEKIYDHRKFTLRITYDQGRPFLWLPSSGLAAVNVSYFFNGRLAGLQGA | 1898 |
| Qy | 1901 | MSERMEYDOAGRIISRIFADGKTWSYTYLEKSMVLLLSHORQYIFEFDKNDRLSSVTMPN | 1960 |
| Db | 1899 | MSERTDIDKQGRIVSRMPADGKWSYSLDKSMVLLLSQSORQYIFEYSSDRLHAUVTPS | 1958 |
| Qy | 1961 | VAROTLETIRSGVYRNIYOPPEGNASVIOQFTEGDHLLHTFVLGTGRRIYIYKGLSKL | 2020 |
| Db | 1959 | VARHSMTHTSIGIRIYNPPESNASVIFDYSDDGRILKTSFLTGCRQFYKYGKLSKL | 2018 |
| Qy | 2021 | AETLYDTKYSFTYDETAGMKTLINLQNEGFTCTIRVQIIGPLIDROIIPFTEEGMVNAR | 2080 |
| Db | 2019 | SEIYVDSTAFTGDETTGVLKMWNLQSGGFSCTIRYRKVGPLVDKQIYRFSBEGMINAR | 2078 |
| Qy | 2081 | FDYNY-DNSPRVTSQMAVINETPLIDLYRYDDVSGKTEQFGKFGVIYIYDINOIITAVM | 2139 |
| Db | 2079 | FDYTYHDSFRIASIKPVISETPLVDLYRYDBISGKVEHFGKFGVIYIYDINOIITAVM | 2138 |
| Qy | 2140 | THTKHFDAYGRMEVOYEIERSLMYMTVQYDNMGVVKKEIKVGPYANTRISYXEYDAD | 2199 |
| Db | 2139 | TLSKHFDTHGRIKEVQYEMPRSLMYMTVQYDSMGVRIKRELLKGPYANTKYTYDYDGD | 2198 |
| Qy | 2200 | GOLQTVSINDKPLWRYSYDNLGNLHLLSPGNSARLTPLRYDIRDTRLGDVQYKMDGEG | 2259 |
| Db | 2199 | GQLQSAVANDRPTWRYSYDLNGLNHLNPGNSARLMPLRYDLRDRITRLGDVQYKIDDDG | 2258 |
| Qy | 2260 | FLQRGGDIIEYNSAGLLIKAYNRASWSVRYRYDGLGRRVSKSSHSHHLQFYADLTN | 2319 |
| Db | 2259 | YLCQRGSDIEEYNSKGLLTRAYNKASGWSVQYRYDGVGRASYKTLGLHHLQFYSDLHN | 2318 |
| Qy | 2320 | PTKVTHLYNHSSEITSLYDLOQHLFAMELSGDEFFYIACDNIGTPLAVFSGTGLMIKQ | 2379 |
| Db | 2319 | PTRIITHVYNSHSSEITSLYDLOQHLFAMESSGSEBYVNASDNTGTPPLAVFSINGLMIKQ | 2378 |
| Qy | 2380 | ILYATGEIYMDTNPNPQIIIGYHGLYDPLTKLVHMGRRDYDVLAGRMTSPDHELWKHL | 2439 |
| Db | 2379 | LQYATGEIYIDSNPQFMWIFGHGGLYDPLTKLVHFTQRDYDVLAGRMTSPDYTWNRV | 2438 |
| Qy | 2440 | SSSNVMPNLYMFKNNPISNOSDICKCFMTDVSMLLTGCFOLHNVI PGYKPEDMDAMEP | 2499 |
| Db | 2439 | GKEPA-PFNLYMFKNNPUSNELQKNYITDVKSWLVMFGFQLSNIIIPGPPRAKMYFVPP | 2497 |
| Qy | 2500 | SYELIHTQMTKEWMDNSKILGVCQBQKQKAFVTLERFDQLYGSTITSQCAPTKK-2558 | |

Db 2498 PYELSESQAS----ENGQLITGVQQTTERHNOAFLALE-----GQVITKCLHASIREKA 2544
 Qy 2559 ---PASSGSVFGKGVFAKLDGRVTTDIIISVANEDGRRVAAIILNHAHYLENLHFTIDGVD 2615
 Db 2548 GHWFATPTPIIGKINWPAKEGKRVTTGVSIASEDSRKVASVLNNAYYLDKKHYSIEGKD 2607
 Qy 2616 THYFVKPGPSEGLAILGSGGRTTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCL 2675
 Db 2608 THYFVKIGAADGDLVTLTGTIGRKVLESGVNVTVSQPTLLVNGRTRRFTNIEFQYSTLLL 2667
 Qy 2676 NTRYG---TTLDEKARVLELORAVROAWAREOQRLREGSEGLRAWTEGEKQOVLSTG 2732
 Db 2668 SIIRYGTPTDLDSEKARVLDQAKQALGATAWAKOOKQKRGESRLWTEGEKQQLLSTG 2727
 Qy 2733 RVQGYDGFVVISVEQYPELSDSANNHFRMQSEMGR 2769
 Db 2728 RVQGYEGYVLPVEQYPELADSSNNIQFLRQNEWGR 2764

 RESULT 10
 Q9DERS_CHICK
 ID Q9DERS_CHICK PRELIMINARY; PRT; 2802 AA.
 AC Q9DERS;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Teneurin-2 (Fragment).
 GN Teneurin-2
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20581705; PubMed=11146505;
 RX DOI=10.1002/1097-0177(2000)999:9999<;AID-DVDY1084>3.0.CO;2-B;
 RA Tucker R.P., Chiquet-Ehrismann R., Chevron M., Martin D., Hall R.J.,
 RA Rubin B.P.;
 RT "Teneurin-2 is expressed in tissues that regulate limb and somite
 RT pattern formation and is induced in vitro and in situ by FGF8."
 RL Dev. Dyn. 220:27-39(2001).
 DR EMBL; AJ279031; CAC09416.1; -; mRNA.
 DR HSSP; P00750; ITPG.
 DR Ensembl; ENSGALG0000001768; Gallus gallus.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001258; NHL.
 DR InterPro; IPR009471; Ten_N.
 DR InterPro; IPR006530; YD.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF01436; NHL_6.
 DR Pfam; PF05593; RNS_repeat; 5.
 DR Pfam; PF06484; Ten_N; 1.
 DR SMART; SM00181; EGF; 6.
 DR TIGRFAMs; TIGR01643; YD_repeat_2x; 5.
 DR PROSITE; PS00022; EGF_1; 8.
 DR PROSITE; PS01186; EGF_2; 7.
 DR PROSITE; PS00266; EGF_3; 5.
 KW EGF-like domain.
 FT CHAIN <1>2802 teneurin-2.
 FT NON TER 1 1
 FT NON TER 2802 2802
 SQ SEQUENCE 2802 AA; 310746 MW; B1FBC2C84EDFA4B3 CRC64;

 Query Match 64.6%; Score 9616.5; DB 2; Length 2802;
 Best Local Similarity 61.3%; Pred. No. 0;
 Matches 1775; Conservative 411; Mismatches 491; Indels 217; Gaps 27;

 Qy 1 MDVKERKPYRSITRRR-DAERYRTSSSADSEEGKAP-QKSYSSSSTLTKAYDQDARLAYGS 58
 Db 1 MDIKRR-HRSITRCGCKEYRTSSSDCRVPAOKSYSSSSTLTKAYGHDTRMHYGN 59

Db 2140 LPVDLYRYDIBSKVEHFGKGVYIYDIINQIITAVMTLSKFDTHGRKEVQYEMFSL 2199
Qy 2163 MYWMTVOYDMGRVVKELKVGYPYANTTRYSEYEDADGQLOQTQVSNIDKPLWRYSDNLGN 2222
Db 2200 MYWMTVOYDSMGRTVRELKGLPYANTTKYTDYDGGQLOQSVAVNDRPTWRYSDNLGN 2259
Qy 2223 LHLSPGNSARLTPLRYDTRDITRLGDVOYKMDDEGFLRQGGDIFEYNSAGLIIKAYN 2282
Db 2260 LHLNFPNSVRLMPLRYDURDRITRUGDIPYKIDDDGFLCQRGSDVFEYNSGGLLTRYN 2319
Qy 2283 RAGSWSVRYRYDGLGRVRSKSSHSHLQFFYADLTNPTKVTHLYNHSSEITSLYDIQ 2342
Db 2320 KANGWNVQYRYDGLGRASCKTNLGHLLQYFYADLHNPTRVTHVYNSHSEITSLYDIQ 2379
Qy 2343 GHLFAMELSGDBFYIACDNIGTPLAVFGTGLMIKQIILYTAGGEIYMDTNNFQIITGY 2402
Db 2380 GHLFAMESSGEEYVASDNTGTPLAVFSGINGLMIKQLQYTAGGEIYYDSNPDQVLIVGF 2439
Qy 2403 HGLGYDPLTKLVHMGRRDDVLGRWTSPOHELWKHLSNVMPPNLYMFKNNPISNSQ 2462
Db 2440 HGLGYDPLTKLVHFTQRDDVLGRWISPDYTMWKNIGREPA-PFNLYMFKNNPISNSQ 2498
Qy 2463 DIKCFMTDVSNTLLTGFQHLNVIPIGYPKPDMDAMEPSYELIHTQMKTOEWDNSKSIILGV 2522
Db 2499 DLKNYVTDVKSMLVMFGQLSNIIPGFPRAKMYFVSPPYEL---TESQACENGQIITGV 2554
Qy 2523 QCEVQKQLKAVTLERFDQLYGSTITSQOAPKTK-----PASSGSVFGKGVKPAKQGR 2578
Db 2555 QOTTERHQAFALE-----GOVISKRLHASIREKAGHWFATSTPIIGKGMFAVYKGR 2608
Qy 2579 VTTDIISVANEQDORRAAIIINHAHYLENLHFTIDGVDTHYFVKPGPSEGDLAILGLSGR 2638
Db 2609 VTTGISIATDSDSKIASVLSNHYLEKMYHIEGKDTHYFKIGSADSDLVTLMTSGR 2668
Qy 2639 RTLENGVNVTVSQINTVLNGRTTRYTDIOLQYCALCLNTRYG---TTLDDEKARVLELAR 2695
Db 2669 KVLDSGVNVTVSQPTLLNGRTTRFTNIBFYSTLLINIRYGLTADTLDDEKARVLDQAR 2728
Qy 2696 ORAVROAWAREOQLREGEGELRAWTEGKQOVLSTGRVQGVDFPVISVEQYPELSDSA 2755
Db 2729 QRALGSAAKEQKQKARDREGSRVMTDGEKQQLNTRVQGVYGYVLPVEQYPELADSS 2788
Qy 2756 NNHFMRQSGEMGRR 2769
Db 2789 SNIQFLRQEMGKR 2802
RESULT 11
Q9WTS5 MOUSE
ID OSWTS5 MOUSE PRELIMINARY; PRT; 2764 AA.
AC Q9WTS5_7
DC 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ten-m2.
GN Name=Odz2; Synonym=ten-m2;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c; TISSUE=Brain;
RA Cohnahti T., Zhou X., Feng K., Richter B., Moergelin M., Perez M.T.,
RA Su W., Chiquet-Ehrismann R., Rauch U., Faessler R.;
RT "Mouse Ten-m/Odz is a new family of dimeric type II transmembrane
RT proteins expressed in many tissues.";
RL J. Cell Biol. 0:0-0(1999).
RL EMBL; AB025411; BAA77397.1; -; mRNA.
DR HSSP; P35555; IEMN.
DR Ensembl; ENSMUSG00000049336; Mus musculus.

DR MGI; 1345184; Odz2.
DR GO; 0016021; C:integral to membrane; TAS.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR009471; Ten_N.
DR InterPro; IPR006530; YD_N.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF01436; NHL; 6.
DR Pfam; PF05593; RNS repeat; 5.
DR Pfam; PF06484; Ten_N; 1.
DR SMART; SM00181; EGF; 7.
DR TIGRFAMs; TIGR01643; YD repeat_2x; 5.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 4.
SQ SEQUENCE 2764 AA; 306465 MW; 73BA3D916D0F0344 CRC64;
Query Match 64.6%; Score 9610.5; DB 2; Length 2764;
Best Local Similarity 61.9%; Pred. No. 0;
Matches 1769; Conservative 418; Mismatches 489; Indels 181; Gaps 28;
Qy 1 MDVKRPYSLTTRR-DAERRYTSASDSEEGKAP-QKSYSSSETLKAYDQDARLAYGS 58
Db 1 MDVKRR-HRSLTRGCGKCRYTSSILDSEDCRVPTQKSYSSSETLKAYDHDHDSRMHYGN 59
Qy 59 RVKDIVQEAEEFRTGANTFLRELGLBEVTPPHGTLYRTDILGPPQCGYSGMAGSDADME 118
Db 60 RVTDLVHRESDEFGRQGTFTLAEGLICEPS-PHRSYGCSDMGTLHQGYSLTSGDADSD 118
Qy 119 ADTVLSPHPVRLWGRSTRGSRSSCLSSRANSNLTLTDTEHENTETDHPG----- 168
Db 119 TEGMSPEHAIRLWGRGIKRRSSGLSRENSALTLDSDNENKSDDDNGRPIPTSSSS 178
Qy 169 ----- 169
Db 179 LLPSAQLPSSHNPPVSCQMPLLDSNTSHQIMDTNPDEEFPNSYLLRACSGPQOASSG 238
Qy 170 LQNH---ARLTTPPPPLSHAHTPNQHHAAASINLRNGNFTPRSN-----PSPAPTDHLSG 222
Db 239 PPNHSSOSTLRPLPLP-PHNHTLSHHH-SSANSLNRLNRRSQIHAPAPAND--LAT 294
Qy 223 EPPAGGAQEPAAQENWLLNSPLNPLTRNLGKQPLGLTQDNLNLTENDILGASRDHGDYSD 282
Db 295 TP-----ESVLQDSWVLSNVPLETR----- 316
Qy 283 GHFLFK-PGTSPLFTTSPGYPLTSTVYSPPPRPLRSTFAPAPNLKKPKSKYCNWKC 341
Db 317 -HFLFKTSSGSTPLFSSSSPGYPLTSGTVTPPPRLLPRNTFSPKAFKPKKPKSKYCSWKC 375
Qy 342 AALSAIVISATLVILLAYFVAMHLFGLNWLHLPMEGOMYEITEDTASSWVPTDVSLYPS 401
Db 376 AALSAIAAALLLAILLAYFTAMHLGLNLQLOQADGHTF--NNGVRTGLPNDGDDVATVPS 433
Qy 402 GGTGLETPDRKGTTEGKSPFPDESFDSDGIDVGRASOKIPPGTFRWSOVFIDHP 461
Db 434 GSK-----VFWSL--KNSSIDSGAEVGRVTVQVPGVFRWSQIHLSQP 476
Qy 462 VHLKFNVSGLKAALVGYIRGKLPSPSHQTFDFVELLDGRLLTQEAARSLBGTTPQSRGTV 521
Db 477 QFLKFNISLGDALFGVYIRRGLPSPSHAQYDFMERLDGK-----EKMSVSVESPRERSIQ 531
Qy 522 PPSSETGTFOYLDSDGIWHLAFYNDGKESVGVFSLTTAIESVNCNPSNCGNGDCISGTC 581
Db 532 TLVQNEAVFQYLDVGLWHLAFYNDGDKEMVFNFTVVLDSVQDCPRNCHNGECVSGLC 591
Qy 582 HCFGLGLGPCGRASCPLVCSGNGQYMKGRCLCHSGWKGAECDDVPTNQCIDVACSNGHGC 641
Db 592 HCFPGFLGADCAKAAACFVLCSGNGQYSKGTQCQYSGWKGAECDDVPMNQCIDPSCGGHGC 651
Qy 642 ITGTICNPQYKGESCEEVDCMDPTCSGRGVYRGECVHGWTGCTTCETPRATCLDQCS 701

Db 652 IDGNCVCAAGYKGRHCEBVDCLDPTCSSHGVCVNGECLCSPGMGLNCELARVQCPCDQCS 711
Qy 702 GHGTFLPDTGLCSCDPSWTHGDCSIEICAADCGHGVCGGTCCRCEDGWMGAACDORACH 761
Db 712 GHGYLPLDPSGLCSDPNWMPDQCSV - VCSVDCGTHGVCI GAACBEGWTGAACDQRVCH 770
Qy 762 PRCAEHGTCDRGKCECSPGNNGEHCCTIAHYLDRVYKGGCPGLCNGNGRCRTLDLNGHVCV 821
Db 771 PRCLIEHTCKDCKCECEGNGEHCCTI - DGCPLCNGNGRCRTLQGNSWQVCV 821
Qy 822 QLWHRGAGCDTSMETACGDSKONDGDLVDCMDPCCQLPCLCHINPLCLGSPNPLDIOE 881
Db 822 QTWGRGPGCNVAMETSCADNKNBEGDLVDCLDCCLOSAQCNSLLCRSGRPLDIOQ 881
Qy 882 TOVPVSQONLHSHFYDRKFLVGRDSTHIIIGENPFDCGHACVIRGQVMTSDGTPLVGVNI 941
Db 882 GQ--TDWPAVKSFYDRIKLAGDKDSTHIIIGDNPFNSLSVLIRGQVVTMDGTPLVGVNV 939
Qy 942 SFVNNPLFGYITISRDQGSFDLVTNGGIIILRFERAPFIQEHTLMTLPWDRFFVMTIIM 1001
Db 940 SFVKYPKYITITQDGTDFLLIANGGSALTILHFERAPFMSQERTVWLPWNSFYAMDITLV 999
Qy 1002 RHENEIPSCLSNFARNPVPSPSLTSPASSCAEKGPIVPEIQALQOEISISGCKORL 1061
Db 1000 KTEENSIPSCDLSGFVRPDP1IISPLSTFFSASPASNPIVPETQVLHEBIEILPFTNVKL 1059
Qy 1062 SYLSRTPGYKSLVRLISLTHPTIIPNLKVKHLMVAVGRLPRKWFAPADLSYVFIWDKT 1121
Db 1060 RYLSRRTAGYKSLKLIKIMTQSTVPLNIRVHLMVAVGHLUFQKSPQASPNLAYTFIWDKT 1119
Qy 1122 DVYNQKVFGLSEAFVSGYYESPCDLTLMKRTTVTLQGVBEIDASKLGGMSLDKHALNI 1181
Db 1120 DAYQORVYGLSDAVVSGVEFETCPSLILMEKRTALLQGFELDPNSLGGMSLDKHTLV 1179
Qy 1182 QSGILHKGNGBNQVSPQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALVTCSDG 1241
Db 1180 KSGILHKGNGENQFLTOQPAITISIMGNRRRSISCPSCNGLAEKGLLAPVALVADIG 1239
Qy 1242 SLYVGDENYIIRIIPSGNVNTHILELNKDPHSHSPAKHYLAITDPMGSAVFLSDNSRR 1301
Db 1240 SLFVGDENYIIRIIPPSRNVTSILERNKBFKSHSPGHKYYLAVDPVTVGSLYSDTNSRR 1299
Qy 1302 VFUKSTVVKDLVKNSEVAGTGDQCLPFDOTRCGGGKATEATLNPGRITVDKFLGI 1361
Db 1300 IYRVKLSLGAADLAGEVNAVGTGEQCLPDEARCGGKAVDATLMSPRGIAVDKNGLM 1359
Qy 1362 YFVBDTMRIRRDQGIISTLGSNDLTSARPLSCDSVNDISQVLEWPTDLAINPMONS 1421
Db 1360 YFVDATMRKVDQNGIISTLGSNDLTAVRPLSCDSMDVAQVLEWPTDLAVNPMONS 1419
Qy 1422 YVLNNVVLQISEKHQVRIVAGRPMHCQVPGIDHFLSKVAIHATLSATALAVSHNGVL 1481
Db 1420 YVLENNVTLRITENHQVSIAGRPMHCQVPGID - YLSKLAIHSALESASAIAISHTGVL 1478
Qy 1482 YIAETDEKINRIQVTTSGEISLVAGAPSCDCNDANCDCFGDDGCAKDAKLNTPSS 1541
Db 1479 YITETDEKINRLKQVTTNGEICLLAGAAOCCDNVNCICYSGDDAYATDALNPS 1538
Qy 1542 LAVCAGDGLYVADLGNIRIRIRKKNKPFNTQNNMYELSSPIDQELYLFDITTKGHLTQSL 1601
Db 1539 LAVAPDGTIYIADLGNIRIRIRAVKKNKPVNLNAPNOYEAASPGQELBYVFNADGIIHOYTSL 1598
Qy 1602 PTGOYLNFYTVGGDITLITDNNGNMNVNRDSTGMPMLVLVDPGQVYVWMTGNSALK 1661
Db 1599 VTGEBLYNFYTSADNDVTTELIDNNGNSLKIRDRSSGMPRHLLMPDNQIITLTVGTNGGLK 1658
Qy 1662 SVTTQGHELAMWTVHNGSGLLATKSNENGWTTTFYEYDSFGBLTNTVPTPGOVSSFRSDTD 1721
Db 1659 AVSTQNLELGLMTYDGTNGLLATKSDGTGWTTFYDIDHEGRLTNTVPTGVTTSIHRME 1718
Qy 1722 SSVHVQVETSSK - DDVITTTNLSASGAFYTLLOQOVNRNSYYIGADGSLRLLLANGMEVAL 1780
Db 1719 KSIITIDIENSRRDDVTVITNLSSEVASYTVVQOVNRNSYQLCNGNGLRVMYANGMAVSF 1778

Qy 1781 QTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEMRQKEQARGQVTVFGRRLRVHNRNLLS 1840
Db 1779 HSEPHVLAGTITPTIGRCNISLPMENGLNSIEWRLRKEQIKGKVTFIFGRKLRVHGRNLLS 1838
Qy 1841 LPDFRVTREKTYDDHRKFTLRLYDOAGRPSSLWSPSSRLNGVNVVTSYSGGYIAGTORG 1900
Db 1839 IDYDRNIRTEKTYDDHRKFTLRLYDOVGRPLFLWPSGLAAVNVVSYFFNGRLAGJORGA 1898
Qy 1901 MSERMEYDOAGRITSIRIFADGKTWSTYILEKSMVLLHSHQROQYIFEFKDNDRSLSSVTMPN 1960
Db 1899 MSERTDIDQGRIVSRNPFADGKWSYSYLDKSNVLLQSORQVIFYEYDSSDLRHAVTMS 1958
Qy 1961 VARQTLTIRSVGYRYNIYQPPPEGNASVIOQFTEDGHLHHTFYLGTGRRVYIYKGLSKL 2020
Db 1959 VARHSNSTHTSIGYIRNIYNPESNASVIFDYSDDCGRILKTSFLGTGRQVYFYKGLSKL 2018
Qy 2021 AETLYDTTKVSYFYDTAGMLKTINIQNEGFTCTIRYQIGPLIDROIIRPTFTEGMVNAR 2080
Db 2019 SEIYVDSATAVTFGYDETTLGVLKMNLOSGGFTIRYKVGPLVDKQIYRFSBEGMINAR 2078
Qy 2081 EDVNY - DNSFRVTSQAVINETPLPIDLYRDDVSGKTEQFGKFGYIYVDINOIITAVM 2139
Db 2079 FDTYHDNSFRASIKPVISETPLPVDLTRYDEISKVEHFGEVGYIYVDINOIITAVM 2138
Qy 2140 THTKHFDAYGRKKEVQYEIERSLMYMTVOYDNMGVWVKELKVGPIANTTRYSEYDAD 2199
Db 2139 TLSKHFDTHGRIKEVQYEMFRSLMYMTVOYDSMGVRIKRELKLGPIANTTRYDYDGD 2198
Qy 2200 GQLQTVSINDKPLWRYSYDLNGLHLLSPONSARLTPLRYDIDRDIRLGRDVOYKWDG 2259
Db 2199 GQLQSVAVNDRPTWRYSYDLNGLHLLNPGNSARLMLRYDLRIDRILGRDVOYKIDDDG 2258
Qy 2260 FLRQCGDIFEYNSAGLILKAYNRAGSWSVRVRYDGLGRVSSKSHSHLQFYYADLTN 2319
Db 2259 YLCQSGDIFEYNSKGLLTRYANKASGWSVQYHYDGVGRASVYKVLGHLLQVYFSDLN 2318
Qy 2320 PTKVTHLYNHSSEITSLYYDLQGLHFLAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQ 2379
Db 2319 PTRITHYVNSSEITSLYYDLQGLHFLAMESSGEEVYVASDNTGTPLAVYSINGLMIKQ 2378
Qy 2380 ILTVAYGEIYMDNPNPQIIIGHGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKHL 2439
Db 2379 LQYTAGGEIYDSDNPDQMVIGVPHGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWRNV 2438
Qy 2440 SSSNWPENLYMFKNNPISNSODIKCFMTDVNSWLLTFGFLHNVIPGYPKPDMAMEP 2499
Db 2439 GKPEPA - PFNLYMFKNNPISNELDLKNYVTDVKSWMVMPGFLSNIIIPGFPRAKMYFVP 2497
Qy 2500 SYELIHTQMKTOEWDNKSITLGVQCEVQKOLKAFVTLERPDQLYGSTITSCOAPKTKK - 2558
Db 2498 PYELSESQAS - ---ENGQITGVQOTTERHNQAFLE - ---GQVITKKLHASIREKA 2547
Qy 2559 ---FASGSGVFGKVPKALOGKRVTTDIIISVANEDGRRVAAIILNHAHYLENLHPTDQVD 2615
Db 2548 GHWFATTPPIIGKINFAIKEGRVTTGVSSIASDSRKVASVLNNAYLDMHYISBGKD 2607
Qy 2616 THYFVPGSPSEGDLAILGLSGRRTLENGVNVTVSQINTVLNGRTRRYTDDIOLQYGLACL 2675
Db 2608 THYFVKIAGADGDLVLTGTTIGRKVLESVGNVTVSQPTLLVNGRTRRFTNIBFYSTLL 2667
Qy 2676 NTRYG - ---TTLDEKARVLELARQVROAWAREQORLREGEGBGLRAWTEGBEQQVLSTG 2732
Db 2668 SIYGLTPTDLDEKARVLDQAGORALGTAWAKEQQKARDGSGRLWTEGBEQQLSTG 2727
Qy 2733 RVQYGDGFFVISVEQPELSDSANNHFRMQSENGRR 2769
Db 2728 RVQYEGYVYLPVEQPELADSSNIQFLRQNEWGR 2764

RESULT 12

Q9WTS4_MOUSE

ID Q9WTS4_MOUSE PRELIMINARY; PRT; 2731 AA.

Db 2326 VFSRRGVKIELLYTPYDGYHDYTPDFQVIIGFHGGLYFLTKLVLHQDQYDVWVAGR 2385
Qy 2429 TSPDHEHLWKHLSSNVN--PBNLYMFKNPNPINSODIKCFMTDVNSWLLTFCGQHNVI 2486
Db 2386 TTPNHHITWQOL--NLLPKPFLNLYSPENNYPVGKIQDVAKYTTDIRSWLELFGQLHNVL 2442
Qy 2487 PGVPKPDMDAMESYELIHTQMKTBQWDNSKSIIGVQCEVQKQKAPVTILERFDQLYGST 2546
Db 2443 GPGPKPLENLELYELLRLQTKQEWDPGKTIIGQCEIQKQLRNPISLDQLPMTPRYN 2502
Qy 2547 ITSQQAPKTKYPASSGVFGKVPKALPDGRVTTDIISVANEDGRRAAILNHAHYLEN 2606
Db 2503 DGRLEGKQPRFAAVPFGKGIKFAIKDGIIVTADIIGVANEDSRRLAAILNHAHYLEN 2562
Qy 2607 LHETIDGVTHFYVKPGPSSGDLAILGLSGRRLTENGVNVTYSQINTVLNGRTRTYDI 2666
Db 2563 LHFTIEGRDTHFYFKGSLBEDLVLCNTGGRILENGVNVTYSQMTSVLNGRTRRPADI 2622
Qy 2667 QLOVGALCLNTRVYTTLDEEKARVLELARQAVRQAWARQORLREGEGLRAWTEGEKQ 2726
Db 2623 QLOHGALCFNIRYGTVEEBKNVHLEIARQAVQAQWTKQORLQEGEGIRAWTEGEKQ 2682
Qy 2727 QVLSTGRVQYDGVFVSVQYPELSDSANNIHPMRQSENGRR 2769
Db 2683 QLLSTGRVQYDGVFVSVQYLELSDSANNIHPMRQSEIGRR 2725
RESULT 15
Q9UKZ4 HUMAN
ID Q9UKZ4 HUMAN PRELIMINARY; PRT; 2725 AA.
AC Q9UKZ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tenascin-M1.
GN Name=OD21; Synonym=TNM1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=20025749; PubMed=10556288; DOI=10.1093/hmg/8.13.2407;
RX Brandau O., Schuster V., Weiss M., Hellebrand H., Fink F.M.,
RA Kreczy A., Friedrich W., Strahm B., Niemeyer C., Belohradsky B.H.,
RA Meindl A.;
RT "Epstein-Barr virus-negative boys with non-Hodgkin lymphoma are
RT mutated in the SH2D1A gene, as are patients with X-linked
RT lymphoproliferative disease (XLP).";
RL Hum. Mol. Genet. 8:2407-2413 (1999).
DR EMBL; AF100772; AAF04723.1; -, mRNA.
DR HSSP; P01135; 1MOX.
DR Ensembl; ENSG0000009694; Homo sapiens.
DR HGNC; HGNC:8117; OD21.
DR GO; GO:0005576; C:extracellular region; TAS.
DR GO; GO:0008201; F:heparin binding; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR009471; Ten_N.
DR InterPro; IPR006530; YD.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF01436; NHL; 6.
DR Pfam; PF05593; RRS repeat; 6.
DR Pfam; PF06484; Ten_N; 1.
DR SMART; SM00181; EGF; 6.
DR TIGRFAMs; TIGR01643; YD_repeat_2x; 5.

DR PROSITE; PS00022; EGF 1; 8.
DR PROSITE; PS01186; EGF 2; 7.
DR PROSITE; PS00026; EGF 3; 5.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
SQ SEQUENCE 2725 AA; 304894 MW; 6F383E64C1B2E1B1 CRC64;
Query Match 63.8%; Score 9501; DB 2; Length 2725;
Best Local Similarity 62.0%; Pred. No. 0;
Matches 1737; Conservative 404; Mismatches 550; Indels 112; Gaps 17;
Qy 1 MDVKERKPRSLTR-RRDAERYTSSADSECKAPQKSYSSSETLKAYDODARLAYS- 58
Db 1 MEQTDCKPYQPLPKVKVHEMDLAYTSSDSEDEGRKPRQSYNSRETHLYNQELRMVNSQ 60
Qy 59 --RVKDIVQEAEE-ECRTIGANFTRELGLEEVTPPHGTLYRTDI--GLPCGYSMGAGSD 114
Db 61 SRKKEVEKSTQMECECTSHLC-----SGYQTDHMSVSRHGQLENGSD 106
Qy 115 ADMEADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGQLQ--- 171
Db 107 VDTETGAASPDHALRMWIRGKMSHSSCLSSRANSALSITDTHHER-KSDGNGFKFSP 165
Qy 172 -----NHAHLR--TPPPPLSHAHTPNQHAASINSLNGRNTPRS 209
Db 166 VCCDMEAQAGSTQDVQSSPHNQFTFRPLPPPPPPHACTCARKPPPAADSQRSMTRTS 225
Qy 210 NPSPAFTDHSLSGEPAGGAQEPAAQENWLLNSNIPLETRNLGKQPFGLTLDQNLTEM 269
Db 226 QPSPA-----APAPPTSDSVHLHNSVWLSNIPLETR----- 259
Qy 270 ILGASRDGAYSDGHFLFKPG-GTSPFLCTTSPGYPLTSTVYSPPPRPLRPTTFARPAP 328
Db 260 -----HSLFKHGGSSAIFSAASQNYPLTSNTVYSPPPRPLRPTTFARPAP 305
Qy 329 NLKPSKYCNWKAALSAIVISATVILLAYFAMHLFGLNWLHQPMEGOMYIETEDTAS 388
Db 306 TENKPRCCNWKCTALSATAITVTALLAYIAVHLFGLTQVPEGLSANGVSKGN 365
Qy 389 SWPVPDVSILYPSGGTGLETPDRKGTTEGKSPSPFPDSFIDSIGDIDVGRASOKIPP 448
Db 366 RGTESMDTTPYSGGKVDKSEKK-----VFKGRAIDTGEVDICAQVMQTIPP 414
Qy 449 GTFWRQVFIIDHPVHLKFNVSLGKAALVGIYGRGLPPSPSTQDFVELLDGRLLLTQEAR 508
Db 415 GLFWRQIITHHPIYLKFNISLAKDSILGIYGRNIPPTHTQDFVKLMGKQLVKQDSK 474
Qy 509 SLBGTQRQRGTVPPSSSHETGFTQYLDSDGIWHLAFYNDKGESEVSLFTTAIESVDNCP 568
Db 475 GSDDTQHSRNLILTSLOETGFTIEYMDQGPWYLAFYNDGKKMEQVFLVTTAIEIMDDCST 534
Qy 569 NCYNGDGI SGTCCHCFGLGPDGRASCPLVCSGNGOYMKGRCLCHSGWKGAECVPTN 628
Db 535 NCNGNGECISGHCHCFPGFLGPDGRASCPLVCGNGEYKGHCVKRGHWKGECDVPEE 594
Qy 629 QCIDVACSNHGTCTITGTICNPGYKGESEVDCMDPTCSGRGVCVRGECHCFVWGQGTN 688
Db 595 QCIDPTCFGHGTCTIMGVCICVPGYKGEI CEEEDCLDPMCSNHGICVKGECSTGSGVNV 654
Qy 689 CETPRATCLDQCSGHGTFLPDTGLSCDPSWTHDCSIEICAADCGHGVGVGTCRCEB 748
Db 655 CETPLPVQBCQCSGHGTFLLDAGVCSCDPKWTGSDCSTELCTMECSHGVCSRGICQCE 714
Qy 749 GWMGAACDORACHPRCAEHGTCDGKCECSPGWNGBHCTIAHYLDRLVVKGGCPLGNGNG 808
Db 715 GWVGPTCEERSCHSHCTEHGQCKDCKCECSPGWEGBHCTIAHYLD-AVRDGCPLGFCNG 773
Qy 809 RCTLDLNGHVCVQLGWRGAGCDTSMETACGDSKMDGDLGVDCMDPDCCQLCHINPL 868
Db 774 RCTLDQNGHVCVQGVSGTGCNVVMEMLCGDNLNDGDLTDCVDPDCCQSNICYISPL 833
Qy 869 CLGSPNPLDI IQETVPVVSQNLNLSHYDRIKFLVGRDSTHIIIPGPNPFDGGHACVIRQV 928
Db 834 CQGSPPDLDI IQQSQTFLFSQHTSRLFYDRIKFLIGKDSHTHVIPEVVSFDSRRACVIRQV 893

| | | | |
|----|------|--|------|
| Qy | 929 | MTSDGTPLVGNVNSIFVANNPLFGYTIISRQDGSFDLVTGGISIIILFRFRAPFITQHEITLWL | 988 |
| Db | 894 | VAIDGTPLVGVNVSVFLHHSDDYGTISRQDGSFDLVAIGGISVILIFORSFPLPEKRTLWL | 953 |
| Qy | 989 | PWDRFFVWETIIMRHEENETPSCDLNFARPNNPVVSPSLTSPASSCAEKGPIVPELOAL | 1048 |
| Db | 954 | PWNQFIVVEKVTMQRVVDPSCDISNFIENPITVLESPSLTSPFGSCPERGTIVPELOVV | 1013 |
| Qy | 1049 | QEEISIGCKMRLSYLSRTPGYKSVLRISLTHPTIPFNLMKWHLMVAVEGRLFRKWFAA | 1108 |
| Db | 1014 | QEEPIPSFVRLSYLSRTPGYKTLRLILLTHSTIPVGMKVHLTVAVEGRLTKQWPPA | 1073 |
| Qy | 1109 | APDLSYFIFWKTVDYVQKVGLESEAFVSVGYEYESCPDILLWEKRTTVLQGYEIDASKL | 1168 |
| Db | 1074 | AINLVYTFAMNKTDIYQKVWGLAEALVSVGYEYETCPDFILWEQRTVWLQGFEMDASLN | 1133 |
| Qy | 1169 | GWQLSDKHHLNIOGSLIHKNGENOFVSOQPPVIGSIMNGRRRSISCPSCNGLADGNK | 1228 |
| Db | 1134 | GDWLNKXHLINPOSGIIHKNGENMFIISOQPPVISTIMNGHORSVACTNCNGPAHNKK | 1193 |
| Qy | 1229 | LLAPVALTCGSDGLVYVGFENYIRRIFFPSGNVTNILELRNKDFRHSHPASHKYYLATDPM | 1288 |
| Db | 1194 | LFAFVALASGPDGSVYVGFENFVRIIFPSGNSVLSLEL-----STSPASHKYYLAMPDV | 1246 |
| Qy | 1289 | SGAVFLSDSNSRRVFKIKSTVVVKDLVKNSEVAGTGDQCLPFDOTRCGDBGXKATEAITL | 1348 |
| Db | 1247 | SESLYLSDTNTRKYVYKLSLVETXDLSKNFEVAGTGDQCLPFPDQSHCGDGRASEASLN | 1306 |
| Qy | 1349 | NPRGITVDKFLIYFVDGTMIRRIDONGIILSTLLGSDNLTSAEPLSCDSVMDISOVRLWEW | 1408 |
| Db | 1307 | SPRGITVDRHGFIYFVDGTMIRKIDENAVITTVIGSNGLTSTQPLSCDSGMDITQVRLEW | 1366 |
| Qy | 1409 | PTDLAINPMDNSLVLDNNVYLOITSENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLE | 1468 |
| Db | 1367 | PTDLAVNPMDNSLVLDNNVILQISENRRVRIIAGRIHCOVPGIDHFLVSKVAIHSTLE | 1426 |
| Qy | 1469 | SATLAVSHNGVLVIATDEKKINRIQVTTSGEISLVAGAPGCDCKNDANDCDCFSGDD | 1528 |
| Db | 1427 | SARAISSVSHGLLPFAETDBRKVNRIQOVTTNGEIIYIAGAPTDCCDKIDPNCDCFSGDG | 1486 |
| Qy | 1529 | GYAKDAKLNTPSSILAVCADGELYVADLGNIRIFIRKKNKFLNTQNMVELSSPIDOLEYL | 1588 |
| Db | 1487 | GYAKDAKNAKAPSSLAWSPDGTLVADLGNVRIRTISRNQAHLDNMNIYEIASPADQELVQ | 1546 |
| Qy | 1589 | FDTTGHLYTQSLPTGTYLNYFTYTGDDITLITDNNGNMNVRRDSTGMPLVLVDPDQG | 1648 |
| Db | 1547 | FTVNGTHLHTLNLITRDYVYVNYTNSBGDLGAIITSSNGNSVHIRRDAGGMPLMLVPGGQ | 1606 |
| Qy | 1649 | VYVYTMGTNSALKSVTTQGHELAMWTHGNSGLLATKNSENGWTTTFEYDSFGRLTNVTF | 1708 |
| Db | 1607 | VYMLTISNGVLKRVSAQGNPALMTPYNGNTGLLATKNSENGWTTVVEYDPEGHLTNATF | 1666 |
| Qy | 1709 | PTGOVSSFRSDTSSVHVQVETSSKDVITITNLSAGAFYTLQLDOVRNYSYIIGADGSL | 1768 |
| Db | 1667 | PTGEVSSFHSDLEKTKVELDTSNRENVLMSTNLTATSTIYLKQENTQSTYRVNPDGSL | 1726 |
| Qy | 1769 | RLLLANGWEVALQTEPHLLAGTVNPTVGKRVNTPIDINGLNLVWEQRKEQARQVTVFG | 1828 |
| Db | 1727 | RVTFASGWEIGLSSEPHILAGAVNPTLGKNCISLPGEHNANLIEWQRKEONKGNVSAFE | 1786 |
| Qy | 1829 | RRLRVNHRNLLSDFDVRTTEKIIYDDHRKFTLRIILYDQAGRSLWSPSSRLNGVNTVYS | 1888 |
| Db | 1787 | RRLRAHNRNLLSIDFDHITRTGKIYDHRKFTLRIILYDQGRFILSPSVSRVNEVNTVYS | 1846 |
| Qy | 1889 | PGGYIAGIQGIMSERMEYDQAGRITSRIEADGKWTSTYVLEKSMVLLHLSHQRYTIFEFD | 1948 |
| Db | 1847 | PSGLVTFIQRTGWNEKMEYDQSGKIISRTWADGKIWSYTYVLEKSMVLLHLSHQRYTIFEYD | 1906 |
| Qy | 1949 | KNDRLSVTPWPNVARQTLFETIRSVGYRYNTIYQPEGNASVIOQFTEBDGHLHLLTFYLGTR | 2008 |
| Db | 1907 | QSDCLLSVTPWPNMVRHSLOTMLSVGYRYNTITPDDSTSTSIQYISDRGRLLQTLHLGTR | 1966 |

| | | | |
|----|------|---|------|
| QY | 2009 | RVIYKYKLSKLAETLYDTTKVSTFTVDETAGMLKTLINLQNEGFTCTIRYRQIGPLIDRQI | 2068 |
| Db | 1967 | RVLYKYTKQARLSEVLYDTTQVTLTYEESGVIKTHLMDHGFICTIRYRQTGPGLIGRQI | 2026 |
| QY | 2069 | PRFTEEGMVARPDYNDNSFRVTSQWAVINETPLPIDLYRYVDVSGKTEQCFKGVIVY | 2128 |
| Db | 2027 | FRFSEELVNARFDYSY--NNFRVTSQWAVINETPLPIDLYRYVDVSGRTEQCFKFSVINY | 2085 |
| QY | 2129 | DINOIITTAVMHTTKGFDAVGRMKVEQYEIIFRSLMYMTVOYDNMGVRVVKELKVGPGYAN | 2188 |
| Db | 2086 | DLNQVITITVMKHTKIFSANGQVIEVQYELLKAIAYWMTIOYDNVGRHGNMCIRVGV DAN | 2145 |
| QY | 2189 | TTRYSEYDADGQLOQTVSINDKPLMRYSYDLNGLHLLSPGNSARLTPURYDIRDIRTRL | 2248 |
| Db | 2146 | ITRYFEYDADGQLOQTVSVDNKTQWYSYDLNGDINLLSHGKSARLTPURYDLDRDIRTRL | 2205 |
| QY | 2249 | GDVOYKMDDEGFLRQRGDIFEYNSAGLLIKAYNRAGSWSRVRYOGLGRRVSSKSSH | 2308 |
| Db | 2206 | GETQYKMDDEGFLRQRGNDIFEYNSNGLLQKAYNKASGWTQVYYDGLGRRVASKSLQG | 2265 |
| QY | 2309 | HLQFFYADLNPNTKVTHLYNHSSEITSLYYDLOQHLFAMELSSGDEFYIACDNICTPLA | 2368 |
| Db | 2266 | HLQFFYDATANPRTVTHLYNHTSSEITSLYYDLOQHLLAMELSSGGEYVACDNTGTPLA | 2325 |
| QY | 2369 | VFGGTGLMIKQIILYAYGEIYMDTPNPFQIIGYHGGLYDPLTKLVHMGRRDYDVLAGRW | 2428 |
| Db | 2326 | VFSSRGQVKEILYTPYGDYIHDTPDPQVIGFHGGLYDFLTKLVHLGORDYDVVAGRW | 2385 |
| QY | 2429 | TSPDHELWKHLSSSNVW--PFNLMPKNNNPISNSODIKCFMTDVNSMLLTGQFQLHNVI | 2486 |
| Db | 2386 | TTYAHHIWKQL--NLLPKPFNLSPENNYPVGKIQDVAKYTTDRKSWELEGFQJLHNVL | 2442 |
| QY | 2487 | PGYKPDMDAMEPSYELIHTOMKTQSDWNSKSTLGVQCEVQKQKAFVTLERFDQLYGST | 2546 |
| Db | 2443 | PGFPKELENLLEYELLRLQTKQWDPKTILGICELQKQJRNFIISLDQLPMTPRYN | 2502 |
| QY | 2547 | ITSQQAPKTKYPASSGSVFGKGVKALKDGRVTTDIIISVANEDGRRVAALINHAHYLEN | 2606 |
| Db | 2503 | DGRLEGKGQPRFAAVPSVFGKIKFAIKDGIVTADIIIGVANEDSRRLAAILNNAHYLEN | 2562 |
| QY | 2607 | LHFTIDGVDRHYFVKGPBEGDLAIIGLSGGRTLENGVNVTVSQINTVLNGTRRYTDI | 2666 |
| Db | 2563 | LHFTIEGRDRHYFIKLGSLUEEDIVLITGNTGRRILENGVNVTVSQMTSLUNGTRRFADI | 2622 |
| QY | 2667 | QLOVGALCLNTRYGTTLDDEKARVLELARORAVROAWAREQORLRGEGSLRAWTEGEKQ | 2726 |
| Db | 2623 | QLQHGAJLCFNIRIGTTVBEEKHVLBIARQAVAQAWKTEQORRLQGBESGIRAWTEGEKQ | 2682 |
| QY | 2727 | QVJLSTGRVQYDGFVVISVEQYPELSDSANNHFMQSEMGRR | 2769 |
| Db | 2683 | QLLSTGRVQYDGFVVISVEQYLELSDSANNHFMQSEIGRR | 2725 |

Search completed: December 11, 2005, 04:48:10
Job time : 254 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2005, 04:48:17 ; Search time 157 Seconds
(without alignments)
7369.232 Million cell updates/sec

Title: US-10-029-020-14
Perfect score: 14887
Sequence: 1 MDVKERKPYSLRRRDAER.....ELSDSANNIHFMQSEMGRR 2769

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|---------|-------------|--------|-------|---------------------|
| 1 | 14887 | 100.0 | 2769 | 4 | US-10-383-201-44 |
| 2 | 14887 | 100.0 | 2769 | 4 | US-10-029-020-14 |
| 3 | 14748.5 | 99.1 | 2758 | 4 | US-10-467-535-10 |
| 4 | 14610 | 98.1 | 2775 | 4 | US-10-383-201-56 |
| 5 | 14529 | 97.6 | 2771 | 3 | US-09-808-602-82 |
| 6 | 14529 | 97.6 | 2771 | 3 | US-09-800-198-70 |
| 7 | 14406.5 | 96.8 | 2794 | 4 | US-10-042-865-2 |
| 8 | 10227 | 68.7 | 2715 | 4 | US-10-042-865-52 |
| 9 | 10227 | 68.7 | 2715 | 4 | US-10-029-020-51 |
| 10 | 10221 | 68.7 | 2721 | 4 | US-10-038-854-38 |
| 11 | 10201 | 68.5 | 2725 | 4 | US-10-038-854-36 |
| 12 | 9888.5 | 66.4 | 2628 | 4 | US-10-038-854-40 |
| 13 | 9856 | 66.2 | 2613 | 4 | US-10-038-854-42 |
| 14 | 9616.5 | 64.6 | 2802 | 3 | US-09-808-602-81 |
| 15 | 9616.5 | 64.6 | 2802 | 3 | US-09-800-198-69 |
| 16 | 9616.5 | 64.6 | 2802 | 4 | US-10-072-012-489 |
| 17 | 9610.5 | 64.6 | 2764 | 3 | US-09-808-602-80 |
| 18 | 9610.5 | 64.6 | 2764 | 3 | US-09-800-198-68 |
| 19 | 9610.5 | 64.6 | 2764 | 4 | US-10-072-012-487 |
| 20 | 9610.5 | 64.6 | 2764 | 5 | US-10-631-467-1514 |
| 21 | 9601 | 64.5 | 2765 | 3 | US-09-808-602-84 |
| 22 | 9601 | 64.5 | 2765 | 3 | US-09-800-198-72 |
| 23 | 9601 | 64.5 | 2765 | 4 | US-10-072-012-488 |
| 24 | 9584 | 64.4 | 2725 | 4 | US-10-029-020-52 |
| 25 | 9584 | 64.4 | 2725 | 4 | US-10-408-765A-1687 |
| 26 | 9536 | 64.1 | 2733 | 3 | US-09-808-602-8 |
| 27 | 9536 | 64.1 | 2733 | 3 | US-09-800-198-8 |

| | | | | | |
|----|--------|------|------|---|--------------------|
| 28 | 9530.5 | 64.0 | 2724 | 3 | US-09-808-602-13 |
| 29 | 9530.5 | 64.0 | 2724 | 3 | US-09-800-198-13 |
| 30 | 9501 | 63.8 | 2725 | 4 | US-10-295-027-928 |
| 31 | 9501 | 63.8 | 2725 | 5 | US-10-723-860-4102 |
| 32 | 9418 | 63.3 | 2759 | 4 | US-10-072-012-144 |
| 33 | 9314 | 62.6 | 2633 | 4 | US-10-144-194A-82 |
| 34 | 9314 | 62.6 | 2633 | 5 | US-10-491-566-82 |
| 35 | 9303 | 62.5 | 2590 | 4 | US-10-072-012-490 |
| 36 | 9145 | 61.4 | 2346 | 4 | US-10-072-012-491 |
| 37 | 8874 | 59.6 | 2551 | 4 | US-10-144-194A-80 |
| 38 | 8874 | 59.6 | 2551 | 5 | US-10-491-566-80 |
| 39 | 8059.5 | 54.1 | 2144 | 5 | US-10-723-860-2303 |
| 40 | 6774 | 45.5 | 1769 | 5 | US-10-723-860-4494 |
| 41 | 6389.5 | 42.9 | 1737 | 3 | US-09-808-602-83 |
| 42 | 6389.5 | 42.9 | 1737 | 3 | US-09-800-198-71 |
| 43 | 6258.5 | 42.0 | 1688 | 4 | US-10-144-194A-113 |
| 44 | 6258.5 | 42.0 | 1688 | 5 | US-10-491-566-113 |
| 45 | 6258.5 | 42.0 | 1688 | 5 | US-10-494-940-52 |

ALIGNMENTS

RESULT 1

US-10-383-201-44
; Sequence 44, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 44
; LENGTH: 2769
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-44

Query Match 100.0%; Score 14887; DB 4; Length 2769;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDVKERKPYSLRRRDAERYYTSSSADSEEGKAPQKYSSTETLKAYDDARLAYGSRV 60
Db 1 MDVKERKPYSLRRRDAERYYTSSSADSEEGKAPQKYSSTETLKAYDDARLAYGSRV 60

Qy 61 KDIVPQAEAEFCRTGANFTLRELGLVTPPHGTLTYRTDGLPQCYSMGAGSDADHEAD 120
Db 61 KDIVPQAEAEFCRTGANFTLRELGLVTPPHGTLTYRTDGLPQCYSMGAGSDADHEAD 120

QY 121 TVLSPHVRWLGRSTRSGRSCSLSSRANSNLTLTDTHEHENTETDHPGGLQNHARLRTPP 180
DB 121 TVLSPHVRWLGRSTRSGRSCSLSSRANSNLTLTDTHEHENTETDHPGGLQNHARLRTPP 180
QY 181 PPLSHAHPNQHHAASINSLNRGNFTPRSNPSAPTDHSLSGEPAGGAQPAHAQENWL 240
DB 181 PPLSHAHPNQHHAASINSLNRGNFTPRSNPSAPTDHSLSGEPAGGAQPAHAQENWL 240
QY 241 LNSNIPLETRNLGKOPFLGTLODNLIEMDIIGASRHDGAYSDGHPLFKPGGTSPFLCFTTS 300
DB 241 LNSNIPLETRNLGKOPFLGTLODNLIEMDIIGASRHDGAYSDGHPLFKPGGTSPFLCFTTS 300
QY 301 PGYPLTSTVSVPPRPLPRSTFARPAFNALKPSKYNKWKCAALSAIVISATLVILLAYF 360
DB 301 PGYPLTSTVSVPPRPLPRSTFARPAFNALKPSKYNKWKCAALSAIVISATLVILLAYF 360
QY 361 VAMHLFGLNHLQPMQEGQMEYIETEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEBK 420
DB 361 VAMHLFGLNHLQPMQEGQMEYIETEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEBK 420
QY 421 PSSFPPEDSFIDSGEIDVGRASQKIPPGTFRWSQVFDHPVHLKFNVSGLKAALVGIIY 480
DB 421 PSSFPPEDSFIDSGEIDVGRASQKIPPGTFRWSQVFDHPVHLKFNVSGLKAALVGIIY 480
QY 481 RKGLPSPHTQDFVELLDGRRLLTOEARSLCTPRQSRGTVPSPSHETGFTQYLDSGIWH 540
DB 481 RKGLPSPHTQDFVELLDGRRLLTOEARSLCTPRQSRGTVPSPSHETGFTQYLDSGIWH 540
QY 541 LAFYNDGKESEVVSFLTTAIESVDNCPNCGNGDCISGTCCHFGLFGLPGDCGRASCPVL 600
DB 541 LAFYNDGKESEVVSFLTTAIESVDNCPNCGNGDCISGTCCHFGLFGLPGDCGRASCPVL 600
QY 601 CSGNGQYMKGRCLCHSGWKABCDVPTNQCIDVACSNHGTCTGTGICINPGYKGBSCREY 660
DB 601 CSGNGQYMKGRCLCHSGWKABCDVPTNQCIDVACSNHGTCTGTGICINPGYKGBSCREY 660
QY 661 DCMDPTCSGRGVVGRGECHCFVWGTCNCTETPRATCLDQCSHGHTFLPDTGLCSDPSWT 720
DB 661 DCMDPTCSGRGVVGRGECHCFVWGTCNCTETPRATCLDQCSHGHTFLPDTGLCSDPSWT 720
QY 721 GHDCSIEICAADCGGHGVCGGTCCEDGMMGAACDQACHPRCAEHGTCRDGKCECSPG 780
DB 721 GHDCSIEICAADCGGHGVCGGTCCEDGMMGAACDQACHPRCAEHGTCRDGKCECSPG 780
QY 781 MNGEHCTIAHYLDVRVYKEGCPGLCNGNRCCTLDLNGWHCVCOLGWRGAGCDTSMETACGD 840
DB 781 MNGEHCTIAHYLDVRVYKEGCPGLCNGNRCCTLDLNGWHCVCOLGWRGAGCDTSMETACGD 840
QY 841 SKDNDDGLVDCMDPCCLOPLCHINPLCLGSPNPLDIIQETQVPVSQONLHSFYDRIKF 900
DB 841 SKDNDDGLVDCMDPCCLOPLCHINPLCLGSPNPLDIIQETQVPVSQONLHSFYDRIKF 900
QY 901 LVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLVGVNISFVNNPLFGYTISRQDGSF 960
DB 901 LVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLVGVNISFVNNPLFGYTISRQDGSF 960
QY 961 DLVTNGGIIILRFRAPAITQEHNTLWLPDRFFVWMETIIMRHEENIEPSCDLSNFARN 1020
DB 961 DLVTNGGIIILRFRAPAITQEHNTLWLPDRFFVWMETIIMRHEENIEPSCDLSNFARN 1020
QY 1021 PVVSPSPLTSFASSCAEKGPVPEIQALQOEIISIGCKMRLSYLSLSTRTPGYKSVLRISLT 1080
DB 1021 PVVSPSPLTSFASSCAEKGPVPEIQALQOEIISIGCKMRLSYLSLSTRTPGYKSVLRISLT 1080
QY 1081 HPTIPFNLMKVLMWAVEGRLFRKWFAPADLSYFFIWDKTDVYNQKVFGLSEAFVSVGY 1140
DB 1081 HPTIPFNLMKVLMWAVEGRLFRKWFAPADLSYFFIWDKTDVYNQKVFGLSEAFVSVGY 1140
QY 1141 EYESCPDLILWEKRTTVLOGYEIDASKLGWSLDKHALNIOSGIILHKGNGENQFVSQQP 1200
DB 1141 EYESCPDLILWEKRTTVLOGYEIDASKLGWSLDKHALNIOSGIILHKGNGENQFVSQQP 1200
QY 1201 PVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRIFPSPGNV 1260

DB 1201 PVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRIFPSPGNV 1260
QY 1261 TNILELRNKDPRSHSHSAHKYKYLATDPMGSAFVLSDSNSRRVPKIKSTVVVKDVLKXSEV 1320
DB 1261 TNILELRNKDPRSHSHSAHKYKYLATDPMGSAFVLSDSNSRRVPKIKSTVVVKDVLKXSEV 1320
QY 1321 VAGTGDQCLPDDTRCDGCGKATEATLTNPRGITVDKFGLIYFYVDGTMIRRIDQNGIIST 1380
DB 1321 VAGTGDQCLPDDTRCDGCGKATEATLTNPRGITVDKFGLIYFYVDGTMIRRIDQNGIIST 1380
QY 1381 LLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDDNNVVLQISENHQVRI 1440
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QY 1441 VAGRPMKCOVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVTTTS 1500
DB 1441 VAGRPMKCOVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVTTTS 1500
QY 1501 GEISLVAGAPSGCDCKNDANCDGSGDDGYAKADAKLNTPPSSLAVCADGELYVADLGNIRI 1560
DB 1501 GEISLVAGAPSGCDCKNDANCDGSGDDGYAKADAKLNTPPSSLAVCADGELYVADLGNIRI 1560
QY 1561 RFIRKNKPFNLTONMYELSSPIDQELYLFDTTGKHLYTQSLPTGDLYNFTYTGDDITL 1620
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QY 1621 ITDNNGNMNVRRDSTGMPLWLVPDGOVYVWVTGNTSALKSVTTQGHELAMTYVHGNSG 1680
DB 1621 ITDNNGNMNVRRDSTGMPLWLVPDGOVYVWVTGNTSALKSVTTQGHELAMTYVHGNSG 1680
QY 1681 LLATKSNENGWTTTFEYVDSFGRLTNVTFPTQOVSSFRSDTSSVHVQVETSSKDDVTITT 1740
DB 1681 LLATKSNENGWTTTFEYVDSFGRLTNVTFPTQOVSSFRSDTSSVHVQVETSSKDDVTITT 1740
QY 1741 NLSASGAPYTLLOQVRNSYYIIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVGKRV 1800
DB 1741 NLSASGAPYTLLOQVRNSYYIIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVGKRV 1800
QY 1801 TLPIDNGLNVEMQRKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIIDHRRKFT 1860
DB 1801 TLPIDNGLNVEMQRKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIIDHRRKFT 1860
QY 1861 LRILYDQAGRPSLWSPSSRLNGVNVYSPGGYIAGIQRIGMSRMEYDQAGRITSRIEAD 1920
DB 1861 LRILYDQAGRPSLWSPSSRLNGVNVYSPGGYIAGIQRIGMSRMEYDQAGRITSRIEAD 1920
QY 1921 GKTWSYTYLEKSMVLLLSHSORQYIPEFDKNDRLSSVTMPNVAROTLETIRSVGYRNIYQ 1980
DB 1921 GKTWSYTYLEKSMVLLLSHSORQYIPEFDKNDRLSSVTMPNVAROTLETIRSVGYRNIYQ 1980
QY 1981 PPEGNASVIQDFTEDGHLHHTFYLGTGRRVYKYGKLSKLAETLYDTTKVSFTYDETAM 2040
DB 1981 PPEGNASVIQDFTEDGHLHHTFYLGTGRRVYKYGKLSKLAETLYDTTKVSFTYDETAM 2040
QY 2041 LKTNLQNEGTCTIRYRQIOPRIDRQIFRFTTEGVNARPDYNDNSFRVTSMAQVINE 2100
DB 2041 LKTNLQNEGTCTIRYRQIOPRIDRQIFRFTTEGVNARPDYNDNSFRVTSMAQVINE 2100
QY 2101 TPLPDLRYDDVSGKTEQFGKFGVIYVDINQIITTAVMTHTKHFDAYGRMEKVOYEIEFR 2160
DB 2101 TPLPDLRYDDVSGKTEQFGKFGVIYVDINQIITTAVMTHTKHFDAYGRMEKVOYEIEFR 2160
QY 2161 SLMWYMWTVQYDNMGVWVKELKVGYPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLN 2220
DB 2161 SLMWYMWTVQYDNMGVWVKELKVGYPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLN 2220
QY 2221 GNLHLLSPGNSARLTPLYDIRIDRITRLGDOVQYKMDGDFLQRQGDIFEYNSAGLIIKA 2280
DB 2221 GNLHLLSPGNSARLTPLYDIRIDRITRLGDOVQYKMDGDFLQRQGDIFEYNSAGLIIKA 2280
QY 2281 YNRAGSWSVRYDGLGRRVSKSSSHHLOQFFYADLTNTPTKVTHTLHNHSSSEITSLYYD 2340

Db 2281 YNRAGSWVRYYDGLGRRVSSKSHSHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340
Qy 2341 LQGHLFAMELSSGDEFYACDNIGTPLAVSGTGLMIKQILLYTAYGIYMDTPNFQII 2400
Db 2341 LQGHLFAMELSSGDEFYACDNIGTPLAVSGTGLMIKQILLYTAYGIYMDTPNFQII 2400
Qy 2401 GYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHLMKHLSSSNVMPFNLYMFKNNPISN 2460
Db 2401 GYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHLMKHLSSSNVMPFNLYMFKNNPISN 2460
Qy 2461 SQDIKFCMTDVNSWLLTFGQLHNVIPGYPKPDMNAMEPSYELIHTQMTQEWDNKSIL 2520
Db 2461 SQDIKFCMTDVNSWLLTFGQLHNVIPGYPKPDMNAMEPSYELIHTQMTQEWDNKSIL 2520
Qy 2521 GVQCEVQKQKAFVTLRFQLYGSTTSCQAPKTKKEASSGVFCGKVKFALKDGRVT 2580
Db 2521 GVQCEVQKQKAFVTLRFQLYGSTTSCQAPKTKKEASSGVFCGKVKFALKDGRVT 2580
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Db 2581 TDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGD LAILGLSGGRT 2640
Qy 2641 LENGVNTVQSINTVLNGRRYTDIQLQYCALCLNTRYGTTLDEEKARVLELARQAVR 2700
Db 2641 LENGVNTVQSINTVLNGRRYTDIQLQYCALCLNTRYGTTLDEEKARVLELARQAVR 2700
Qy 2701 QAWAREOORLEBEGIRAWTEGKQOVLSTGRVOGYDGRFVISEQYBELSDSANNIH 2760
Db 2701 QAWAREOORLEBEGIRAWTEGKQOVLSTGRVOGYDGRFVISEQYBELSDSANNIH 2760
Qy 2761 MRQSEMR 2769
Db 2761 MRQSEMR 2769

RESULT 2

US-10-029-020-14
; Sequence 14, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 2769
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-020-14

Query Match 100.0%; Score 14887; DB 4; Length 2769;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDVKERKPYRSLTRRDAERRYTSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
Db 1 MDVKERKPYRSLTRRDAERRYTSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
Qy 61 KDIVPOEAEFEFCRTGANFTLRELGLBEVTPPHGTLRYRTDGLPQCYSMGAGSDADMEAD 120
Db 61 KDIVPOEAEFEFCRTGANFTLRELGLBEVTPPHGTLRYRTDGLPQCYSMGAGSDADMEAD 120
Qy 121 TVLSPEHPVRLWGRSTRSGSSCLSRANSNLTLTTEHENTETDHPGGIQLNHLRLTTP 180
Db 121 TVLSPEHPVRLWGRSTRSGSSCLSRANSNLTLTTEHENTETDHPGGIQLNHLRLTTP 180
Qy 181 PPLSHAHTPNQHAASINLSNRGNFTPRSNPSPAPTDHSLSGPPAGGAPAHQAQENWL 240
Db 181 PPLSHAHTPNQHAASINLSNRGNFTPRSNPSPAPTDHSLSGPPAGGAPAHQAQENWL 240
Qy 241 LNSNI PLETRNLGKQPFGLTQDNLIEMDILGASRHGAYS DGHFLFKPGGTSP LFCCTS 300
Db 241 LNSNI PLETRNLGKQPFGLTQDNLIEMDILGASRHGAYS DGHFLFKPGGTSP LFCCTS 300
Qy 301 PGVPLTSSVTSYSPPPRLPRSTFARPAFNLKKPSKYNMKCAALSAIVISATVILLAYF 360
Db 301 PGVPLTSSVTSYSPPPRLPRSTFARPAFNLKKPSKYNMKCAALSAIVISATVILLAYF 360
Qy 361 VAMHLGLNWHLOPMEGOMYEITETDASSWPVPTDVS LYPGSGTGLETDPKKGKGTTEGK 420
Db 361 VAMHLGLNWHLOPMEGOMYEITETDASSWPVPTDVS LYPGSGTGLETDPKKGKGTTEGK 420
Qy 421 PSSFFPPEDSFDSGEIDVGRRASQKIPPGTFMRSQVFI DHPVHLKFNVS LGKAALVGIYG 480
Db 421 PSSFFPPEDSFDSGEIDVGRRASQKIPPGTFMRSQVFI DHPVHLKFNVS LGKAALVGIYG 480
Qy 481 RKGLPPSHQTFDFVELLDGRRLLTOEARSLEGTPROSRGTVPSSSHETGTIYLD SGIMH 540
Db 481 RKGLPPSHQTFDFVELLDGRRLLTOEARSLEGTPROSRGTVPSSSHETGTIYLD SGIMH 540
Qy 541 LAFYNDGKSEVVSFLTATAESVNDCPNVCNGDCISGTC HCFGLGFLGPD CGRASCPVL 600
Db 541 LAFYNDGKSEVVSFLTATAESVNDCPNVCNGDCISGTC HCFGLGFLGPD CGRASCPVL 600
Qy 601 CSGNGQYMKGRCLCHSGWKGAECDVPTNQICIDVACS NHGTCITGTCTCNPGYKGESCEEV 660
Db 601 CSGNGQYMKGRCLCHSGWKGAECDVPTNQICIDVACS NHGTCITGTCTCNPGYKGESCEEV 660
Qy 661 DCMDP TCGRGVCVRGECGCHCFVWG GTNCTBPATCLDQCSGHGTFLPDTGLSCDPSWT 720
Db 661 DCMDP TCGRGVCVRGECGCHCFVWG GTNCTBPATCLDQCSGHGTFLPDTGLSCDPSWT 720
Qy 721 GHDCSIEICAADCGHGVCGVGGTCRCEDGWMGAACDORACHPRCAEHGTCRDGKCECSPG 780
Db 721 GHDCSIEICAADCGHGVCGVGGTCRCEDGWMGAACDORACHPRCAEHGTCRDGKCECSPG 780
Qy 781 WNGEHCTIAHYLDRVVKEGCPGLCNGNRCCTLDLNGWHCVCLGWRCAGCDTSMETACGD 840
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Qy 841 SKNDGGLVDCMDPCCCLQPLCHINPLCLGSPNPLDIIQETQVPVQQNLHSHFYDIK 900
Db 841 SKNDGGLVDCMDPCCCLQPLCHINPLCLGSPNPLDIIQETQVPVQQNLHSHFYDIK 900
Qy 901 LVGRDSTHIIIPGENPDGGHACVIRGOVMTSDGTPLVGVNISFVNPNLFGVTTISRQDGSF 960
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Qy 961 DLVTNGGISIIILRFERAPFITQBSHTLWLPWDRFFVVMETIIMRHEENEIPSCDLSNFARPN 1020
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DB 1081 HPTIPENLAKVHLMVAVGRLFRKWFAPADLSYFPIWDKTDVYNQKVFGLSEAFVSVCY 1140
QY 1141 EYESCPDLILWEKRTTTLVQGYEIDASKLGGWSLDKXHALNIQSGILHKGNGENQFVSQOP 1200
DB 1141 EYESCPDLILWEKRTTTLVQGYEIDASKLGGWSLDKXHALNIQSGILHKGNGENQFVSQOP 1200
QY 1201 PVIQSTMGNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFPNYIRRIIPSGNV 1260
DB 1201 PVIQSTMGNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFPNYIRRIIPSGNV 1260
QY 1261 TNLIELRNKDFRHSHPAHKYIATDPMMSGAVFLSDSNSRRVFKIKSTVVVKDLVKNSEV 1320
DB 1261 TNLIELRNKDFRHSHPAHKYIATDPMMSGAVFLSDSNSRRVFKIKSTVVVKDLVKNSEV 1320
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DB 1321 VAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDTGTMIRRIDQNGIIST 1380
QY 1381 LLGSDNLTSAEPLSCDSVNDISQVRLEWPTDLAINPMDNSLYVLONNVVLQISENHQVRI 1440
DB 1381 LLGSDNLTSAEPLSCDSVNDISQVRLEWPTDLAINPMDNSLYVLONNVVLQISENHQVRI 1440
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QY 1561 RPIRKNKPELNTQNMVELSSPIDQELYLFDTTGKHLYTQSLPTGDYLYNFYTTGCGDITL 1620
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DB 1621 ITDNNGMNVNRDSTGMPLWLVPDGOVYWTMTGNSALKSVTTQGHELAMTTHVGNNG 1680
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QY 1861 LRILYDQAGRPSLWSPSSRLNGVNTYSPGGYIAGIQRGINSERMEYDQAGRITSRIPAD 1920
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QY 1921 GHTWSYTYLEKSMVLLSHSQRQYIIEFDDKNDRLSSVTPNVARQTLTIRSGVYRNIYQ 1980
DB 1921 GHTWSYTYLEKSMVLLSHSQRQYIIEFDDKNDRLSSVTPNVARQTLTIRSGVYRNIYQ 1980
QY 1981 PPEGNASVIQDFTEDGHLHLHTPYLGTGRRVYKYGKLSKLAETLYDTHKVSFTYDETAGM 2040
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QY 2101 TPLPDLVRYDDVSKTEQFGKFGVIVYDINQIITTAWTHTKHPDAYGRMKVEQYEIFR 2160
DB 2101 TPLPDLVRYDDVSKTEQFGKFGVIVYDINQIITTAWTHTKHPDAYGRMKVEQYEIFR 2160

QY 2161 SLMTWMTVQYDNMGRVVKKELKVGYPYANTTRYSYEYDADGLOQTIVSINDKPLWRYSDLN 2220
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DB 2221 GNLHLLSPGNSARLTPLRYDIRDIRITRLGDVQYKWDGDFLRQRGDIFFEYNSAGLLIKA 2280
QY 2281 YNRAGSVRYRYDGLGRRVSSKSSHHLQFFVADLTNPTKVTHLYNHSSEITSLYYD 2340
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QY 2461 SQDIKCFMTDVNSWLLTFQGLHNVIPGYPKPDMDAMEPSYELIHTQMKTQEWDSKSIL 2520
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QY 2581 TDIISVANEDGRRVAAIILNHAHYLENLHFTIDGVDTHTYFVKPSPSEGDAILGLSGGRT 2640
DB 2581 TDIISVANEDGRRVAAIILNHAHYLENLHFTIDGVDTHTYFVKPSPSEGDAILGLSGGRT 2640
QY 2641 LENGVNVTVOINTVLNGRTRRYTDLOQYCALCLNTRYGTTLDDEKARVLELQARAVR 2700
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QY 2701 QAWAREOORLREGEGLRAMTEGEKQOVLSTGRVQGYDGFVIVSVEQYPELSDSANNIHF 2760
DB 2701 QAWAREOORLREGEGLRAMTEGEKQOVLSTGRVQGYDGFVIVSVEQYPELSDSANNIHF 2760
QY 2761 MRQSEMGR 2769
DB 2761 MRQSEMGR 2769
RESULT 3
US-10-467-535-10
; Sequence 10, Application US/10467535
; Publication No. US20040146970A1
; GENERAL INFORMATION:
; APPLICANT: YUE, Henry; YAO, Monique G.
; APPLICANT: ISON, Craig H.; LU, Yan
; APPLICANT: WARREN, Bridget A.; ELLIOTT, Vicki S.
; APPLICANT: BAUGHN, Mariah R.; DING, Li
; APPLICANT: XU, Yuming; GIETZEN, Kimberly J.
; APPLICANT: TANG, Tom Y.; LAL, Preeti G.
; APPLICANT: DUGGAN, Brendan M.; BURFORD, Neil
; APPLICANT: LU, Dyung Aina M.; RICHARDSON, Thomas W.
; APPLICANT: TRAN, Uyen K.; KHARE, Reena
; APPLICANT: CHAWLA, Narinder K.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
; FILE REFERENCE: PF-0903 USN
; CURRENT APPLICATION NUMBER: US/10/467,535
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/US02/03715
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/268,111
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/271,175
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,503
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/274,552

;; PRIOR FILING DATE: 2001-03-09
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PERL Program
;; SEQ ID NO 10
;; LENGTH: 2758
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No: 7488573CD1
US-10-467-535-10

Query Match 99.1%; Score 14748.5; DB 4; Length 2758;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2753; Conservative 0; Mismatches 7; Indels 11; Gaps 3;
Qy 1 MDVKERKPYSLTRRRDAERRYSSADSBEGKAPQKYSYSSSETLKAYDQDARLAYGSRV 60
Db 1 MDVKERKPYSLTRRRDAERRYSSADSBEGKAPQKYSYSSSETLKAYDQDARLAYGSRV 60
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Db 61 KDIVPOQAEBCFRTGANFTLRELGLEEVTPPHGTLVETDGLPCOGYSMGAGSDADMEAD 120
Qy 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHENTETDHPGGLQNHARLTTP 180
Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHENTET - FGGGLQNHARLTTP 178
Qy 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDSHLSGEPAGGAQEPAAHQENWL 240
Db 179 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDSHLSGEPAGGAQEPAAHQENWL 238
Qy 241 LNSNIPLETNLGKOPFLGTLODNLIMDILGASRHGDAYSDDGHFLPKPGGTSLPFCCTS 300
Db 239 LNSNIPLETNLGKOPFLGTLODNLIMDILGASRHGDAYSDDGHFLPKPGGTSLPFCCTS 298
Qy 301 PGYPLTSSVYSPRPLRSTFARPAFNLLKPKSKYCNWKAALSAIVISATLVILLAYF 360
Db 299 PGYPLTSSVYSPRPLRSTFARPAFNLLKPKSKYCNWKAALSAIVISATLVILLAYF 358
Qy 361 VAMHLFGLNHLQPMQEQMYEITDITASWPVPTDVSLYPSGGTGLTPDRKGKGTTEGK 420
Db 359 VGKHLF--NWLQPMQEQMYEITDITASWPVPTDVSLYPSGGTGLTPDRKGKGTTEGK 416
Qy 421 PSSFPFDESDISGEIDVGRASQKIPPGTFWRSQVFIIDHPVHLKFNVLGKAALVGIY 480
Db 417 PSSFPFDESDISGEIDVGRASQKIPPGTFWRSQVFIIDHPVHLKFNVLGKAALVGIY 476
Qy 481 RKGLPPSHQTQDFVELLDGRLLTQEARSLBGTPRQSRGTVPSPSHETGFTQYLDGSIWH 540
Db 477 RKGLPPSHQTQDFVELLDGRLLTQEARSLBGTPRQSRGTVPSPSHETGFTQYLDGSIWH 536
Qy 541 LAFYNDGKESVVSFLTTAIBSVNCPNSCYNGDCISGTCFCFLGFLGPDGCRASCPLV 600
Db 537 LAFYNDGKESVVSFLTTAIBSVNCPNSCYNGDCISGTCFCFLGFLGPDGCRASCPLV 596
Qy 601 CSNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCITGTCTCNPGYKGESCEEV 660
Db 597 CSNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCIMGTCTCNPGYKGESCEEV 656
Qy 661 DCMPTCSGRGVCVRGECGFCVGGGTNCETPRATCLDQCSGHGTFLPDTGLSCSDPSWT 720
Db 657 DCMPTCSGRGVCVRGECGFCVGGGTNCETPRATCLDQCSGHGTFLPDTGLSCSDPSWT 716
Qy 721 GHDCSIEICAAACGCGHGVCGVGTCTCRCEGMMGAACDQACRACHGTCRDKGCECSPG 780
Db 717 GHDCSIEICAAACGCGHGVCGVGTCTCRCEGMMGAACDQACRACHGTCRDKGCECSPG 776
Qy 781 WNGBHCCTIAHYLDVRVVGKCGFLCNNGRCRTLDLNGWHVCQLWRGAGCDTSMETACGD 840
Db 777 WNGBHCCTIAHYLDVRVVGKCGFLCNNGRCRTLDLNGWHVCQLWRGAGCDTSMETACGD 836
Qy 841 SKDNDGDLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVPSQQNLHSFYDRIKF 900

Db 837 SKDNDGDLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVPSQQNLHSFYDRIKF 896
Qy 901 LVGRDSTHIIIPGENPFDGGHACVIRQVMTSDGTPLVGVNISFVNNPLFGYTTISRDQGSF 960
Db 897 LVGRDSTHIIIPGENPFDGGHACVIRQVMTSDGTPLVGVNISFVNNPLFGYTTISRDQGSF 956
Qy 961 DLVTNGGSIILIRFERAPFITQHTLWLPMDFRFFVMTETIMRHEHENEIPSCDLSNFARPN 1020
Db 957 DLVTNGGSIILIRFERAPFITQHTLWLPMDFRFFVMTETIMRHEHENEIPSCDLSNFARPN 1016
Qy 1021 PVVSPSPLTSFASCAEKGPIVPEIQALOEIISICCKMRSLVLSRTPGYKSVLRISLT 1080
Db 1017 PVVSPSPLTSFASCAEKGPIVPEIQALOEIISICCKMRSLVLSRTPGYKSVLRISLT 1076
Qy 1081 HPTIPNLKMKVHLMAVEGRLEFRKWFAPADLSYFIWDKTDVYNQKVFGLSBAFVSVG 1140
Db 1077 HPTIPNLKMKVHLMAVEGRLEFRKWFAPADLSYFIWDKTDVYNQKVFGLSBAFVSVG 1136
Qy 1141 EYESCPDLILWEKRTTTLQOYEIDASKLGGWSLDKHALNIQSGILHKGNGENQFVSQQP 1200
Db 1137 EYESCPDLILWEKRTTTLQOYEIDASKLGGWSLDKHALNIQSGILHKGNGENQFVSQQP 1196
Qy 1201 PVTGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDPNVIRIFPSGNV 1260
Db 1197 PVTGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDPNVIRIFPSGNV 1256
Qy 1261 TNLLELRNKDFRSHSHPAHKYILATDPMGAVFLSDSNSRRVPFKIKSTVVVKDLVKNSEV 1320
Db 1257 TNLLEL-----SHSPAHKYILATDPMGAVFLSDSNSRRVPFKIKSTVVVKDLVKNSEV 1309
Qy 1321 VAGTGQCQLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDONGIIST 1380
Db 1310 VAGTGQCQLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDONGIIST 1369
Qy 1381 LLGSNDLTSARPLSCDSVMDISQVRLWPTDLAINPMDNSLYVLDNNVVLQISENHQVRI 1440
Db 1370 LLGSNDLTSARPLSCDSVMDISQVHLEWPTDLAINPMDNSLYVLDNNVVLQISENHQVRI 1429
Qy 1441 VAGRPHMCQVPGDHFLLSKVAIHTALESATALAVSHNGVLYIAETDEKKINRIQVTTTS 1500
Db 1430 VAGRPHMCQVPGDHFLLSKVAIHTALESATALAVSHNGVLYIAETDEKKINRIQVTTTS 1489
Qy 1501 GEISLVAGAPSGDCCKNDANCDGSGDDGYAKDAKLTNPSSLAVCADGELYVADLGNIRI 1560
Db 1490 GEISLVAGAPSGDCCKNDANCDGSGDDGYAKDAKLTNPSSLAVCADGELYVADLGNIRI 1549
Qy 1561 RPIRKONKPFLLNTQNMVELSSPIDOELYLFTTQKHLYTQSLPTGDIYLYNTYITGDDITL 1620
Db 1550 RPIRKONKPFLLNTQNMVELSSPIDOELYLFTTQKHLYTQSLPTGDIYLYNTYITGDDITL 1609
Qy 1621 ITDNGNMVNRDSTGMPMLVVPDQVYVMTGNTSNALSKSVTTQGHLEAMMTYHNSG 1680
Db 1610 ITDNGNMVNRDSTGMPMLVVPDQVYVMTGNTSNALSKSVTTQGHLEAMMTYHNSG 1669
Qy 1681 LLATKSNENGTTFYEYDSFGRLTNTVFTPTQGVSSFRSDTSSVHVQVETSSKDDVTITT 1740
Db 1670 LLATKSNENGTTFYEYDSFGRLTNTVFTPTQGVSSFRSDTSSVHVQVETSSKDDVTITT 1729
Qy 1741 NLSASGAFYTLQDQVRNSYIIGADSLRLLLANGMEVALQTBPHLLAGTVNPTVGRNV 1800
Db 1730 NLSASGAFYTLQDQVRNSYIIGADSLRLLLANGMEVALQTBPHLLAGTVNPTVGRNV 1789
Qy 1801 TLPIDNGLNLVWRQKEQARGVTFGRRLRVHNRNLLSIDFDRVTRTEKIYDDHRKFT 1860
Db 1790 TLPIDNGLNLVWRQKEQARGVTFGRRLRVHNRNLLSIDFDRVTRTEKIYDDHRKFT 1849
Qy 1861 LRILYDQAGRPSSLWSPSSRLNGVNTYSPGCIAGIORGIMSERMEYDQAGRITSRIFAD 1920
Db 1850 LRILYDQAGRPSSLWSPSSRLNGVNTYSPGCIAGIORGIMSERMEYDQAGRITSRIFAD 1909
Qy 1921 GKTWSYTYLBSKSMVLLHLSQRQYIFEPDKNDRILSSVTMPNVARQTLTETIRSIVGYRIYQ 1980

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Db 1910 GKTWSYLEKSMVLLLSHQRYIFBFDKNDRLSSVTMPNVARQTLETIRSVGYRNIIYQ 1969
Qy 1981 PPEGNASVIODFTEDEGHLLHTFVLGTRRRVIYKXGKLSKLAETLYTTKVSFTYDETACM 2040
Db 1970 PPEGNASVIODFTEDEGHLLHTFVLGTRRRVIYKXGKLSKLAETLYTTKVSFTYDETACM 2029
Qy 2041 LKTIINLQNEGTCCTIRYRQIGPLIDRQIFRFTBEGMVNARFDVYDNSFRVTSMAQVINE 2100
Db 2030 LKTIINLQNEGTCCTIRYRQIGPLIDRQIFRFTBEGMVNARFDVYDNSFRVTSMAQVINE 2089
Qy 2101 TPLPIDLYRDDVSGKTEQFGKFGVIYYDINQIITAVMTHKHFDAYGRMKVEQVYEIPR 2160
Db 2090 TPLPIDLYRDDVSGKTEQFGKFGVIYYDINQIITAVMTHKHFDAYGRMKVEQVYEIPR 2149
Qy 2161 SLMYMWTVOYDNNMGRVVVKELKVPYANTTRYSYEDADGQLOQTVSINDKPLWRYSYDLN 2220
Db 2150 SLMYMWTVOYDNNMGRVVVKELKVPYANTTRYSYEDADGQLOQTVSINDKPLWRYSYDLN 2209
Qy 2221 GNLHLLSPGNSARLTPLRYDIRDRIITRLGDVOYKMDDEDGFLRQRGDIFEYNSAGLLIKA 2280
Db 2210 GNLHLLSPGNSARLTPLRYDIRDRIITRLGDVOYKMDDEDGFLRQRGDIFEYNSAGLLIKA 2269
Qy 2281 YNRAGSWVRYYRVDGLGRRVSSKSHHLLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340
Db 2270 YNRAGSWVRYYRVDGLGRRVSSKSHHLLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2329
Qy 2341 LQGHFLAMELSSGDEFYIACDNIIGTPLAVFSGTGLMIKOILYATAYGEIYMDTNPNFQIII 2400
Db 2330 LQGHFLAMELSSGDEFYIACDNIIGTPLAVFSGTGLMIKOILYATAYGEIYMDTNPNFQIII 2389
Qy 2401 GYHGGLYDPLTKLVHMRDYYDLAGRMTSPDHELWKHLSSSNVMPFNLYMFKNPNPISN 2460
Db 2390 GYHGGLYDPLTKLVHMRDYYDLAGRMTSPDHELWKHLSSSNVMPFNLYMFKNPNPISN 2449
Qy 2461 SQDIKCFMTDVNSWLLTFQOLHNVIIPGYPKDMDAMEPSYELIHTQMTQBDWNSKIL 2520
Db 2450 SQDIKCFMTDVNSWLLTFQOLHNVIIPGYPKDMDAMEPSYELIHTQMTQBDWNSKIL 2509
Qy 2521 GVQCEVQOKKAFVTLERFDQLYGSTITSCQAQPKTKFPASSGSVFGKGVKFPALXDGRTV 2580
Db 2510 GVQCEVQOKKAFVTLERFDQLYGSTITSCQAQPKTKFPASSGSVFGKGVKFPALXDGRTV 2569
Qy 2581 TDIISVANEDGRVRAAILNHAHYLENLHFTIDGVDPHYFVKPGPSEGDLAILGLSGGRT 2640
Db 2570 TDIISVANEDGRVRAAILNHAHYLENLHFTIDGVDPHYFVKPGPSEGDLAILGLSGGRT 2629
Qy 2641 LENGVNVTYSQINTVLNGTRTRYTDIOLQYGCALCLNTRYGTTLDDEKARVLELARQAVR 2700
Db 2630 LENGVNVTYSQINTVLNGTRTRYTDIOLQYGCALCLNTRYGTTLDDEKARVLELARQAVR 2689
Qy 2701 QAWAREQORLRBEGEGLRAWTEGEXQOVLSTGRVOGYDGFVVISVEQYPELSDSANNIHF 2760
Db 2690 QAWAREQORLRBEGEGLRAWTEGEXQOVLSTGRVOGYDGFVVISVEQYPELSDSANNIHF 2749
Qy 2761 MRQSENGRR 2769
Db 2750 MRQSENGRR 2758

RESULT 4
US-10-383-201-56
; Sequence 56, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
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; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 56
; LENGTH: 2775
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-383-201-56

Query Match 98.1%; Score 14610; DB 4; Length 2775;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 2743; Conservative 2; Mismatches 6; Indels 42; Gaps 12;

Qy 1 MDVKERKPYRLTRRRDAERRYTSSSADSEBKAPQKSYSSSETLKAYDQDARLAYGSRV 60
Db 1 MDVKERKPYRLTRRRDAERRYTSSSADSEBKAPQKSYSSSETLKAYDQDARLAYGSRV 60
Qy 61 KDIVPQAEAEFCRTGANFTLRELGLEEVTPPHGTLVYTDIGLPCQGYSMGAGSDADMEAD 120
Db 61 KDIVPQAEAEFCRTGANFTLRELGLEEVTPPHGTLVYTDIGLPCQGYSMGAGSDADMEAD 120
Qy 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTETDHPGGLQNHARLTTP 180
Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTETDHPGGLQNHARLTTP 180
Qy 181 PPLSHAHTPNQHAASINSLNRGNTFPRSNPSPAPTSHLSGEBPPAGGAQEPAAHQENWL 240
Db 181 PPLSHAHTPNQHAASINSLNRGNTFPRSNPSPAPTSHLSGEBPPAGGAQEPAAHQENWL 240
Qy 241 LNSNIPILETNLGKQPLGTLQNLLEMDILGASRHDGAYSDGHFLPKPGTSPFLCTTS 300
Db 241 LNSNIPILETNLGKQPLGTLQNLLEMDILGASRHDGAYSDGHFLPKPGTSPFLCTTS 300
Qy 301 PGYPLTSSVYSPPPRPLPRSTFARPAFNLKFPKSKYCNWKCAALSATVILVILAYF 360
Db 301 PGYPLTSSVYSPPPRPLPRSTFARPAFNLKFPKSKYCNWKCAALSATVILVILAYF 360
Qy 361 VAMHLFGLNHLQPMQEQMYEITETASSWPVPTDVSILYPSGGTGLTTPRKGKGTTEGK 420
Db 361 VAMHLFGLNHLQPMQEQMYEITETASSWPVPTDVSILYPSGGTGLTTPRKGKGTTEGK 420
Qy 421 PSSFFFPEDSFIDSGEIDVGRASQKPPGTFWRSQVFIIDHPVHLKFNVSIGKAAALVGIY 480
Db 421 PSSFFFPEDSFIDSGEIDVGRASQKPPGTFWRSQVFIIDHPVHLKFNVSIGKAAALVGIY 480
Qy 481 RKGLPPSHTQDFVELLDGRRLLTQBARSLLEGTPROSRGTVPFPSSSHETGFIQYLDSGIWH 540
Db 481 RKGLPPSHTQDFVELLDGRRLLTQBARSLLEGTPROSRGTVPFPSSSHETGFIQYLDSGIWH 540
Qy 541 LAFYNDGKSESVYFLTTAIESVDNCPNSCYNGDCISGTCCHCFGLGPDCCGRASCPVL 600
Db 541 LAFYNDGKSESVYFLISP--ESVDNCPNSCYNGDCISGTCCHCFGLGPDCCGRASCPVL 598
Qy 601 CSGNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCTGTCTICNPYKGSCEEV 660
Db 599 CSGNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCTGTCTICNPYKGSCEEV - 657
Qy 661 DCMDDPTCSGRGVCVRGECHCFVGVGNGTNCNTPRATCLDQCSGHGTFLPDTGLSCDPSWT 720
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| | | | | | | | |
|----|------|---|------|----|------|--|------|
| Db | 658 | DCMDPTCSGRGVCVRGCHCVSGVGGTNCETPRATCLDQCSGHGTFLPDTGLCSDCPSWT | 717 | Db | 1738 | VETSSKDDVTITTNLSAGAFY-----DQVRNSYIIGADGSLRLLLLANGMEVALQTEPHLL | 1793 |
| Qy | 721 | GHDCSIIEICAADCGGHCVCVGGTCRCEDGHWGAACDORACHPCBAEHGTCRDCCKCSPG | 780 | Qy | 1788 | AGTVNPTVGRNVTLPIIDNGLNLVWRQKEQARGQVTVFGRRLR--VHNRLNLLSLDFD | 1844 |
| Db | 718 | GHDCSIIEICAADCGGHCVCVGGTCRCEDGHWGAACDORACHPCBAEHGTCRDCCKCSPG | 777 | Db | 1794 | AGTVNPTVGRNVTLPIIDNGLNLVWRQKEQARGQVTVFGRRLRVLQVHNRNLLSLDFD | 1853 |
| Qy | 781 | WNGEHCITII--AHYLDLRVVK--EGCPGLCNGNGRCTLIDLNGWHVCQOLGMRGACDTSMET | 836 | Qy | 1845 | RVTRETEKIYDDHRKFTLRILYDOAGRPSLWSPSSRLNGVNVTVYSPGGYIAGIORGIMSER | 1904 |
| Db | 778 | WNGEHCITISLAHYLDVRVVKLSECGPGLCNGNGRCTLIDLNGWHVCQOLGMRGACDTSMET | 837 | Db | 1854 | RVTRETEKIYDDHRKFTLRILYDOAGRPSLWSPSSRLNGVNVTVYSPGGYIAGIORGIMSER | 1913 |
| Qy | 837 | ACGDSKNDGDGLVDCMDPCCLOPLCHINPLCLGSPNPLDIIQETQVPVSOQNLSHYD | 896 | Qy | 1905 | MEYDOAGRITTSRIFADGKTWSYTYLEKSMVLLLSHQRYIFBPDKNDRLLSSVTMPNVARQ | 1964 |
| Db | 838 | ACGDSKNDGDGLVDCMDPCCLOPLCHINPLCLGSPNPLDIIQETQVPVSOQNLSHYD | 897 | Db | 1914 | MEYDOAGRITTSRIFADGKTWSYTYLEKAGV-----EPDKNDRLLSSVTMPNVARQ | 1962 |
| Qy | 897 | RIKFLVGRDSTHIIIPGENPDGSHACVIRGOVMTSDGTPLVGVNI SPVNNPLFGYTSRQ | 956 | Qy | 1965 | TLTETRSVGYRNIYQPPPEGNASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKLSKLAETL | 2024 |
| Db | 898 | RIKFLVGRDSTHIIIPGENPDGSHACVIRGOVMTSDGTPLVGVNI SPVNNPLFGYTSRQ | 957 | Db | 1963 | TLTETRSVGYRNIYQPPPEGNASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKLSKLAETL | 2022 |
| Qy | 957 | DGSFDLVTNGGIIILIRFERAPFITOEHTLWLWDRFPFVNMETIIMRHEENEIPSCDLSNF | 1016 | Qy | 2025 | YDTTKVSYFYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTBEGMVARFEDYN | 2084 |
| Db | 958 | DGSFDLVTNGGIIILIRFERAPFITOEHTLWLWDRFPFVNMETIIMRHEENEIPSCDLSNF | 1017 | Db | 2023 | YDTTKVSYFYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTBEGMVARFEDYN | 2082 |
| Qy | 1017 | ARENPNVPSPLTSFASSCAKEGPIVPEIQALQEEIISGCKMRLSYLSRTPGYKSCLR | 1076 | Qy | 2085 | YDNSPRVTSQMAVINETPLPIDLYRYDDVSGKTEQFGKGVYVDINQIIITTAVMTHTKH | 2144 |
| Db | 1018 | ARENPNVPSPLTSFASSCAKEGPIVPEIQALQEEIISGCKMRLSYLSRTPGYKSCLR | 1077 | Db | 2083 | YDNSPRVTSQMAVINETPLPIDLYRYDDVSGKTEQFGKGVYVDINQIIITTAVMTHTKH | 2142 |
| Qy | 1077 | ISLTHPTIIPNLMKVHLMAVEGRLPKWFAPPAADLSYYFIWKTQVYNQKVGCLSEAFV | 1136 | Qy | 2145 | FDAYGRMKEVOVEIIFRSLMYMTVOYDNMGRVVKELKVGVPYANTTRYSEYDADGLOQT | 2204 |
| Db | 1078 | ISLTHPTIIPNLMKVHLMAVEGRLPKWFAPPAADLSYYFIWKTQVYNQKVGCLSEAFV | 1137 | Db | 2143 | FDAYGRMKEVOVEIIFRSLMYMTVOYDNMGRVVKELKVGVPYANTTRYSEYDADGLOQT | 2202 |
| Qy | 1137 | SVGYEYESCPDLLWEKRTTVLOQYEIDASKLGWSLDKHALNIOS-GTLHKNGENQF | 1195 | Qy | 2205 | VSINDKPLWRYSYDLNGLNHLSPGNSARLTPLRYDIRDIRITRLGDVQVYKMDDEGFLQR | 2264 |
| Db | 1138 | SVGYEYESCPDLLWEKRTTVLOQYEIDASKLGWSLDKHALNIOS-GTLHKNGENQF | 1197 | Db | 2203 | VSINDKPLWRYSYDLNGLNHLSPGNSARLTPLRYDIRDIRITRLGDVQVYKMDDEGFLQR | 2262 |
| Qy | 1196 | VSQOPPVIISGMNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYYVGDYFNIRIF | 1255 | Qy | 2265 | GGDIPEYNAGLIIKAYNRAGSWSVRYDGLGRRYSSKSSHHLQFFVADITNPTKVT | 2324 |
| Db | 1198 | VSQOPPVIISGMNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYYVGDYFNIRIF | 1257 | Db | 2263 | GGDIPEYNAGLIIKAYNRAGSWSVRYDGLGRRYSSKSSHHLQFFVADITNPTKVT | 2322 |
| Qy | 1256 | PSGNVTNILEL--RNKDFRSHSPAHKYIATDPMGSAVFLSDNSRRVFKIKSTVVVKD | 1313 | Qy | 2325 | HLYNHSSSETLSLYDLOQHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQLIYTA | 2384 |
| Db | 1258 | PSGNVTNILELRNKNDFRSHSPAHKYIATDPMGSAVFLSDNSRRVFKIKSTVVVKD | 1317 | Db | 2323 | HLYNHSSSETLSLYDLOQHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQLIYTA | 2382 |
| Qy | 1314 | LVKNSEVVAGTGDQCLPFDTRCDGGKATEATLTNPR--GITVDKFGLIYFVDTGTMIR | 1370 | Qy | 2385 | YGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRDYDVLAGRWTSPDHLMKHLSSNV | 2444 |
| Db | 1318 | LVKNSEVVAGTGDQCLPFDTRCDGGKATEATLTNPRGPPGITYDKFGLIYFVDTGTMIR | 1377 | Db | 2383 | YGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRDYDVLAGRWTSPDHLMKHLSSNV | 2442 |
| Qy | 1371 | RIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVR--LEWPTDLAINPMDNSLYVLDDN | 1427 | Qy | 2445 | MPENLYMFKNNPISNSODIKCFMTDVNSWLLTFGQLHNVI PGYKPKDMDAMEPSYELI | 2504 |
| Db | 1378 | RIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRQVHLEWPTDLAINPMDNSLYVLDDN | 1437 | Db | 2443 | MPENLYMFKNNPISNSODIKCFMTDVNSWLLTFGQLHNVI PGYKPKDMDAMEPSYELI | 2502 |
| Qy | 1428 | VVLQISENHQVRIVAGRPMECQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYTAETD | 1487 | Qy | 2505 | HTQMTQOEWDNSK-----SILGVQCEVQKQKAFVTLERFDQLYGSTITSQQAAPT | 2556 |
| Db | 1438 | VVLQISENHQVRIVAGRPMECQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYTAETD | 1497 | Db | 2503 | HTQMTQOEWDNSKVIIPAQCQSILGVQCEVQKQKAFVTLERFDQLYGSTITSQQAAPT | 2562 |
| Qy | 1488 | EKKNIRQVTTSGEISILVAGAPSGCDKNDANCDGSGDDGVAKADAKLNTPPSLVACAD | 1547 | Qy | 2557 | KKFASSGSVFGKGVKFPALXDGRVTDDIIISVANEDGRRVAAILNHAHYLENLHFTIDGVDT | 2616 |
| Db | 1498 | EKKNIRQVTTSGEISILVAGAPSGCDKNDANCDGSGDDGVAKADAKLNTPPSLVACAD | 1557 | Db | 2563 | KKFASSGSVFGKGVKFPALXDGRVTDDIIISVANEDGRRVAAILNHAHYLENLHFTIDGVDT | 2622 |
| Qy | 1548 | GELYVADLGNIRIFIRKNKPFPLNTQNNYELSSPIDQELYLFDTTGKHLTYQSILPTGDYL | 1607 | Qy | 2617 | HYVPKGPSEGDIAIILGSGRRTLENGVNVTVSQINTVLNGRTRTYTDIOLQYGALCLN | 2676 |
| Db | 1558 | GELYVADLGNIRIFIRKNKPFPLNTQNNYELSSPIDQELYLFDTTGKHLTYQSILPTGDYL | 1617 | Db | 2623 | HYVPKGPSEGDIAIILGSGRRTLENGVNVTVSQINTVLNGRTRTYTDIOLQYGALCLN | 2682 |
| Qy | 1608 | YNFTYTGDDITLITDNNGNVNRDSTGMLPLMLVVPDGGVYVWVTGNTSALKSVTTQG | 1667 | Qy | 2677 | TRYGTTLDREKARVLELQRAVRQAWAREQOBLREGEGLRAWTEGEKQOVLSTGRVQG | 2736 |
| Db | 1618 | YNFTYTGDDITLITDNNGNVNRDSTGMLPLMLVVPDGGVYVWVTGNTSALKSVTTQG | 1677 | Db | 2683 | TRYGTTLDREKARVLELQRAVRQAWAREQOBLREGEGLRAWTEGEKQOVLSTGRVQG | 2742 |
| Qy | 1668 | HELAMTYHGNISGLLATKSNENGWTTTFEYDVSFGLTNVTTFPGQVSSFRSDTSSVHVQ | 1727 | Qy | 2737 | YDGFVVISVEQYPELSDSANNIHFMRQSEMGRR 2769 | |
| Db | 1678 | HELAMTYHGNISGLLATKSNENGWTTTFEYDVSFGLTNVTTFPGQVSSFRSDTSSVHVQ | 1737 | Db | 2743 | YDGFVVISVEQYPELSDSANNIHFMRQSEMGRR 2775 | |
| Qy | 1728 | VETSSKDDVTITTNLSAGAFYITLLOQVRNSYIIGADGSLRLLLLANGMEVALQTEPHLL | 1787 | | | | |

; Sequence 82, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US20020155115A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 2771
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-808-602-82

Query Match 97.6%; Score 14529; DB 3; Length 2771;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 2688; Conservative 40; Mismatches 41; Indels 2; Gaps 1;

QY 1 MDVKERKPYRSTRTRRDARRYTSSADSEEGKAPKQSYSSSETLKYDQDARLAYGSRV 60
DB 1 MDVKERKPYRSTRTRRDARRYTSSADSEEGKQKQSYSSSETLKYDQDARLAYGSRV 60

QY 61 KDIVPOAEBCFRTGANFTLRLGLLEEVTPPHGTLYRTDGLPQCGYSGAGSDADMEAD 120
DB 61 KDWVPOAEBCFRTGNFTLRLGLGEMTPPHGTLYRTDGLPCHGYSAGSSADLEAD 120

QY 121 TVLSPEHPVRLNGRSTRGRSSCLSRANSNLTLTDTEHENTETDHPGLQNHARLTPP 180
DB 121 TVLSPEHPVRLNGRSTRGRSSCLSRANSNLTLTDTEHENTETDHPSSLQNHRLTPP 180

QY 181 PPLSHAHTNQHAASINSLNKGNFTPRNSPAPTDHSLGEPAGGAQPAHAQENWL 240
DB 181 PPLPHAHTNQHAASINSLNKGNFTPRNSPAPTDHSLGEPAGGAQPAHAQENWL 240

QY 241 LNSNIPLETRNLGKQFFLGTLDQNLIEMDILGASRDGAYSQDHPFKPGGTSPLFCCTS 300
DB 241 LNSNIPLETRNLGKQFFLGTLDQNLIEMDILSASRDGAYSQDHPFKPGGTSPLFCCTS 300

QY 301 PGVPLTSSVYSPPPRPLPRSTFAPAPNLKPKSKYCNWKAALSAIVISATLVLLAYF 360
DB 301 PGVPLTSSVYSPPPRPLPRSTFAPAPNLKPKSKYCNWKAALSAIVISATLVLLAYF 360

QY 361 VAMHFLGFWHLQMEG--QMYEITETASSVPVPTDVSYPGSGTGLETPDRKGKGTTE 418
DB 361 VAMHFLGFWHLQMEGQMYEITETASSVPVPTDVSYPGSGTGLETPDRKGKGAAB 420

QY 419 GKPSSEFPEDSDISGEIDVGRASQKTPPGTFMRSQVFIQHPVHLKFNVSIGKAALVGI 478
DB 421 GKPSSEFPEDSDISGEIDVGRASQKTPPGTFMRSQVFIQHPVHLKFNVSIGKAALVGI 480

QY 479 YQRKGLPPSHQTFDFVELLDGRLLTQEARSLLEGTPROSRGTVPPSSSHETGFIQVLDGI 538
DB 481 YQRKGLPPSHQTFDFVELLDGRLLTQEARSLLEGTPROSRGTVPPSSSHETGFIQVLDGI 540

QY 539 WHLAFYNDGKESEVVSFLTTAIESVDNCFNSYNGDCISGTCFGLGFLGPDGCRASCP 598
DB 541 WHLAFYNDGKESEVVSFLTTAIESVDNCFNSYNGDCISGTCFGLGFLGPDGCRASCP 600

QY 599 VLCSNGQYMKGRCLCHSGWKAECDDVPTNQCIDVACSNHGTCTGTCTICINPGYKGSCE 658
DB 599 VLCSNGQYMKGRCLCHSGWKAECDDVPTNQCIDVACSNHGTCTGTCTICINPGYKGSCE 658

DB 601 VLCSNGQYMKGRCLCHSGWKAECDDVPTNQCIDVACSSHGTCIMGTCTICINPGYKGSCE 660
QY 659 EVDKMDPTCSRGVGVVGECHCFVGMGTNCETPRATCLDQCSHGHTPLPDTGLCSDDPS 718
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QY 719 WTGHDCSTEICAADCGGHGVCVGGTCRCEDGMMGAACDQACHPRCAHBGTCRDKKCCS 778
DB 721 WTGHDCSTEICAADCGGHGVCVGGTCRCEDGMMGAACDQACHPRCAHBGTCRDKKCCS 780
QY 779 PGWNGEHTCTIAHYLDREVVKKEGCPGLCNGNGRCTLDLNGWHCVCLGMRGAGCDSMETAC 838
DB 781 PGWNGEHTCTIAHYLDREVVKKEGCPGLCNGNGRCTLDLNGWHCVCLGMRGAGCDSMETAC 840
QY 839 GDSKNDGDGLVDCMDPDCCLOPLCHINPLCLGSPNPLDIIQETQVPSQNLHSFVDRI 898
DB 841 GDGKNDGDGLVDCMDPDCCLOPLCHVNPCLGSPNPLDIIQETQVPSQNLHSFVDRI 900
QY 899 KFLVGRDSTHIIIPGENPFDGHCACVIRGOVMTSGTPLVGNISFVNPLFGYTIISQDG 958
DB 901 KFLVGRDSTHIIIPGENPFDGHCACVIRGOVMTSGTPLVGNISFVNPLFGYTIISQDG 960
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DB 961 SFDLVNTGGISIIILRFERAPFIIQETHTLWLPWDRFFVYMETIIMRHEBNEIPSCDLSNFAR 1020
QY 1019 PNPVVSPLTSPASSCAEKGPVPEIQALQEBEISISGCKMRLSYLSRTPGYKSVLRIS 1078
DB 1021 PNPVVSPLTSPASSCAEKGPVPEIQALQEBEISISGCKMRLSYLSRTPGYKSVLRIS 1080
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DB 1081 LTHPTIFPNLMKHLMAVAVEGRLPRKWFAPAAAPDLSYFIFWDKTDVYNQKVGFLSEAFVSU 1140
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QY 1199 QPPVIGSIMGNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDVNYIRRIIPSG 1258
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QY 1259 NVTNILELRNKDPFHSHSPAHKYYLATDPMGSAFVFLSDSNSRRVFKTKSTVVKDLVKNS 1318
DB 1261 NVTNILEMRNKDPFHSHSPAHKYYLATDPMGSAFVFLSDTNSRRVFKTKSTVVKDLVKNS 1320
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DB 1321 EVAGTGDDQLPDDTTRCGDGGKATEATLNPGRITVDFKGLIYFVDGTMIRRIDQNGII 1380
QY 1379 STLGSNDLTSAKPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLNNVVLQISENHQV 1438
DB 1381 STLGSNDLTSAKPLSCDSVNEISQVRLEWPTDLAINPMDNSLYVLNNVVLQISENHQV 1440
QY 1439 RIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKNIRIQVT 1498
DB 1441 RIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKNIRIQVT 1500
QY 1499 TSSEISLVAGAPSGCDCKNDANCDGAGYAKADAKLNTNPSSSLAVCADGELYVADLGN 1558
DB 1501 TSSEISLVAGAPSGCDCKNDANCDGAGYAKADAKLNTNPSSSLAVCADGELYVADLGN 1560
QY 1559 RIRFIRKNKPFNTQNMVELSSPIDQLYLFDTTGGKLYTQSLPTGDLNYFTYTGDDI 1618
DB 1561 RIRFIRKNKPFNTQNMVELSSPIDQLYLFDTTGGKLYTQSLPTGDLNYFTYTGDDI 1620
QY 1619 TLITDNNGNMVRSTGMPLWLVPDQGVYVMTGMTNSALKSVTTQGHELAMMTYHGN 1678
DB 1621 THITDNNGNMVRSTGMPLWLVPDQGVYVMTGMTNSALKSVTTQGHELAMMTYHGN 1680
QY 1679 SGLLATKSNENGTTFYEYDSFORLNTNPTQOVSSFRSDTSSVHVQVETSKDDVTI 1738
DB 1681 SGLLATKSNENGTTFYEYDSFORLNTNPTQOVSSFRSDTSSVHVQVETSKDDVTI 1740

QY 1739 TTNLASGAFYTLLODVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKR 1798
DB 1741 TTNLASGAFYTLLODVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKR 1800
QY 1799 NVTLPIDNGLNVEWRQKQARQGVTVFGRRRLRVHNRNLLSLDFORVTRTEKIYDDHRK 1858
DB 1801 NVTLPIDNGLNVEWRQKQARQGVTVFGRRRLRVHNRNLLSLDFORVTRTEKIYDDHRK 1860
QY 1859 FTLRILYDQAGRLSPSLSPSLRLGNVNTYSPGGVIAGIQGIMSERMEYDQAGRIISRIF 1918
DB 1861 FTLRILYDQAGRLSPSLSPSLRLGNVNTYSPGGVIAGIQGIMSERMEYDQAGRIISRIF 1920
QY 1919 ADGKTWYTYLXKSMVLLLSHQRYIFEFDKNDRLSSVTMPNVARQTLTIRSGYGRNI 1978
DB 1921 ADGKWSYTYLXKSMVLLLSHQRYIFEFDKNDRLSSVTMPNVARQTLTIRSGYGRNI 1980
QY 1979 YQPPEGNASVIQDPTDGHLLHTFYLGTGRVYKYKLSKLAETLYDITTKVSFTYDETA 2038
DB 1981 YQPPEGNASVIQDPTDGHLLHTFYLGTGRVYKYKLSKLAETLYDITTKVSFTYDETA 2040
QY 2039 GMLKTINLQNEGFTCTIRYQIGPLIDROJIFRFTTEGKVNARPDYNDNSFRVTSQAVI 2098
DB 2041 GMLKTINLQNEGFTCTIRYQIGPLIDROJIFRFTTEGKVNARPDYNDNSFRVTSQAVI 2100
QY 2099 NETPLPIDLYDDVSKTEQFGKFGVIYDINOIITAVMTHTKHFDAYGRMKEVOYEI 2158
DB 2101 NETPLPIDLYDDVSKTEQFGKFGVIYDINOIITAVMTHTKHFDAYGRMKEVOYEI 2160
QY 2159 FRSLMYWMTVQYDNMGVRVKKELKVPYANTTRYSYEYDADGQLQTVSINDKPLWRYSD 2218
DB 2161 FRSLMYWMTVQYDNMGVRVKKELKVPYANTTRYSYEYDADGQLQTVSINDKPLWRYSD 2220
QY 2219 LKGNLHLLSPGNSARLTPRYDIDRITRLGDVQYKMDGFLRQCGDIFEYNSAGLLI 2278
DB 2221 LKGNLHLLSPGNSARLTPRYDIDRITRLGDVQYKMDGFLRQCGDIFEYNSAGLLI 2280
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DB 2281 KAYNRAGWSVRYRYDGLGRVSSKSHHLQFPFYADLTNPTKVTHLYNHSSEITSY 2340
QY 2339 YDLQGLFAMELSSGDFYIACDNIGTFLAVFSGTGLMIKQILLYTAYGEIYMDTNPFI 2398
DB 2341 YDLQGLFAMELSSGDFYIACDNIGTFLAVFSGTGLMIKQILLYTAYGEIYMDTNPFI 2400
QY 2399 IIGYHGGLYDPLTKLVHMGRRDYDLVLAGRWTSPDHLEWKLSSNVMPFNLYMFKNNPI 2458
DB 2401 IIGYHGGLYDPLTKLVHMGRRDYDLVLAGRWTSPDHLEWKLSSNVMPFNLYMFKNNPI 2460
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DB 2461 SNSODIKCFMTDVNSWLLTFQGLHNVIPGYPKPDMAMEPSYELIHTQMTQSDWNSKS 2520
QY 2519 ILGVQCEVQKQKAFVTLERDQLYGSTITSCQAPKTKFPASSGSVFGKGVKFAKDGR 2578
DB 2521 ILGVQCEVQKQKAFVTLERDQLYGSTITSCQAPKTKFPASSGSVFGKGVKFAKDGR 2580
QY 2579 VTTDIIISVANEDGRRAAILNNAHYLENLHFTIDGVTHYVFKPGPSEGDLAILGLSGGR 2638
DB 2581 VTTDIIISVANEDGRRAAILNNAHYLENLHFTIDGVTHYVFKPGPSEGDLAILGLSGGR 2640
QY 2639 RTLENGVNTVQINTVLNGTRRYTDIOLOYGALCLNTRYGTTLDREKARVLELARORA 2698
DB 2641 RTLENGVNTVQINTVLNGTRRYTDIOLOYGALCLNTRYGTTLDREKARVLELARORA 2700
QY 2699 VRQAWARQOQLREGEGLRAWTEGEKQOVLSTGRVQGYDGFVVISVEQYPELSDSANNI 2758
DB 2701 VRQAWARQOQLREGEGLRAWTEGEKQOVLSTGRVQGYDGFVVISVEQYPELSDSANNI 2760
QY 2759 HFMRSQSEMR 2769
DB 2761 HFMRSQSEMR 2771

RESULT 6
US-09-800-198-70
; Sequence 70, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Cornie AM
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herkmann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 2771
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-800-198-70

Query Match 97.6%; Score 14529; DB 3; Length 2771;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 2689; Conservative 40; Mismatches 41; Indels 2; Gaps 1;

QY 1 MDVKERKPYRSLTRRRDAERRYTSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
DB 1 MDVKERKPYRSLTRRRDAERYTSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
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DB 61 KDMVPQAEAEFCRTGNFTLRELGLGEMTPPHGLTVRTDGLQCGYSGMAGSDADHEAD 120
QY 121 TVLSPEHPVRLWGRSTRSGRSSCLSSPANSNLTDTTEHENTETDHPGGIQLNHARLTTP 180
DB 121 TVLSPEHPVRLWGRSTRSGRSSCLSSPANSNLTDTTEHENTETDHPGGIQLNHARLTTP 180
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DB 181 PPLPHAHTPNQHAASINSLNRGNFTPRSNPSPAPTDHLSLGGPPAGGAQEPHAQAQNW 240
QY 241 LNSNI PLETRNLGKQPFGLTLDNLIEMDILGASRHDGAYSDGHFLPKPGGTSPLFCTTS 300
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QY 301 PGYPLTSSVTYSPPPRPLPRSTFARPAFNLLKPSKYNWKAALSAITVILLAYF 360
DB 301 PGYPLTSSVTYSPPPRPLPRSTFARPAFNLLKPSKYNWKAALSAITVILLAYF 360
QY 361 VAMHLFGLNHLQPMEG- -QMYETTEDTASSWPVPTDVSLYPSGGTGLETPDRKKGKYTE 418
DB 361 VAMHLFGLNHLQPMEGQMYETTEDTASSWPVPTDVSLYPSGGTGLETPDRKKGKAAE 420
QY 419 GKPSSEFPEDSFIDSGEIDVGRASQKIPPGTFTWRSQVFDHPVHLKFNVSGLKAALVGI 478
DB 421 GKPSSEFPEDSFIDSGEIDVGRASQKIPPGTFTWRSQVFDHPVHLKFNVSGLKAALVGI 480
QY 479 YGRKGLPPSHTQDQFVLLDGRLLLTQEARSLGCTPQSRGTVPSPSHETGFIQYLDOSGI 538
DB 481 YGRKGLPPSHTQDQFVLLDGRLLLTQEARSLGCTPQSRGTVPSPSHETGFIQYLDOSGI 540
QY 539 WHLAFYNDGKSESEVVSFLTTAIESVDNCPNCGVNGDCISGTCHCFGLGPDGCRASCP 598
DB 541 WHLAFYNDGKSESEVVSFLTTAIESVDNCPNCGVNGDCISGTCHCFGLGPDGCRASCP 600
QY 599 VLCSGNQYMKGRCLCHSGWKGAECVDVPTNQCIDVACSNHGTCTGTCTCNPGYKGSCE 658

Db 601 VILCSNGQYMKGRCLCHSKWGAECVPTNQCIDVACSSHGTCIMGTCLCNPGYKGSCE 660
QY 659 EVDCHMDPTCSRGVGVCRGCHCFVGVGGTNCETPRATCLDQCSHGHTFLPDTGLCSDPS 718
Db 661 EVDCHMDPTCSRGVGVCRGCHCSVGVGGTNCETPRATCLDQCSHGHTFLPDTGLCNCDDPS 720
QY 719 WTGHDCSIEICAADCGGHGVCVGGTCRCEDGHWGAACDORACHPCABEHGTCRCCKCECS 778
Db 721 WTGHDCSIEICAADCGGHGVCVGGTCRCEDGHWGAACDORACHPCABEHGTCRCCKCECS 780
QY 779 PGWNGEHCTIAHYLDVRVKEGCPGLCNGNGRCTLDLNGWHVCVQLGWRGAGCDTSMETAC 838
Db 781 PGWNGEHCTIAHYLDVRVKEGCPGLCNGNGRCTLDLNGWHVCVQLGWRGAGCDTSMETGC 840
QY 839 GSKONDDGLVDCMDPCCLQPLCHINPLCLGSPNPLDIIQETQVPVPSQQMLHGFYDRI 898
Db 841 GSKONDDGLVDCMDPCCLQPLCHVNPCLCLGSPDPLDIIQETQAPVSQQNLNPFYDRI 900
QY 899 KEFLVGRDSTHIIIPGENPPDGGHACVIRGOVMTSDGTPLVGVNISFVNPNPLFCYTTISRODG 958
Db 901 KEFLVGRDSTHIIIPGENPPDGGHACVIRGOVMTSDGTPLVGVNISFINNPLPFGYTTISRODG 960
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Db 961 SFDLVNTGGISIIILPERAPFITQEBHTLWLPMDRFFVMEETIIMRHEENEIPSCDLSNFAR 1020
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Db 1021 PNPVSPSPLTSPASSCAEBGPIVPEIQALQBEISISGCKMRLSYLSRTPGYKSVLRIS 1080
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QY 1199 QPVTGSIINGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSIYVGDVFNIRIPFSG 1258
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QY 1559 RIRFIRKKNPFLNTQMYELSPIDQELYLFTTGKHLVYQSLPTGVDLYNFTYTGDDGI 1618
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QY 1619 TLIITDNGNMVNRDSTGMPMLVVPDGOVYVMTGTNSALKSVTTQGHELAMMTYHGN 1678
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Db 1681 SGLLATKSNENGWTTTFYEDSFGRLTNVTFPTGOVSSFRSDTSSHVHVQVETSSKDDVTI 1740
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QY 1859 FTLRILYDQAGRPSSLSPSSRLNGVNTYSPGGYIAGIQRIGIMSERMEYDQAGRITSRIF 1918
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QY 1919 ADGKTWSTYILEKSMVLLHLSORQYIPEFDKNDRLSSVTMBNVAROTLETIRSVGYVYNI 1978
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QY 1979 YQPEGNASVIQDFTEDGHLHHTFYLGTGRVVIYKYGKLSKLAETLYDTTTKVSFTYDETA 2038
Db 1981 YQPEGNASVIQDFTEDGHLHHTFYLGTGRVVIYKYGKLSKLAETLYDTTTKVSFTYDETA 2040
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Db 2041 GMLKTIINLQNEGFTCTIRYRQIGPLIDRQIPRFTBEGMVNARFDYNDNSPRVTSMQAVI 2100
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Db 2161 FRSLMYNMTVOYDNMGVWVKELKVGYPYANTTRYSYEYDADGQLOTVSINDKPLWRYSYD 2220
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QY 2279 KAYNRASWSVRYRVDGLGRRVSSKSSHHLQFADLTNPTKVTHLYNHSSSEITSLY 2338
Db 2281 KAYNRASWSVRYRVDGLGRRVSSKSSHHLQFADLTNPTKVTHLYNHSSSEITSLY 2340
QY 2339 YDLQGLHLPAMELSSGDEFYIACDNIGTFLAVFSGTGLMIKQILYATGEIYMDTNPNFQI 2398
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Db 2401 IIGYHGGLYDPLTKLVHMGRRDYDLVLAGRWTSDPHELWKHLSSNVIPFHLMPKNNNPI 2460
QY 2459 SNSODIKCFWTDVNSWLLTTFGQLHNVIPGYPKPDMDAMESYELIHTOMKTOEWDNSKS 2518
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QY 2579 VTTDIIISVANEDGRRVAAIILNHAHYLENLHPTIDGVTHYFVKPSPSEGDALAILGLSGGR 2638
Db 2581 VTTDIIISVANEDGRRVAAIILNHAHYLENLHPTIDGVTHYFVKPSPSEGDALAILGLSGGR 2640
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Db 2641 RTLENGVNTVSOINTVLNGRTRYTDIOLQYGCALCLNTRYGTTLDDEKARVLEIARORA 2700
QY 2699 VROAWAREQORLRGEBGLRAWTEGEKQVVLSTGRVQYDGFVVISVEQYPELSDSANNI 2758
Db 2701 VROAWAREQORLRGEBGLRAWTEGEKQVVLSTGRVQYDGFVVISVEQYPELSDSANNI 2760
QY 2759 HFMRQSEMGRR 2769
Db 2761 HFMRQSEMGRR 2771

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RESULT 7
US-10-042-865-2
; Sequence 2, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangoli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2794
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-042-865-2

Query Match 96.8%; Score 14406.5; DB 4; Length 2794;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 2704; Conservative 21; Mismatches 41; Indels 31; Gaps 11;

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Db 61 KDIVPQAEFCRTGANFTLRELGLEEVTTPHGTLYRTDGLPCGYSMGAGSDADMEAD 120
Qy 121 TVLSPEHPVRLWGRSTRSGRSCSSLRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180
Db 121 TVLSPEHPVRLWGRSTRSGRSCSSLRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180
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Db 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGBPAPAGGAQEPAAHQAENWL 240
Qy 241 LNSNIPLERNLGKQPFLGTLQDNLIEMDILGASRHDGAYS DGHFUKPGGTSPLFCFCTS 300
Db 241 LNSNIPLERNLGKQPFLGTLQDNLIEMDILGASRHDGAYS DGHFUKPGGTSPLFCFCTS 300
Qy 301 PGYPLTSSVTYSPPPPLPRSPFARFNLKPKSKYCNMKCAALSALVATVILLAYF 360
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Qy 361 VAMHFLGLNWLQPMEGOMYEITETASSWPVPTDVSLYPSGGTGLTETPRKKGKGTTEGK 420
Db 361 VAMHFLGLNWLQPMEGOMYEITETASSWPVPTDVSLYPSGGTGLTETPRKKGKGTTEGK 420
Qy 421 PSSFFPEDSFIDSGEIDVGRRASOKIPPGTFWRSQVFIIDHPVHLKFNVSGLKAALVGIYG 480
Db 421 PSSFFPEASGIDSGEIDVGRRASOKIPPGTFWRSQVFIIDHPVHLKFNVSGLKAALVGIYG 480
Qy 481 RKGLPFSHTQDFVELLDGRRLLTOBARSLEGTPROSRGTVPSSSHETGFIQYLDSDGIWH 540
Db 481 RKGLPFSHTQDFVELLDGRRLLTOBARSLEGTPROSRGTVPSSSHETGFIQYLDSDGIWH 540
Qy 541 LAFYNDGKESEVVSFLTATAESVNDNCPSNCGNGDCISGTCFGLGFLGPDCCGRASCPVL 600
Db 541 LAFYNDGKESEVVSFLTATAESVNDNCPSNCGNGDCISGTCFGLGFLGPDCCGRASCPVL 600
Qy 601 CSGNGQYMKGRCLCHSGWGAECDVPTNQCIDVACSNHGTCTTGTCICNPGYKGESCEEV 660
Db 601 CSGNGQYMKGRCLCHSGWGAECDVPTNQCIDVACSNHGTCTTGTCICNPGYKGESCEEV 660
Qy 661 DCMPTCSRGVGVRCBCHFCVGGTNCETPRATCLDQCSHGTFPLDGLCSCDSWT 720
Db 661 DCMPTCSRGVGVRCBCHFCVGGTNCETPRATCLDQCSHGTFPLDGLCSCDSWT 720
Qy 721 GHDCSIEICAAACGGHGVCGGTCCEDGMMGAACDORACHPRCAEHGTCRDGKCECSPG 780
Db 721 GHDCSIEICAAACGGHGVCGGTCCEDGMMGAACDORACHPRCAEHGTCRDGKCECSPG 780
Qy 781 WNGEHCTI--AHYLDRVK--EGCPGLCNGNGRCTLDLNMGHVCVQLGWRGAGCDTSMET 836
Db 781 WNGEHCTI--AHYLDRVK--EGCPGLCNGNGRCTLDLNMGHVCVQLGWRGAGCDTSMET 836
Qy 837 ACSDSKNDGDGLVDCMDPCCLOPLCHINPLCLGSPNPLDIIQETQVPSQQNLHGFYD 896
Db 837 ACSDSKNDGDGLVDCMDPCCLOPLCHINPLCLGSPNPLDIIQETQVPSQQNLHGFYD 896
Qy 897 RIKPLVGRDSTHIIIPGENPFDGGHACVIRQVMTSDGTPLVGVNISPNNPLFGYTISRQ 956
Db 897 RIKPLVGRDSTHIIIPGENPFDGGHACVIRQVMTSDGTPLVGVNISPNNPLFGYTISRQ 956
Qy 957 DGSFDLVTNGGIIILRERAPFITQHTLWLWDRFVFMETIIMRHEENIPSCDLSNF 1016
Db 957 DGSFDLVTNGGIIILRERAPFITQHTLWLWDRFVFMETIIMRHEENIPSCDLSNF 1016
Qy 1017 ARNPVVPSPPLTSFASSCAEKGPVPEIQALQBEISISCKMKRLSYLSRSTPGYKSVLR 1076
Db 1017 ARNPVVPSPPLTSFASSCAEKGPVPEIQALQBEISISCKMKRLSYLSRSTPGYKSVLR 1076
Qy 1077 ISLTHPTIPENLMKVLHMAVEGRLPFKFAAADPLSYFIWDKTDVYNNOKVFCLSAFAV 1136
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Qy 1137 SVGYEYESCPDLILWEKRTTVLQGYEIDASKGWSLDKHALNIQS--GILHKGNGENQF 1195
Db 1137 SVGYEYESCPDLILWEKRTTVLQGYEIDASKGWSLDKHALNIQS--GILHKGNGENQF 1195
Qy 1196 VSQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDVFIIRIF 1255
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Qy 1257 VSQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDVFIIRIF 1257
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QY 1256 PSNVNTHLEL--RNKDPHSHSPAHHYLYLATDPMGAVFLSDNSRRVFKIKSTVVVKD 1313
DB 1258 PSNVNTHLELRVRNKDFRHSHPAHHYLYLATDPMGAVFLSDNSRRVFKIKSTVVVKD 1317
QY 1314 LVKNSEVAGTGQCLPFDDTRCGDGKATEATLTNPR---GITVDKFGLIYFVDTMTIR 1370
DB 1318 LVKNSEVAGTGQCLPFDDTRCGDGKATEATLTNPRGPPGITYVDKFGLIYFVDTMTIR 1377
QY 1371 RIDQNGIISTLGSNDLTSGARPLSCDSVMDISQVR---LEWPTDLAINPMDNSLYVLNN 1427
DB 1378 RIDQNGIISTLGSNDLTSGARPLSCDSVMDISQVRQVHLEWPTDLAINPMDNSLYVLNN 1437
QY 1428 VUQISENHQVRIVACRPHMCQVPGIDHFLSKVAIHATLESATALAVSHNGVLYAETD 1487
DB 1438 VUQISENHQVRIVACRPHMCQVPGIDHFLSKVAIHATLESATALAVSHNGVLYAETD 1497
QY 1488 EKKINRIQVTTSGEISLVAGAPSGCDCKNDANCDFSGDDGYAKDAKLNTPSSLAVCAD 1547
DB 1498 EKKINRIQVTTSGEISLVAGAPSGCDCKNDANCDFSGDDGYAKDAKLNTPSSLAVCAD 1557
QY 1548 GELYVADLGNIRIRFKKPKPLNTQMYELSPIDQELYLFDTTGKHLIYTOSLPTGDYL 1607
DB 1558 GELYVADLGNIRIRFKKPKPLNTQMYELSPIDQELYLFDTTGKHLIYTOSLPTGDYL 1617
QY 1608 YNFTYTGDDGITLITDNNGMVNVRRDSTGMPLMLVVPDQVYVMTGNTNSALKSVTTQG 1667
DB 1618 YNFTYTGDDGITLITDNNGMVNVRRDSTGMPLMLVVPDQVYVMTGNTNSALKSVTTQG 1677
QY 1668 HELAMWYHNGSGLATKSNENGTTFYBDFSGRLTNVTPFTQGVSPRSDTSSVHVQ 1727
DB 1678 HELAMWYHNGSGLATKSNENGTTFYBDFSGRLTNVTPFTQGVSPRSDTSSVHVQ 1737
QY 1728 VETSSKDDVTITNLSASAFYTLQDOVRNSYIIGADGSLRLLANGMEVALQTEPHLL 1787
DB 1738 VETSSKDDVTITNLSASAFYTLQDOVRNSYIIGADGSLRLLANGMEVALQTEPHLL 1797
QY 1788 AGTVNPTVGRNVNTPIDNGLNLVWQRKEAQGVTVFGRRLR---VHNRLNLSLDFD 1844
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QY 1845 RVTRTEKIYDDHKKFTLRILYDQAGRPSLWSPSSRLNGVNVYSPGGYIAGIQGIMSER 1904
DB 1858 RVTRTEKIYDDHKKFTLRILYDQAGRPSLWSPSSRLNGVNVYSPGGYIAGIQGIMSER 1917
QY 1905 MEYDOAGRTISRIFADGKTWSYTYLEK---SMVLLLSQROYIPEFDKNDRLSSVTMPN 1960
DB 1918 MEYDOAGRTISRIFADGKTWSYTYLEKAGVQSMVLLLSQROYIPEFDKNDRLSSVTMPN 1977
QY 1961 VARQTLTIRSVGYRNIIQPPEGNASVIQDFTEDGHLHTFYLGTGRRVIYKYGKLSKL 2020
DB 1978 VARQTLTIRSVGYRNIIQPPEGNASVIQDFTEDGHLHTFYLGTGRRVIYKYGKLSKL 2037
QY 2021 AETLYDVTTKVSTYDETAGMLKTIINLQNEGFTCTIRYQIGPLIDRQIFRTEEGMVNAR 2080
DB 2038 AETLYDVTTKVSTYDETAGMLKTIINLQNEGFTCTIRYQIGPLIDRQIFRTEEGMVNAR 2097
QY 2081 FQYNDNSFRVTSMAOVINETPLPDLVRYDDVSGKTEQFGKFGVIYVDINQIITTAVMT 2140
DB 2098 FQYNDNSFRVTSMAOVINETPLPDLVRYDDVSGKTEQFGKFGVIYVDINQIITTAVMT 2157
QY 2141 HTKHFDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVKKELKVGYPYANTTRYSEYDADG 2200
DB 2158 HTKHFDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVKKELKVGYPYANTTRYSEYDADG 2217
QY 2201 QLOTVSIINDKPLWRYSDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEGF 2260
DB 2218 QLOTVSIINDKPLWRYSDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEGF 2277
QY 2261 LRQRGDDIFEYNSAGLLIKAYNRAGSWSVRYRQDGLGRVSKSHSHHLOFFFYADLTNP 2320
DB 2278 LRQRGDDIFEYNSAGLLIKAYNRAGSWSVRYRQDGLGRVSKSHSHHLOFFFYADLTNP 2337

QY 2321 TKVTHLYNHSSEITSLYYDLQGHLFAMELSSGDEFYIACDNIPTGLAVFSGTGLMIKOI 2380
DB 2338 TKVTHLYNHSSEITSLYYDLQGHLFAMELSSGDEFYIACDNIPTGLAVFSGTGLMIKOI 2397
QY 2381 LYTAYGEIYMDTNFNFOIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHLELWKHLS 2440
DB 2398 LYTAYGEIYMDTNFNFOIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHLELWKHLS 2457
QY 2441 SSNVMPNLYNFKKNNPISNSQDIKCFMTDVNSMLLTFGOLFHNVIPOGYPKPDMDAMEPS 2500
DB 2458 SSNVMPNLYNFKKNNPISNSQDIKCFMTDVNSMLLTFGOLFHNVIPOGYPKPDMDAMEPS 2517
QY 2501 YELIHTQKTKTEWPNK-----SILGVOCEVQKOLKAPVTILERPDOLYGSTITSQOQ 2552
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QY 2553 APKTKKFASSGSVFGKGVKFKALDKGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTID 2612
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DB 2638 GVDTHYFVKPSPSGDLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRTYDILQLOYGA 2697
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DB 2698 LCLNTRYGTTLDDEKARVLELQARAVRQAWARQORLREGEGLRAWTEGEKQOVLSTG 2757
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DB 2758 RVQCYDGFVVISVQYPELSDSANNIHFMRQSEMGRR 2794

RESULT 8

US-10-042-865-52
; Sequence 52, Application US/10042865
; Publication No. US20040029216A1

GENERAL INFORMATION:

; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
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; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417

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; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 52
; LENGTH: 2715
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-042-865--52

Query Match      68.7%; Score 10227; DB 4; Length 2715;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 1864; Conservative 370; Mismatches 457; Indels 102; Gaps 19;

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Qy 58 SRVKDIYPOEAEEFCRTGANFTLRELGLEEVTPPHGTLVYRTDGLPCQGYMGAGSDADM 117
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Qy 118 EADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHN---TETDHPGLQNH 174
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Qy 231 -EPAAHQENWLLNSINPLETRNLGKQPLFLGTLDNLNLEMDILGASRHGDAYSDGHFLFKP 289
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Db 230 PESVLQDQSVWLVGNSVPLESR-----HFLFKT 256
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Qy 290 G-GTSPFLCFTTSPGYPLTSTVTSPPPRPLPRSTFARPAFLNKKPKSKYCNWKAALS 348
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Db 317 VSVLLAILLSYFIAMHLFGLNWHLQQTENDTFENGKVNSDT-----VPTNTVSLPSG-- 368
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Db 369 -----DNGKLGFTHENNTIDSGELDIDGRRAIQEVPPGIFWRSQLFIDQPOFLK 417
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Db 598 CACNSGYKGENCEADCLDPCCSNHGVCIHGECHCNFGWGSNCIEILKTCWADQCSGHT 657
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Qy 706 FLPDTGLCSDPSTGHDGCSIEICAADCGGHGVCGVGTGTCEDGWMGAACDQRACHPRCA 765
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Db 658 YLQESSGCTCDPNWTGTPDCSNEICSVDCSGSHGVCMWGSRCCEEGMTGPACNQRACHPRCA 717
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Db 718 EHGTCRDGKCECSPGMNGBEHCTIAHYLDKIVKEGCGPLCNSNGRCCTLDQNGHVCVQPGW 777
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Qy 886 VSQOQLHSFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLGVNLSFVN 945
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Db 838 PSQQAASFYDRI SFLIGSDSTHVLPGESPFNKSLASVIRGOVLTADGTPLIGVNVSLH 897
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Qy 946 NPLFGYTIQRQGSFDLVNNGISIIILRPERAPPTQEHNTLMLPWRFPFMTIIRHBE 1005
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Db 898 YSEYGYTITRQDGMFPLVANGASLTLPERSPFLTYHTVWIPMWVFMVMDLVNKKBE 957
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    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1066 SRTPGVKSVLRISLTHPTIPFNLKVLMAVEGRFLRKWFAAAPOLSYFFIWDKTDVYN 1125
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1018 SRAAGYKSVLKTMTQAVIPFNLKVLMAVVGRLFKQKFPASPPLATYFFIWDKTDAYN 1077
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1126 QKVFGLEAFVSVGYEYESCPDLILWEKRTTVLQGYEIDASKLGGWSLDRKHALNTQSGI 1185
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1078 QKVYGLSEAVSVVGYEYESCLDLTLWEKRTAVLQGYELDASNNMGWTLDKHHVLDVQNGI 1137
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1186 LHKNGENQFVSQOPPVIGSIMNGRRRSISCPSCNGLADGNKLLAPALVATCGSDGLYV 1245
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1138 LYKNGENQFISQOPPVVSSIMNGRRRSISCPSCNGQADGNKLLAPALVACGIDGLYV 1197
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1246 GDFNYIRRIIPPSGNVTNILELRNKPFRHSHSPAHKYLLATDPMGSAVFLSDSNSRRVFKI 1305
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1198 GDFNYIRRIIPPSGNVTNILELRNKPFRHSHSNPAHRYLLATDPTGDLVSDTNTTIRYR 1257
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1306 KSTVVVVKLVKNSVAVAGTGDQCLPDDTRCGDGGKATBATLNPRGITVDKFLIYFVD 1365
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1258 KSLTGAKDLTKNAEVVAGTGEQCLPFDEARCGDGGKAVEATLMSPKGMAIDKNGLIYFVD 1317
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1366 GTMIRIDONGIISTLLGNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMNSLVLD 1425
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1318 GTMIRVQDNGIISTLLGNDLTSARPLSCDTSMHISQVRLEWPTDLAINPMNSIYVLD 1377
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1426 NNVLQIISNHQVRIVAGRPMHCOVPGIDHFLLSKVAIATLESATALAVSHNGVLYIAE 1485
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1378 NNVLQITENRQVRIAGRPMHCOVPGV-YPVGKIAVQTTLESATAIAIVSGVLYITE 1436
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1486 TDEKKNIRQVTTSGEISLVAGAPSGCDCKNDANCDGSGDGYAKADAKLNTPSSLAVC 1545
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1437 TDEKKNIRQVTTDGEISLVAGIPSECDCKNDANCDGSGDGYAKADAKLNAAPSSLAAS 1496
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1546 ADGELVADLGNIRIRFIRKNRPFNTONMYELSSPIDQELYLFDITGKHLITQSLPTGD 1605
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1497 PDGTLTIADLGNIRIRAVSKNPKLLNSMNFYVASPTDQELYIPDINGTHQYTVSLVTD 1556
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1606 YLNFYTYTGDGDTLITDNNGNMNVYRDSGTGMLVLPDGOVYVYVMTGNTSALKSVTT 1665
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1557 YLNFYSYNDNDVATVDSNGNTLRIRRDNRNMPRVVSPDNQVIMLTIGTNGCLKSMTA 1616
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1666 QGHELAMMTYHNGSGLLATKSNENGMTTFYEDYSFGRLTNVTPTQGVSSFRSDTSSVH 1725
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1617 QGLLELVLFYHNGSGLLATKSDETGTTTFDYDSEGRLLTNVTFTGVVTLHGDMDKAIT 1676
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1726 VQVETSSK-DDVTITNLSAGAFYTLQDQVNSYIIGADGSIIRLLLANGMEVALQTEP 1784
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1677 VDIESSRREBDVSITNSLSDISFYTMVQDLNRSYQIGYDGLRIFAYASGLDSSHQYTEP 1736
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1785 HLAGTVPNTVGRKNTLPIDNGLNIVEMRQEQARGOVTVFGRRLRVHNRNLLSLDFFD 1844
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1737 HVLAGTANPTVAKRNTLPGENQNLVEMRFRKEAQKQVNVFGRKLRVGNRNLSSVDFD 1796
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 1845 RVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVITYSPGYIAGIQRMISER 1904
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 1797 RTTKTEKLYDDHRKFLRLRIAYDTSCHPTLWLPSSKLMANNVTVSSGTQIASQRTGTSBK 1856
Qy 1905 MEYDQAGRITSRIPADGKTSWYTYLEKSMVLLHSHQRYIFEPDKNDRLSSVTMPNVARQ 1964
Db 1857 VDYSQGRIVSRVFAADGKTSWYTYLEKSMVLLHSHQRYIFEDMDRLSAITMPSVARH 1916
Qy 1965 TLETIRSVGYRNITQOPPEGNASVIOFTEDGHLLHTFVLTGRRVYIKYKLSKUAETL 2024
Db 1917 TMTOTIRSIGYRNINYPPEASNAIITDYNEBEGLLQTAFLGTSRRVLFYRRQTRLSEIL 1976
Qy 2025 YDTTKVSFTYDETAGMLKTNLQNEGTCTIRYRQIGPLIDROIPTFTBEGMVNARFDYN 2084
Db 1977 YDSTRVSFTYDETAGVLKTNVLSQDGFICTIRYRQIGPLIDROIPTFTBEGMVNARFDYS 2036
Qy 2085 YDNSFRVTSQAVINETPLPIDLYRVDVSGTEQFGKFGVYIYDINQIITAVMPTTKH 2144
Db 2037 YDNSFRVTSQGVINETPLPIDLYQFDDISGKVEQFGVYIYDINQIITAVMPTTKH 2096
Qy 2145 FDAYGRMKEVOYEIIFSLMVMYTVQDNNMGRVVKKELKVPYANTTRYSEYVDAGLOLT 2204
Db 2097 FDAHGRKEIYQYEIFSLMVMYTVQDNNMGRVVKKELKVPYANTTRYSEYVDAGLOLT 2156
Qy 2205 VSINDKPLMRYSDYDLNGLNLLSPGNSARLITPLRYDIRITRLGVDVQYKMDDEDFLQR 2264
Db 2157 VYLNKIMRYNDYDLNGLNLLSPGNSARLITPLRYDIRITRLGVDVQYKMDDEDFLQR 2216
Qy 2265 GGDIFPYNAGLLIKAYNRAGSWVRVYDGLGRRVSSKSHHLOFFYADLTNPTKVT 2324
Db 2217 GTEIFYSKGLLTRYVSGMGTVIYRYDGLGRRVSSKSHHLOFFYADLTNPTKVT 2276
Qy 2325 HLYNHSSEITSLYDLOGLHFAELSSGDEFVIAACDNIGTPLAVFSGTGLMIKILYTA 2384
Db 2277 HLYNHSSEITSLYDLOGLHFAELSSGDEFVIAACDNIGTPLAVFSGTGLMIKILYTA 2336
Qy 2385 YGEIYNMTPNFQIITGYHGGLYDPLTKLVHMRDYYDLVAGRWTSPOHMLKHLSSNV 2444
Db 2337 YGEIYFDSNVDFQVIFGHGGLYDPLTKLVHMRDYYDLVAGRWTSPOHMLKHLSSNV 2395
Qy 2445 MPNLVMPKNNPISNSQDIKCFMTDVSNSLWLTGFGOLHNVIPGYKPDMDAMEPSYELI 2504
Db 2396 APNLVMPKNNPISNSQDIKCFMTDVSNSLWLTGFGOLHNVIPGYKPDMDAMEPSYELI 2455
Qy 2505 HTQMTQWENDSKSLGVQCEVQKQKAFVTLERFDQLYGTSITSCQAPKTK----- 2558
Db 2456 -----KSQWEDVPPFVGVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 2502
Qy 2559 --PASSGSVFGKVKFALKDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVD 2616
Db 2503 LMFATVKSLSIGKVMWLVASQGRVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 2562
Qy 2617 HYFVKPGPSEGDLAILGLSGRRRTLENGVNVTVSQTINTVLRGTRRYTDIOLQVGCALCN 2676
Db 2563 HYFIKTTTPESDLTGTLRLTSGRKALENGVNVTVSQTINTVLRGTRRYTDIOLQVGCALCN 2622
Qy 2677 TRYGTTLDBEKARVLELAFQRAVQAWAREQQRLREGEGLRAMTEGEKQQLVSTGRVQG 2736
Db 2623 VRYGTMTLDBEKARVLELAFQRAVQAWAREQQRLREGEGLRAMTEGEKQQLVSTGRVQG 2682
Qy 2737 YDGFVVISVEYQYPELSDSANNHFMROSEMGR 2769
Db 2683 YDGYVVLVSVEYQYPELSDSANNHFMROSEMGR 2715
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RESULT 9

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US-10-029-020-51
; Sequence 51, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
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; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 51
; LENGTH: 2715
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-029-020-51

Query Match 69.7%; Score 10227; DB 4; Length 2715;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 1864; Conservative 370; Mismatches 457; Indels 102; Gaps 19;

Qy 1 MDVKERPKYSLTR-RDAERRVYTSADSEEGKAP-OXSYSSSETLKAYDQD-ARLAYG 57
Db 1 MDVKERPKYSLTR-RDAERRVYTSADSEEGKAP-OXSYSSSETLKAYDQD-ARLAYG 57
Qy 58 SRVKDIPQBAEFCRTGANFTLRLELCEEVTPPHGTYLRTDGLPCQGYSMGASDAD 117
Db 61 NRVKDLVHREADEVTGQGNFTLRQLGVCSATRGVAFCAEMGLPHRGYSIAGSDAD 120
Qy 118 EADTVLSPHVPRLWGRSTRSGRSSCLSSRANSLTLTDTEHEN---TETDHPGGLQ 174
Db 121 ENEAVMSPEHAMRLWGRGVKSGRSSCLSSRANSLTLTDTEHENRSDSESEQSP 180
Qy 175 RLRTPPPLSHANTPOHHAASINSLNRGNFTPRSNPSPAPTDHLSGEPAGAGQ--- 230
Db 181 TLQPLP--SHKQHPAQHH-PSITSLNRLNLTNRNQSPAP-----PAALPAELQ 229
Qy 231 -EPAAQENWLLNSNIPLETNRNLGKQPLGTLQDNLNLIEMDILGASRHDGAYS 289
Db 230 PESVQLQDSWVLGSNVPLESR-----HFLFKT 256
Qy 290 G-GTSPFLCTTSRGYPLTSTVYSPRPRLPRSTFAPAPNLPKPSKYCNWKAALSA 348
Db 257 GTGTTPFLSTATPGYTMASGVYSPRPRLPRNLTLSRSAPFKFKSKSKYSWRCT 316
Qy 349 ISATLVLLIAYFYVAMHLFGLNHLQVMEQMYE---ITEATSSWPVPTDVSIVPS 405
Db 317 VSVLLAILLSYFIAMHLFGLNHLQVMEQMYE---ITEATSSWPVPTDVSIVPS 368
Qy 406 LETPDRKKGTTTEGKPSFPPEDSFIDSGEIDVGRRAASKIPPGTFRSQVFI 465
Db 369 -----DNGKLGGEFTHENNTIDSGELDITGRRAIQEVPPGIWRSOLFIDQ 417
Qy 466 FNVSLGKAALVIGYGRKGLPPSHSTQDFVELLDGRLLTQEARSLBGTQRSGTVP 525
Db 418 FNLQKDALIGYGRKGLPPSHSTQDFVELLDGRLLTQEARSLBGTQRSGTVP 477
Qy 526 HETGFIQYLDSDGIWHLAFYNDGKESVWVSLTTAIESVDNCPNSCYCNGDCISG 585
Db 478 HEAGFIQYLDSDGIWHLAFYNDGKESVWVSLTTAIESVDNCPNSCYCNGDCISG 537
Qy 586 GFILGPGCGRASCPVLCSGNGQYMKGRCLCHSGWKGAECDDVPTNQCIDVACS 645
Db 586 GFILGPGCGRASCPVLCSGNGQYMKGRCLCHSGWKGAECDDVPTNQCIDVACS 645
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|----|------|---|------|
| Db | 538 | GFLGPDCSRACPVLCSGNGQYSGRCLCFSGMKGTECDVPTTQCIDPQCGRGICIMGS | 597 |
| Qy | 646 | CICNPGYKGSCEBVDCHDPTCSGRGVVCECHCFVGMGTWCETPRATCLDQCSGHT | 705 |
| Db | 598 | CACNSGYKGENCEADCLDPCSGNHGVCIIHGBCHCNPGWGSNCCEILUKTWCADQCSGHT | 657 |
| Qy | 706 | FLPDTGLSCDSPWTHGDCSIEICAAACGGHGVCGGTCTCEDGWMGAACDQACHPRCA | 765 |
| Db | 658 | YLQBSGCTCDPNWTPDCSNEICSVDCGSHGVCGSGCRCEBGTGWCACQACHPRCA | 717 |
| Qy | 766 | EHGTCRDGCKECSPGWNGEHCIIAHYLDRVVVKBCPGLCNGNGRCHTDLNMGHCVCOLGW | 825 |
| Db | 718 | EHGTCRDGCKECSQWNGEHCIIAHYLDKI VKEGCPGLCNSNGRCHTDLQNGWHVCVCPGW | 777 |
| Qy | 826 | RGACDTSMETACGDSKXNDGDLVDCMDPCCLOPLCHINPLCLGSPNPLDIIQETQVP | 885 |
| Db | 778 | RGAGCDVAMETLCTDSKXNDGDLVDCMDPCCLOQSSCQNPYCRGLPDPQDIIISQSLQT | 837 |
| Qy | 886 | VSQQLNHSFYDRIKFLVGRDSTHIIIPGENPPDGGHACVIRQVMTSDGTPLVGVNISFVN | 945 |
| Db | 838 | PSQQAASFYDRIKFLVGRDSTHIIIPGENPPDGGHACVIRQVMTSDGTPLVGVNISFVN | 897 |
| Qy | 946 | NPLFGYITISRDGSDFLVNGGIIILIFERAPFITQSHLWLPWDRFFVNETIIMRHEE | 1005 |
| Db | 898 | YSEGYITITRODGMFDLVANGASITLVFERSPELTQVHTVMI PMNVFYVMDTLVMKKEE | 957 |
| Qy | 1006 | NEIPSCDLSNPARNPVSPGLTSPASSCAEKGPIVPEIQALQBEISISCKXRLSYLS | 1065 |
| Db | 958 | NDIPSCDLSGFRVSPPIVSSPLSTFFRSPSPEDSPIIPETQVLHEETITPOTDLKLSYLS | 1017 |
| Qy | 1066 | SRTFGYKSVLISLTHPTIPENLMKVLHMAVEGRLEFRKFAAAPPDLSYYPFWDKTDVYN | 1125 |
| Db | 1018 | SRAAGYKSVLKITQAVIPENLMKVLHMAVAVGRLFOKFPAPSPALYTFIWDKTDAYN | 1077 |
| Qy | 1126 | QKVFGLSBAFVSGVEYESCDPLIILWEKRTTVLQGYEIDASKLGWSLDKHHALNIQSGI | 1185 |
| Db | 1078 | QKVYGLSBAFVSGVEYESCDPLIILWEKRTTVLQGYEIDASKLGWSLDKHHALNIQSGI | 1137 |
| Qy | 1186 | LHKNGENQFVSQBPVITGSMNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYV | 1245 |
| Db | 1138 | LYKNGENQFVSQBPVITGSMNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYV | 1197 |
| Qy | 1246 | GDFNYIRIPFSGNVTNILELRNKDFRSHSHPAHKYILATPDMGSAVPLDSNSRRVPKI | 1305 |
| Db | 1198 | GDFNYIRIPFSGNVTNILELRNKDFRSHSHPAHKYILATPDMGSAVPLDSNSRRVPKI | 1257 |
| Qy | 1306 | KSTVVVKDLVKNSEVAGTGDQCLPDDTRCGDGGKATEALTNPGRITVDKFGILYFVD | 1365 |
| Db | 1258 | KSLTGAKULTKNAEVVAGTGEQCLPFDEARCGDGGKATEALTNPGRITVDKFGILYFVD | 1317 |
| Qy | 1366 | GTMRIRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLD | 1425 |
| Db | 1318 | GTMRIRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLD | 1377 |
| Qy | 1426 | NNVVLQIENHQRIVRAGPMPHCQVPGIDHFLSKVAIHTLESATALVSHNGVLYTAE | 1485 |
| Db | 1378 | NNVVLQIENHQRIVRAGPMPHCQVPGIDHFLSKVAIHTLESATALVSHNGVLYTAE | 1436 |
| Qy | 1486 | TDEKINRIQVTTTSGEISLVAGSGCDCKNDANCDCFSGDGDAKADKALNPSSLAVC | 1545 |
| Db | 1437 | TDEKINRIQVTTTSGEISLVAGSGCDCKNDANCDCFSGDGDAKADKALNPSSLAVC | 1496 |
| Qy | 1546 | ADGELYVADLGNIRIRIRKPNFLNTQNMYSLSPIQELYFDPTTGKHYTQSLPTGD | 1605 |
| Db | 1497 | PDGLYIADLGNIRIRIRKPNFLNTQNMYSLSPIQELYFDPTTGKHYTQSLPTGD | 1556 |
| Qy | 1606 | YLYNFTYTGDDITLITDNGNMVNRDSTGMPHLVVPDQVQVWVTMGNTSALKSVYT | 1665 |
| Db | 1557 | YLYNFTYTGDDITLITDNGNMVNRDSTGMPHLVVPDQVQVWVTMGNTSALKSVYT | 1616 |
| Qy | 1666 | QGHAMMYHGNISGLLTKSNENGWTFYEDSFGRLTNVTFPTGOVSSFRSDTSSVH | 1725 |
| Db | 1617 | QGHAMMYHGNISGLLTKSNENGWTFYEDSFGRLTNVTFPTGOVSSFRSDTSSVH | 1676 |
| Qy | 1726 | VQVETSSK-DDVTTITNLSASGAFYTLQDQVRNSYIIGADGSLRLLLLANGMEVALQTEP | 1784 |
| Db | 1677 | VQVETSSK-DDVTTITNLSASGAFYTLQDQVRNSYIIGADGSLRLLLLANGMEVALQTEP | 1736 |
| Qy | 1785 | HLLAGTVNTVTKRNTLPIIDNGLNLVWRQKQARGOVTVFGRBLRVHNRNLLSLDQD | 1844 |
| Db | 1737 | HLLAGTVNTVTKRNTLPIIDNGLNLVWRQKQARGOVTVFGRBLRVHNRNLLSLDQD | 1796 |
| Qy | 1845 | RVTREKIIYDHRKFTLRILYDOAGRPGLWSRSSRLNGVNVITYSPGGYIAGIQRGIMSER | 1904 |
| Db | 1797 | RVTREKIIYDHRKFTLRILYDOAGRPGLWSRSSRLNGVNVITYSPGGYIAGIQRGIMSER | 1856 |
| Qy | 1905 | MEYDQAGRITSIRIFADGKTWSYTYLEKSVLLHLSQRQVIFEPDKNDRLSSVTPMNVARQ | 1964 |
| Db | 1857 | MEYDQAGRITSIRIFADGKTWSYTYLEKSVLLHLSQRQVIFEPDKNDRLSSVTPMNVARQ | 1916 |
| Qy | 1965 | TLBTISVGYRNIYOPPEGNASVIOFDTEGDLHLHTFVLTGGRVRYKYKGLSKLAETL | 2024 |
| Db | 1917 | TLBTISVGYRNIYOPPEGNASVIOFDTEGDLHLHTFVLTGGRVRYKYKGLSKLAETL | 1976 |
| Qy | 2025 | YDTTKVSYTDETAGMLKTINLQNEGFTCTIRVQIGPLIDROI FRFTEEGMVARPDYN | 2084 |
| Db | 1977 | YDTTKVSYTDETAGMLKTINLQNEGFTCTIRVQIGPLIDROI FRFTEEGMVARPDYN | 2036 |
| Qy | 2085 | YDMSFRVTSQMAVINETPLPIDLYRDVDSGKTEQKFGVYIYDINQIITTAVMTHTKH | 2144 |
| Db | 2037 | YDMSFRVTSQMAVINETPLPIDLYRDVDSGKTEQKFGVYIYDINQIITTAVMTHTKH | 2096 |
| Qy | 2145 | FDAYGRMEVQYBEIFRSLMYMTVQVDMGRVVKKELKVGPYANTTRYSEYDADGLOQT | 2204 |
| Db | 2097 | FDAYGRMEVQYBEIFRSLMYMTVQVDMGRVVKKELKVGPYANTTRYSEYDADGLOQT | 2156 |
| Qy | 2205 | VSINDPLWYSYDLNGLNHLSPGASARLTPLRYDIRDRITRLGDVQYKMDGDFLRQR | 2264 |
| Db | 2157 | VSINDPLWYSYDLNGLNHLSPGASARLTPLRYDIRDRITRLGDVQYKMDGDFLRQR | 2216 |
| Qy | 2265 | GGDIFEYNSAGLLIKAYNRAGSWSRYRYDGLGRRVSSKSSHSHHLOFFFYADLTNPTKVT | 2324 |
| Db | 2217 | GGDIFEYNSAGLLIKAYNRAGSWSRYRYDGLGRRVSSKSSHSHHLOFFFYADLTNPTKVT | 2276 |
| Qy | 2325 | HLNHSSEITSYLYDLOGLHFAWELSSGDEFYIACDNITGTLAVFSGTGLMIKQIYTA | 2384 |
| Db | 2277 | HLNHSSEITSYLYDLOGLHFAWELSSGDEFYIACDNITGTLAVFSGTGLMIKQIYTA | 2336 |
| Qy | 2385 | YGEIYMDTNFQIIIGYHGLYDPLTKLVHMGDRDYDLVLAGRWTS PDHKLHLSSSNV | 2444 |
| Db | 2337 | YGEIYMDTNFQIIIGYHGLYDPLTKLVHMGDRDYDLVLAGRWTS PDHKLHLSSSNV | 2395 |
| Qy | 2445 | MPFNLYMFKNNPISNSQDIKCFMTDVNSWLLTFGQLHNVIPGYPKPDMDAMEPSYELI | 2504 |
| Db | 2396 | MPFNLYMFKNNPISNSQDIKCFMTDVNSWLLTFGQLHNVIPGYPKPDMDAMEPSYELI | 2455 |
| Qy | 2505 | HTQMKTOEWDNSKSIILGVQCEVQKQKAFVTLERFDQYLGSTTSCQOAPKTKK----- | 2558 |
| Db | 2456 | HTQMKTOEWDNSKSIILGVQCEVQKQKAFVTLERFDQYLGSTTSCQOAPKTKK----- | 2502 |
| Qy | 2559 | ---PASSGSVFGKVPKALKDGRVTTDIIIVANEDGRVAAIILNHAHVLNHLFTIDGVDOT | 2616 |
| Db | 2503 | ---PASSGSVFGKVPKALKDGRVTTDIIIVANEDGRVAAIILNHAHVLNHLFTIDGVDOT | 2562 |
| Qy | 2617 | HYFVKPSPSGDLAILGLSGRRRTLENGVNVVTSQINTVLNNGRTRRTYDIOLOYGALCLN | 2676 |
| Db | 2563 | HYFVKPSPSGDLAILGLSGRRRTLENGVNVVTSQINTVLNNGRTRRTYDIOLOYGALCLN | 2622 |
| Qy | 2677 | TRYGTTLDEEKARVLELQARQAVRQAWAREQORLREGEELRAWTEGEKQVLTSGRVQG | 2736 |
| Db | 2623 | TRYGTTLDEEKARVLELQARQAVRQAWAREQORLREGEELRAWTEGEKQVLTSGRVQG | 2682 |
| Qy | 2737 | YDGFVYSVEQYPELSANNIHPMROSEMGRR | 2769 |
| Db | 2683 | YDGFVYSVEQYPELSANNIHPMROSEMGRR | 2715 |

| | | | | |
|--|----|------|--|------|
| RESULT 10 | Qy | 58 | SRVKDIYPOAEERECRTGANFTLRELGLBEEVTPPHGTLTYRTDGLGPOCGYSMGAGSDADM | 117 |
| US-10-038-854-38 | Db | 61 | NRVKDLVHREADEFTROQNFTRLQOLGCEPATRRGLAFCAEMGLPHRGYSISAGSDADT | 120 |
| Sequence 38, Application US/10038854 | Qy | 118 | EADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEH-----TETHPGGLQNH | 174 |
| Publication No. US20040022781A1 | Db | 121 | ENEAVMSEHAMRLWGRGVKSGRSSCLSSRNSALTTLTDEHENKSDSENQPSASNOQS | 180 |
| GENERAL INFORMATION: | Qy | 175 | RLRTPPPPLSHAHTPNQHHAASINSLRGNFTPRNSPSPAPTDHSLSGEPAGAAQ---- | 230 |
| APPLICANT: Spytex, Kimberly A | Db | 181 | TLQPLPP--SHKQSAQHH-PSITSLNRSLTNRNQSPAP-----PAALPAELQTT | 229 |
| APPLICANT: Li, Li | Qy | 231 | -EPAHAQENMLNSNIPLETENLCKQPLGTLQDNLIEMDILGASRHDGAYSDGHFLFKP | 289 |
| APPLICANT: Wolenc, Adam R | Db | 230 | PESVOLQDSWVLGNSVPLESR-----HFLFKT | 256 |
| APPLICANT: Vernet, Corine | Qy | 290 | G-GTSPFLCTTSPGYPLTSTVYSPPPRPLPRSTFARPAFLNKKPKSKYCNWKAALSIV | 348 |
| APPLICANT: Eissen, Andrew J | Db | 257 | GTGTTPLFSTATPGYTMASGSVYSPTRPLPRNLTLSRSAPFKFKSKSKYCSMKTALCAVG | 316 |
| APPLICANT: Liu, Xiaohong | Qy | 349 | ISATLVILLAYFVAMHLFGLNWLQPMEGQWYE---ITEDTASSWPVPTDVSLLYPSGGTG | 405 |
| APPLICANT: Malvankar, Uriel M | Db | 317 | VSULLAILLSYFIAMHLFGLNWLQQTENDTFENGKVNSDT-----MPTNTVSLPSG--- | 368 |
| APPLICANT: Shinkets, Richard A | Qy | 406 | LETPDRKGKGTTECKPSPFPEDSFIDSGEIDVGRASOKIPPGTFWRISOVFIDHPVHLK | 465 |
| APPLICANT: Tchernev, Velizar | Db | 369 | -----DNKLGKGTQENNTIDSGEIDIGRRAIQEIIPPGIFWRSQFIDQOPFLK | 417 |
| APPLICANT: Spaderne, Steven K | Qy | 466 | FNVSILGKAALVGIYGRKGLPPSHQTFDFVELLDGRRLLTQEARSLGETPRSGRTVPSS | 525 |
| APPLICANT: Gorman, Linda | Db | 418 | FNISLQXDALLIGVYGRKGLPPSHQTYDFVELLDGRLIAREQSLLETERAGRAQARSVSL | 477 |
| APPLICANT: Kekuda, Ramesh | Qy | 526 | HETGFIQVLDGSIWHLAFYNDGKESEVVSFLTTAIESVDNCPNSCYNGDCISGTCHCFL | 585 |
| APPLICANT: Patturajan, Meera | Db | 478 | HEAGFIQVLDGSIWHLAFYNDGKNAEQVSFNTIVIESVVECPRNCHGNGECVSGTCHCFP | 537 |
| APPLICANT: Gusev, Vladimiry | Qy | 586 | GFLGPDGCRASCPVLCGNGOYMKRGCLCHSGWGAECDVPTNOCIDVACSNHGTCTIGT | 645 |
| APPLICANT: Gangolli, Bsha A | Db | 538 | GFLGPDCSRACPVLCGNGOYSGKRGCLCFSGWGTGTECDVPTTQCIDPQCGRGICINGS | 597 |
| APPLICANT: Guo, Xiaojia S | Qy | 646 | CICNPGYKGESCEBVDQMDPTCSGRGVYVRGECHCFVWGWTNCTETPRATCLDQCSHGHT | 705 |
| APPLICANT: Sheno, Suresh G | Db | 598 | CACSSGYKGESCEADCIDPGCSNHGVCIHGECHCSPWGGSNCEILKTMCPDQCSHGHT | 657 |
| APPLICANT: Rastelli, Luca | Qy | 706 | PLPDTGLCSDPWSWTHGDCSIEICAAACGGHVCVGTGTCRCEDEWMAACDQACHPRCA | 765 |
| APPLICANT: Casman, Stacie J | Db | 658 | YLBESGSCCTDPNWTGPDGCSNEICSVDCSGSHGVCMGGTCRCEBGTGPACNQACHPRCA | 717 |
| APPLICANT: Boldog, Ferenc | Qy | 766 | BHGTCDGKCECSPGWNGEHCTIAHYLDRVV-----KEGCPGLCNGNGRCTLDLNGWHC | 819 |
| APPLICANT: Burgess, Catherine E | Db | 718 | BHGTCDGKCECSPGWNGEHCTIAHYLDRVV-----KEGCPGLCNGNGRCTLDLNGWHC | 819 |
| APPLICANT: Edinger, Shlomit R | Qy | 820 | VCQLGWRGAGCDTSMETACGDSKNDGDLVDCMDPCCLOPLCHINPLCLGSPNPLDII | 879 |
| APPLICANT: Ellerman, Karen | Db | 778 | VCQPGWRGAGCDVAMETLCTDSKNEGDLIDCMDPCCLOQSSQCONQYCRGLPDPQDII | 837 |
| APPLICANT: Gunther, Erik | Qy | 880 | QETQVPSVQNLHSHFYDRIFKFLVGRDSTHIIIPGNPFDGCHACVIRGOVMTSDGTPLGV | 939 |
| APPLICANT: Smithson, Glenda | Db | 838 | SQSLQSPSQAAKSFYDRISFLIGSDSTHVIIPGSPFNKSLASVIRGOVLADGTPLIGV | 897 |
| APPLICANT: Millet, Isabelle | Qy | 940 | NISFVNNPLGTYTISRQDGSFDLVNGGISLILFERAPFITQSBHTLWLPDRFVMTETI | 999 |
| APPLICANT: MacDougall, John R | Db | 998 | NVSFFHYPEYGYTLTROGDMFDLVANGASLULVFERSPFLTQVHTVWPNVFWMDTL | 957 |
| TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same | Qy | 1000 | IMRHEENEIPSCDLNFAFPNPVPSPLTSFASSCAEKGPVPEIQALOEIISIGCKM | 1059 |
| FILE REFERENCE: 21402-230 | Db | 958 | VMEKEENDIPSCDLNFAFPNPVPSPLTSFASSCAEKGPVPEIQALOEIISIGCKM | 1017 |
| CURRENT APPLICATION NUMBER: US/10/038,854 | Qy | 1060 | RLSVLSRTPGYKSVLRIISLTHPTIPNLMKVHLMVAEGRLFRKWFNFAAADLSYFFIWD | 1119 |
| CURRENT FILING DATE: 2003-01-22 | Db | 1018 | KLSYLSRAAGYKSVLRIISLTHPTIPNLMKVHLMVAEGRLFRKWFNFAAADLSYFFIWD | 1077 |
| PRIOR APPLICATION NUMBER: 60/258,928 | | | | |
| PRIOR FILING DATE: 2000-12-29 | | | | |
| PRIOR APPLICATION NUMBER: 60/259,415 | | | | |
| PRIOR FILING DATE: 2001-01-02 | | | | |
| PRIOR APPLICATION NUMBER: 60/259,785 | | | | |
| PRIOR FILING DATE: 2001-01-04 | | | | |
| PRIOR APPLICATION NUMBER: 60/269,814 | | | | |
| PRIOR FILING DATE: 2001-02-20 | | | | |
| PRIOR APPLICATION NUMBER: 60/279,832 | | | | |
| PRIOR FILING DATE: 2001-03-29 | | | | |
| PRIOR APPLICATION NUMBER: 60/279,833 | | | | |
| PRIOR FILING DATE: 2001-03-29 | | | | |
| PRIOR APPLICATION NUMBER: 60/279,863 | | | | |
| PRIOR FILING DATE: 2001-03-29 | | | | |
| PRIOR APPLICATION NUMBER: 60/283,889 | | | | |
| PRIOR FILING DATE: 2001-04-13 | | | | |
| PRIOR APPLICATION NUMBER: 60/284,447 | | | | |
| PRIOR FILING DATE: 2001-04-18 | | | | |
| PRIOR APPLICATION NUMBER: 60/286,683 | | | | |
| PRIOR FILING DATE: 2001-04-25 | | | | |
| Remaining Prior Application data removed - See File Wrapper or PALM. | | | | |
| NUMBER OF SEQ ID NOS: 411 | | | | |
| SOFTWARE: patentin Ver. 2.1 | | | | |
| SEQ ID NO 38 | | | | |
| LENGTH: 2721 | | | | |
| TYPE: PRT | | | | |
| ORGANISM: Homo sapiens | | | | |
| US-10-038-854-38 | | | | |
| Query Match | | | | |
| Best Local Similarity | | | | |
| Matches 1873; Conservative 362; Mismatches 461; Indels 98; Gaps 20; | | | | |
| Score 68.7%; Pred. No. 0; | | | | |
| Length 2721; | | | | |
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| Db | | 1 | MDVKERRPYCSLTKSRREKERRYTNSSADNEECRVPYTKQSYSSSRTLKAFDHDSSRLLYG | 60 |

Qy 1120 KTDVYNQKVFGLSEAFVSVGEYESCPDLILWEKRTTVLQGYEIDASKLGSNLDKXHAL 1179
Db 1078 KTDAYNKVYGLSEAVVSVGEYESCLDLTLWEKRTAILQGYELDASNMCGWTLDKXHV 1137
Qy 1180 NIOGILHKGNGENQFVSOQPPVIGSMNGRRRSISCPSCNGLADGNKLLAPVALTCGS 1239
Db 1138 DVQNGILYKNGENQFISQOPPVVSSIMNGRRRSISCPSCNGQADGNKLLAPVALACGI 1197
Qy 1240 DGSILYVGDFFNYIRIPPSGNVTNILELRNKDFRHSHPAKHYLATDPMGSAVFLSDSNS 1299
Db 1198 DGSILYVGDFFNYIRIPPSGNVTNILELRNKDFRHSHPAKHYLATDPMGSAVFLSDSNS 1257
Qy 1300 RRVFKISTVVVVDLVNSENVAAGTGDQCLPFDDTRCGDGKXATEFLTNPRGITVDKFG 1359
Db 1258 RRIYRPSKLTGAKDLTKNAEVVAGTGFQCLPFDEARCGDGKXATEFLTNPRGITVDKFG 1317
Qy 1360 LIYFVDTMIRRDONGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDN 1419
Db 1318 LIYFVDTMIRKVDONGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAINPMDN 1377
Qy 1420 SLVYLDNNVLOISENHQVIRIVAGRPMHCOVPGIDHFLLSKVAIHATLESATALAVSHNG 1479
Db 1378 SIYVLDNNVLOITENQVIRIAGRPMHCOVPGVE-YPVGKHAVQITLESATALAVSYG 1436
Qy 1480 VLYIAETDEKKINRIROVTTSGEISLVAGAPSGCDCKNDANCDGDDGYAKDAKLNT 1539
Db 1437 VLYIETDEKKINRIROVTTDGEISLVAGIPSECDCKNDANCDGDDGYAKDAKLNT 1496
Qy 1540 SSLAVCADGELYVADLNIRIRFIRKNKPFINTQNMVELSPIDQELLYFTDTGKHLYTQ 1599
Db 1497 SSIAASPDGTLYIADLNIRIRAVSKNPLNSMNFYEVASPTDQELYIFDINGTHQYTV 1556
Qy 1600 SLPTGDLVNYFTYDGDGDIILITDNNGMNVNVRDSTGMPMLVVPDGVVYVMTGNTSA 1659
Db 1557 SLVTGDLVNYFSYNDNDITAVTDSNGNTLRIRDRPNRMPVRVVPDQVIMLTGIGNC 1616
Qy 1660 LKSVTTQGHAMMTYHNGSGLATKSNENGWTTFFEYDYSFGRLTNTVTFPTGVSSPRSD 1719
Db 1617 LKGMTAGLEVLFTYHNGSGLATKSDGTGTTFFDYDSEGRLTNTVTFPTGVVNLHGD 1676
Qy 1720 TDSVVHVQVETSSK-DDVTITNLSASGAFYTLLOQDVRSYIYGADGSLRLLLANGMEV 1778
Db 1677 MDKAITVDIESSSREEDVSITNSLSDSFVTWQDLRNSYQIGDGLRIIYASGLDS 1736
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Qy 1899 GIMSERMEYDOAGRITSRIFADGKTWSYTYLEKSMVLLHSQRQYIFEPDKNDRLSSVTM 1958
Db 1857 GTTSEKVDYDQOGRIVSRVFPADGKTWSYTYLEKSMVLLHSQRQYIFEYDMDRLSAITM 1916
Qy 1959 PNVARQTELTRSVGYRYNIYQPEGNASVUQDTEFCHLLHTPYLGTGRVYKYKLS 2018
Db 1917 PSVARHTMQTIRSGYRYNIYNPPEASIIITDNEEGLLQTAFLGTSRRVLPKYRQT 1976
Qy 2019 KLAETLYDVTTSVFTYDGTAGMLKTINLONEGFTCTIRYQIGPLIDROQFRPFTPEGWVN 2078
Db 1977 RLSEILYDSTRVSTYDGTAGLVNLQSDGFTCTIRYQIGPLIDROQFRPFTPEGWVN 2036
Qy 2079 ARFDYNDNSPRVTSMAVINETPLDLYRYDDVSGKTEQFGKFGYIYDINOIITAV 2138
Db 2037 ARFDYSYDNSPRVTSMQVINETPLDLYQDDBISGKVEQFGKFGYIYDINOIITAV 2096
Qy 2139 MTHYKHFDAVGRMEKVEQYIEPRSLMYMTVOYDNMGRVVKELKVGPYANTTRYSYEDA 2198
Db 2097 MTYTKHFDAHGRKEIQEYIEPRSLMYMTVOYDNMGRVVKELKVGPYANTTRYSYEDA 2156
Qy 2199 DGQLOQTVSINDKPLWRYSYDLNGLNHLSPGNSARLTPLRYDIRITRLGDVQYKWD 2258

Db 2157 DGQLOQTVYLNKIMRWYNYDLNGLNHLNPSARLTPLRYDLRDRITRLGDVQYKWD 2216
Qy 2259 GFLRQSGGDIFFEYNSAGLLIKAVNRAGSVVRVYDGLGRRVSSKSSHSHHLOFFFYADLT 2318
Db 2217 GFLRQSGTEIFEYSSKGLLTVYKSGGWIVYRYDGLGRRVSSKSLGQHLQFFFYADLT 2276
Qy 2319 NPTKVTHLYNHSSEITSLYDLOQHLFAMELSSGDEFYIACDNICTPLAVFSGTGLMIK 2378
Db 2277 YPRTIHTVYNHSSEITSLYDLOQHLFAMELSSGDEFYIASDNTGTPLAVPSSNGLMLK 2336
Qy 2379 QILYTAIGIYMDTNFNQIITGYHGLYDPLTKLVHMGRRDYDLVLAGRWTSDPHELKX 2438
Db 2337 QIQTAYAGIYFDSNIDFQLVIGFHHGLYDPLTKLVHMGRRDYDLVLAGRWTSDPHELKX 2396
Qy 2439 LSSSNVMPNLYMFKNNPISNSQDIKCFMTDVSMLLTFGOLHNVIPGYKPKDMDAME 2498
Db 2397 I-KGDPAPNLYMFRNNPASKIHDVDTITDVNSMLVTFGFLHNAIPGPPVFKFDL 2455
Qy 2499 PSYELIHTQMTQOEWDNKSILGVQCEVQKQKAFVTLERFDQLYGSTITSCQOAPKTK 2558
Db 2456 PSYELV-----KSQWDDIPPIFGVQOQVARQAKAFSLGMAEVQ----VSRRRAGGAQS 2507
Qy 2559 ---FASGVSFGKGVFKALXGRTVTTDIISVANEDGRRVAAIILNHAHYLENLHFTIDCVD 2615
Db 2508 WLMFATVKSILIGKGVMLAVSQGRVQTNVLNIANEDCIKVAALVNNAPYLENLHFTIEBK 2567
Qy 2616 THYFVFKPSEGLATILGLSGGRRTLENGVNVTVSIOINTVLNGRTRRYTDIOLQYGA 2675
Db 2568 THYFIKTTTTPESDLGTLRTSGRKALENGINVTVSOSTTVVNGRTRRFADEVHQFGALAL 2627
Qy 2676 NTRYGYTTLDEKARVLELARAQRAVROAWAREQORLREGEGLRAWTEGEKQOVLSTGRVQ 2735
Db 2628 HVRYGWTLEDEKARILEQARALARAWAREQORVRDGBEGARLWTEGEKQOLLSACKVQ 2687
Qy 2736 GYDGFVVISVEQYPELSDSANNTHMRQSEMGR 2769
Db 2688 GYDGYVLSVEQYPELSDSANNTHMRQSEMGR 2721

RESULT 11

US-10-038-854-36
; Sequence 36, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

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; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-038-854-36

Query Match      68.5%; Score 10201; DB 4; Length 2725;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 1872; Conservative 362; Mismatches 462; Indels 102; Gaps 21;

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Db 598 IMGSCACSGYKGBSCBEADCDIFCCSNHGVCIHGECHCSFGWGSNCEIILKTCWCPDQCS 657
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Db 838 QDIISQSLQSPSQAAKSFYDRIISFLIGSDSTHVPGESPENKSLASVIRQVLTADGTP 897
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 936 LVGVNISFVNPLFGYTIISQDGSFDLVNTGGISIIILFRERAPFITQHTLWLPDRFFV 995
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 898 LIGVNVSFHYPEYGYTITRQDGMFVLVANGGASLTLLVFERSPELTQVHTVMIWNVPYV 957
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 996 METIIMRHEENIEIPSCDLSNFARNPVVPSPTLTSFASSCAEKGPIVPEIQALOEISIS 1055
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 958 MDLVMKEENDIIPSCDLSGFVRNPILVSSPLSTFFRSPEDSPILPETQVLEETIP 1017
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1056 GCKMLSYLSRSTPGYKSLRISLTHPTIPNLMKVHLMAVEGRLFRKFAAPADISYY 1115
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1018 GTDLKLSYLSRAAGYKSLKTIWTQSIIPNLMKVHLMAVAVGRLFKWPPASPILAYT 1077
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1116 FIWKTIVYQKVGLESEAFVSVGYEYESCPDLLMEKRTVLOGYEIDASKLGSWLDK 1175
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1078 FIWKTDAYNQKVGLESEAVVSVGYEYESCLDLTMEKRTAILQGYELDASNMNGWTLDK 1137
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1176 HHALNIOGILLHKGNGENQFVQOQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVAL 1235
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1236 TCGSDGLYVGDFNYIRRIIPPSGNVTNILELRNKDPRHSHSPAHKYYLATDPMGAVPLS 1295
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1198 ACGIDGSLYVGDFNYVRRIPPSGNVTNILELRNKDPRHSHSPAHRYLATDPMVTDLYVS 1257
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1296 DSNRRVPFKIKSTVVVKDLVKNSVAVAGTDOCLPFDDTRCGDGGKATEALTNPRTTV 1355
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1258 DTNTRIRYPSKLTGAKDLTKNAEVAVAGTGEQCPLPFDEARCGDGGKAVEATLMSPKGNV 1317
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1356 DKFGLYFVDTMIRRIDQNGIISTLLGSNDLTLSARPLSCDSVMDISOVRLEWPTDLAIN 1415
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1318 DXGLIIFVDTMIRKVDQNGIISTLLGSNDLTLSARPLTCDTSMHISOVRLEWPTDLAIN 1377
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1416 PMDNSLYLDNNVVLQISENHQVIRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAV 1475
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1378 PMDNSIVYLDNNVVLQITENRQVRIAAGRPMHCQVPGVE-YPVGKHAQVTTLESATAIAV 1436
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1476 SHNGVLIAETDEKKINRIQVTTSGEISLVAGAPSGCDCKNDANCDFSGDDGYAKDAK 1535
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1437 SYSGLVITETDEKKINRIQVTTDGEISLVAGIPSECDCKNDANCDFSGDDGYAKDAK 1496
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1536 LNTFSSLAACDGLYVADLGNIRIFIRKKNKPLNTONMYELSSPDIOELYLPDTTGKH 1595
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Db 1497 LSAFSSLAASPDGLTYIADLGNIRIVAKKNKPLNSNMFYEVASPTDQELYIFDINGTH 1556
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1596 LYTOSLTGDIYLFNTYTGDDITLITDNNNGMNVNRRDSTGMPLMLVVPDQVYVWTMG 1655
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```


Matches 1821; Conservative 348; Mismatches 437; Indels 185; Gaps 21;

| | | | |
|----|------|---|------|
| Qy | 1 | MDVKEKPYSLTR--REDARERYTSSADSSECKAP--OKSYSSSETLKAYDOD--ARLAYG | 57 |
| Dd | 1 | MDVKEHRRPYCSLUTKSRKERYTNTSSADNEBCRVPTQKSYSSSETLKAFDHDSSRLLYG | 60 |
| Qy | 58 | SRVKOTVPOAEBEFCRTGANFTLRELGLBEVTPPHGTLRYRTDGLPQCGSYMGAGSDADM | 117 |
| Dd | 61 | NRVKOLVHREADEFTR----- | 76 |
| Qy | 118 | EADTVLSPHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGQLONHARLR | 177 |
| Dd | 77 | -----QEQPASNOQOST-----LQ----- | 90 |
| Qy | 178 | TPPPPLSHAHTNQHAAASINSINLRGNFTPRNSPAPDTHLSGCEPPAGGAQ-----EP | 232 |
| Dd | 91 | --PLPPSHKQHAQH--PSITSILNRSLNRRNRQSPAP-----PAALPAELQTTPEES | 139 |
| Qy | 233 | AHAQENWLLNSNIPIETRLNLRKQPFGLTLQDNLIEMDILGASRRHDGAYSDGHFLFKPG--G | 291 |
| Dd | 140 | VQLQDSMWLGSNVPLESR-----HFLFKTGTG | 166 |
| Qy | 292 | TSPLFCTTSPGYPPLTSSVTYSPPPRPLPRSTFARPAFNLKPSKYCNWKCAALSAIVISA | 351 |
| Dd | 167 | TTPLFSTATPGYTMASGSYSPPTPLPRNTLSRSFAFKPKSKSKYCSWKCTALCAVGSV | 226 |
| Qy | 352 | TLVILLAYFVAMHLFGLNHLQPMQOMEY-----ITEDTASSWPVPTDVSXPSGGTGLET | 408 |
| Dd | 227 | LIALILUSYFIAMHLFGLNWLQOOTENDTFENKGVASDT-----MPTNTVSLPSG----- | 275 |
| Qy | 409 | PDRKGKGTGTFSPSPFPFSDSIDSGEIDVGRASQKIPPGTFWRSQVPIDHPVHLKFNV | 468 |
| Dd | 276 | -----DNGKLGGTQENNTIDSGELDIGRAIQEIPPGIFWRSQFLDQPQFLKFN | 327 |
| Qy | 469 | SLGKAALVGIYGRKGLPSPHTQDFVELLDGRLLLTQEARSLLEGTPRQSRGTVPSSSHEH | 528 |
| Dd | 328 | SLQKALIGYVRKGLPSPHTQYDFVELLDGSLRLIAREQSRSLLETERAGRARSVSLHEA | 387 |
| Qy | 529 | GFIQYLDGSIWHLAFVNDKSEVVSFLTATIESVDNCSNCGNGDCISGTCFCHFLGFL | 588 |
| Dd | 388 | GFIQYLDGSIWHLAFVNDKNAEQVSFNTIVIESVVECPNCHNGECVSGTCFCHFPGL | 447 |
| Qy | 589 | GPDCGRASCPVLCSNGQYMKRCCLCHSGWKAECDDVPTNQDINVACSNHGTCITGTCIC | 648 |
| Dd | 448 | GPDCSRAACPVLCSNGQYSGKRCCLFCSCWKMGTECDVPTTQCIDPQCGGRGICINGSCAC | 507 |
| Qy | 649 | NGFYKGESCEEVDCHMDPTCSGRGVCVRGECHCFVCGWGTNCETPRATCLDQCDSHGTFPL | 708 |
| Dd | 508 | NSGYKGKSCSEADCIDPGCSNHRGVCIHGECHCSPGMGGSNCBILKTMCPDQCSGHGTYLQ | 567 |
| Qy | 709 | DTGLCSCDPSWTGHDCSIEICAADCGHGVCGVGTCCRCBDGMWGAACDQACHPCABHG | 768 |
| Dd | 568 | EGSGCTCDPNWTGDCSNFICSVDCSGHGVCMGGTCRCBEGWTGPACNQRACHPCABHG | 627 |
| Qy | 769 | TCRDGKCECSPGMNGBHCITIAHYLDRW-----KEGCPGLCNGRCRTLDLNGWHVCVQ | 822 |
| Dd | 628 | TKDGKCECQGMNGBHCITIAHYLDKIVKDIGYKEGCPGLCNSNGRCRTLDQNGGHVCVQ | 687 |
| Qy | 823 | LWHRGAGCSTMETACGDSKNDGDGLVDCMDPDCLQLCHINPLCLGSPNPLDIIQET | 882 |
| Dd | 688 | PGMRGAGCDVAMETLCTDSKDNREGDLIDCMPDCCLOSSCQNYCYCRGLPDQDIIISQS | 747 |
| Qy | 883 | QVPVSOQLNHSFVDRIKFLVLRDSDTHIIPGENPFGGHACVIRGQVMTSDGTFPLVGVNIS | 942 |
| Dd | 748 | LQSPSQAAKSYFDRLISFLIGSDSTHVPGESFPFKSLASVIRGQVLTADGTPPLGVNVS | 807 |
| Qy | 943 | FVNNPLFGYTIQRQGSFPLVTNGGSIILRPERAPFITQETHLWLPMDRFPFWMETIMR | 1002 |
| Dd | 808 | FFHYPEYGYTIRQDGMFPLVANGASLTLPERSPFLOTQYHTVMI PMNVFYVMDTLVME | 867 |
| Qy | 1003 | HEENETPSCDLSNFARNPNVSPSLTSPASSCAEKGPVPEIQALQEBEISISGCKMRLS | 1062 |
| Dd | 868 | KEENDIPSCDLSGFRPNPIIVSSPLSTFRSSPEDSPIIPETQVLHBETTIPGTDLKL | 927 |

| | | | |
|----|------|--|------|
| Qy | 1063 | YLSRTPGYSVLRIISLTHPTIPENLMKVLHMAVEGRLPKWFAAAAPDLGVYFIWDKTD | 1122 |
| Dd | 928 | YLSRAAGYSVLKLTWTQSIIPENLMKVLHMAVAVGRLFOKNFPASPENLAYTFIWDKTD | 987 |
| Qy | 1123 | VYNQKVPGLSBAFVSUGEYESCPDLILWEKRTTVLQGYEIDASKLGGWSLDKHALNIQ | 1182 |
| Dd | 988 | AYNQKVYGLSEAVVSGVEYESCLDLTLWEKRTAILQGYELDASNMGGWTLDKHHVLDDQ | 1047 |
| Qy | 1183 | SGILHKGNGENQFVSQQPPVIGSIMGNGRRRSISCPSCNGLADGNKLLAPALVTCGSDGS | 1242 |
| Dd | 1048 | NGILYKNGENQFISQQPPVVSSIMGNGRRRSISCPSCNGQADGNKLLAPALVACGIDGS | 1107 |
| Qy | 1243 | LYVGDFNYIRIPFSGNVNILELRNKDFRSHSPAHKYLYLATPMSGAVFLSDSNSRRV | 1302 |
| Dd | 1108 | LYVGDFNYVRIIPFSGNVTSVLELRNKDFRSHSNPAHRYLYLATDVTGDLVSDNTNRI | 1167 |
| Qy | 1303 | FKIKSTVVVVDLVKNSEVVAGTGOCLPFDTRCGDGGKATEATLTNPRGTVTDKFGLIY | 1362 |
| Dd | 1168 | YRPKSLTGAKDLTKNAEVVAGTGOCLPFDREARCGDGGKAVEATLMSPGMAVDKNGLIY | 1227 |
| Qy | 1363 | FVDCGTMIRRIDONGIISTLLGSNDLTSARPPLSCDSVMDISOVRLEWPTDLAINPMDNSLY | 1422 |
| Dd | 1228 | FVDCGTMIRKVDQNGIISTLLGSNDLTSARPPLTCDTSMHISOVRLEWPTDLAINPMDNSIY | 1287 |
| Qy | 1423 | VLDNNVLIQISENHQVRIVAGRPMHCOVPGIDHPLLSKVAIHATLESATALAVSHNGVLY | 1482 |
| Dd | 1288 | VLDNNVLIQITENQVRIAGRPMHCOVPGVE--YVKGHVAQVTTLESATALAVSYSGVLY | 1346 |
| Qy | 1483 | IAETDEKINKIRQVTTSGEISLVAGAPSGCDCCKNDANCDCFSDDGDAKAKLNTPSSL | 1542 |
| Dd | 1347 | ITETDEKINKIRQVTTDGEISLVAGIPSECDCKNDANCDCYQSGDGYAKDAKLAPSSL | 1406 |
| Qy | 1543 | AVCAGELYADLGNIRIRFIRKKNPFLNTQNMVELSPDIOELYLDPDTCCKHYTQSLP | 1602 |
| Dd | 1407 | AASPDGLTYADLGNIRIRAVSKNKPLLNSMNFYEVASPTDQELYIFDINGTHQVTVSLV | 1466 |
| Qy | 1603 | TG DYLNFTYTGDDITLITDNNGMNVNRRDSTGMPLWLVPDGVQVYVVTMTGNSALKS | 1662 |
| Dd | 1467 | TG DYLYNFSYNDNDITAVTDSNGNLTIRIRDPNRMPPRVVSPDNQVILWLTIGTCLGK | 1526 |
| Qy | 1663 | VTTQGHELAMWYHNGSGLIATKSNENGWTTFFYDYSFGRLTNTVFTTQGVSSPSRSDTS | 1722 |
| Dd | 1527 | MTAQGLELVFTYHNGSGLIATKSDETGTTTFFDYDSEGRLTNTVFTTGVVNTNLHGMDK | 1586 |
| Qy | 1723 | SVHYQVETSSK--DDVTITNLASGAFVTLQDOVRNSYYIGADGSLRLLLANGMEVALQ | 1781 |
| Dd | 1587 | AITVDIESSSREEDVSITSNLSSIDSFTYVQDQLRNSYQIGYDGSURIIYASGUDSHYQ | 1646 |
| Qy | 1782 | TEPHLLAGTVNPTVGKENVTLPIDNGNLNVEWRQKEQARGQVTVFGRRLRVHNRNLLSL | 1841 |
| Dd | 1647 | TEPHVLAGTANPTVAKENMTLPGENGQNLVEWRPRKEQAQGVNVPFGRKLRVNGRNLLSV | 1706 |
| Qy | 1842 | DFDRVTRTEKIYDHRKFTLRILYDQAGRPSLWSPSSRLNGVNTYSPGGVIAGIQGIM | 1901 |
| Dd | 1707 | DFDRTTTEKIYDHRKFLRLRIAYDTSCHPTLWLPSSKLMAVNTYTSSTGQIASIQRTT | 1766 |
| Qy | 1902 | SERMEYDOAGRITSIRIPADGKTWSYTYLEKSMVLLLSHOROYIPEFDKNDRLSVTWPNV | 1961 |
| Dd | 1767 | SEKVDYDQGGRIYSRVFADGKTWSYTYLEKSMVLLLSHOROYIPEYDMDRLSAITWPSV | 1826 |
| Qy | 1962 | AROTLETIRSVGYRYNIYQPEGNASVIQDPTEDGHLHHTPYLGTGRVRYKYKGLSKLA | 2021 |
| Dd | 1827 | ARHTMQTIRSIGYRYNIYNPPESNASIITDYNEEGLLQTAFLGTSRRVLFKYRQTRLS | 1886 |
| Qy | 2022 | ETLVDTTKVSTYDETHAGMLKTNLQNEGTCTTIRYQIIGPLIDRQIRFRFTEEGWVARF | 2081 |
| Dd | 1887 | EILYDSTRVSTYDETHAGVLTNQLSDGFTCTTIRYQIIGPLIDRQIRFRFSEDGCVNARF | 1946 |
| Qy | 2082 | DYNDNSFRVTSMAVINETPLPIDLYRDDVSKTEQFGKFGVIYDINOIITAVNTH | 2141 |
| Dd | 1947 | DYSYDNSFRVTSMOGVINETPLPIDLIYQFDDISKVEQFGKFGVIYDINOIITAVNWTY | 2006 |

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Qy 2142 TKHFDAYGRMKVEYQYEIFRSLMTYMTVQYDNMGRVVKVKKLVGYANTTRYSEYEDADGQ 2201
Db 2007 TKHFDAGRIKEIQEYEIFRSLMYWITIQYDNMGRVTKREIKIGFANTTKYAYEYVDGQ 2066
Qy 2202 LQTVSINDKPLWRYSDYDNLNHLHLLSPGNSARLTPLRYDIRDRITRLGDVQYQMDDEGFL 2261
Db 2067 LQTVYLNEMKMYRYDNLNHLNPNPSNSARLTPLRYDLRDRITRLGDVQYRLDEGFL 2126
Qy 2262 RQGGDIFENYSAGLLIKAYNRAGSVRYRYDGLGRVRVSKSSSHSHHLOFFVADLTNPT 2321
Db 2127 RQGTETFEYSKGLLTVYSGSGTWIYRYDGLGRVRVSKSLGQHLQFFVADLTPT 2186
Qy 2322 KVTHLNVHSSSEITSLYDILQGHFLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMTKQIL 2381
Db 2187 RITHVNVHSSSEITSLYDILQGHFLFAMEISSGDEFYIASDNTGTPLAVFSSGLMLKQIQ 2246
Qy 2382 YTAIGEIMTNNFNQIIIGHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHLELWHLSS 2441
Db 2247 YTAIGEIFYDSNIDFQLVIGHGGLYDPLTKLIHFGGRDYDILAGRWTTPDIEWKRI-G 2305
Qy 2442 SNVMPENLYMFKNNPISNSQDIKCFMTDYNVSNLLTFGFLHNVIPGYPKPMDAMEPSY 2501
Db 2306 KDPAPENLYMFRNNPNASKIHDVKDYITDYNVSNLLTVTFGLHNAIPGFPVKFDLTPEPSY 2365
Qy 2502 ELIHTOMKTQEWNSKSIILGVQCEVQKQKAFVTLERFDQLYGSTITSQQQAPKTK- 2558
Db 2366 ELV-----KSQWDDIPPIFGVQOQVAKAFSLGMAEVQ-----VSRERAGGAQSWLW 2417
Qy 2559 FASSGSVFGKGVKPKALDKGRVTTDIIISVANEDGRVAAIINHAHYLENLHFTTIDGVTHY 2618
Db 2418 FATVKSILGKGVMLAVSQGRVQTNVLNANEDCIKVAVALNNAFYLENLHFTTIEGKDYTHY 2477
Qy 2619 FVKGPSGEGIALILGSGGRTLENGVNVTVSQINTVLNGRTBRYTDIQLQYCALCINTR 2678
Db 2478 FIKTTPESDLGLRLTSGSKALENGINVTVSQSTTVVNGRTRRRFADVENQFQALALHR 2537
Qy 2679 YGTTLDEKARVLELARAQRAVQAWAREQORLREGEGLRAWTEGEKQQVLSGTRVQYD 2738
Db 2538 YGTTLDEKARILEQARQALARAWAREQORVRDGEGLRWTEGEKQQLLSAGKQVQYD 2597
Qy 2739 GFFVISVEQYPELSDSANNIHFMRQSEMGR 2769
Db 2598 GYVYLSVEQYPELADSANNIQLRQSEIGRR 2628

RESULT 13
US-10-038-854-42
; Sequence 42, Application US/10038854
; Publication No. US2004002781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
```

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; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 42
; LENGTH: 2613
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-038-854-42

Query Match 66.2%; Score 9856; DB 4; Length 2613;
Best Local Similarity 65.2%; Pred. No. 0;
Matches 1815; Conservative 345; Mismatches 437; Indels 188; Gaps 21;

Qy 1 MDVKRRKPYRSLTR-RRDAERRYTTSSADSEEGKAP-QKSYSSSETLKAYDQD-ARLAYG 57
Db 1 MDVKRRPYCSLTKSRREKERRYTNSSADNEECRVPTQKSYSSSETLKAFDHDHDSRLLYG 60
Qy 58 SRVKDIPQEAEEFCRTGANFTLRLECLBEVTPPHGTLXRTDIGLPCQGYSMGAGSDAM 117
Db 61 NRVKDLVHREADEFT- 76
Qy 118 EADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHARLR 177
Db 77 -----QEOPASNQSGST-----LQ----- 90
Qy 178 TPPPPLSHAHTPNQHUAASINSLNRGNFTPRSPSPAPTDHSLSGEPAGAQ-----EP 232
Db 91 --PLPPSHKQHSQHH-PSITSLNRNSLTNRNQSPAP-----PAALPAELQTTPTES 139
Qy 233 AHAEQWLLNSNIPLETNRNLGKQFPFLGTLQDNLEMDILCASRDGAYSQGHFLFKPG-G 291
Db 140 VQLQDSWVLGNSVPLESR-----HFLFKTGTG 166
Qy 292 TSPFLCTTSPGYPLTSTVYSPPPRPLPRSTFARPAFNKKPKSKYCNWKAALSAIVISA 351
Db 167 TTFELFSTATGYTWASGVSPPTRPPLRNTLSRSAPFKKSSKSKYCSMKCTALCAVGVS 226
Qy 352 TLVILLAYFVAMHLFGLNHLQPMEGQMYE---ITEDTASWVPVPTDVSYPSCGTGLET 408
Db 227 LLAILLSYFIAMHLFGLNWLQQTENDTFENGKVNST-----MPTNTVSLPSC----- 275
Qy 409 PDRKGKTTTEKSSPPPEPDSFIDSGEIDVGRASOKIPBCTFWRSQVFIIDHPVHLKFN 468
Db 276 -----DNKGLGGFTQENNTIDSGELDIGRAIQSIPIPGIFWRSOLFIDQPOFLKPN 327
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| | | | |
|----|------|--|------|
| Qy | 469 | SLGKAALVGYIRKGLPPSHQTFDFVBLLDGRLLLTQEARSLBGTTPRQSRGTVPVPSHET | 528 |
| Db | 328 | SLQXDALITGVYGRKGLPPSHQTFDFVBLLDGRSLIAREQSRLLLETERAGRQARSVSLHEA | 387 |
| Qy | 529 | GFIOYLDSGIWHLAFYNDGKSEVVSFLTTAISVDNCPNCYCGNDICISGTCHCFGL | 588 |
| Db | 388 | GFIOYLDSGIWHLAFYNDGNABQVSFNTIIVISWVECPNCHNGECVSGTCHCFPGFL | 447 |
| Qy | 589 | GPDCGRASCPVLCSGNGOYMKGRCLCHSGWKGAECDPVTMQCITDVACSNNHGTCTIGTCIC | 648 |
| Db | 448 | GPDCSRAACPVLCSGNGOYSKGRCLCFSGWKGTEDCVPTTQCIDPQCGRGICIMGSCAC | 507 |
| Qy | 649 | NPYKGBSCEBVD CMDPTCSGRGYCVRGECHCFVGMGGTNCETPRATCLDQCDSHGHTFLP | 708 |
| Db | 508 | NSGYKGBSCEADCIDPGCSNHGVCIHGECHCSPMGWGSNCEILKTMCPDQCSGHGTYLQ | 567 |
| Qy | 709 | DTGLCSDDPSWTHDCHSIEICTAADCGSHGVCVGTCRCEGDGWAACDQACRHPRAEHG | 768 |
| Db | 568 | ESGSCTCDPNWTPDSCSNEICSVDCGSHGVCMGTGTCRCEGWTGPTCNQACHPRCAEHG | 627 |
| Qy | 769 | TCRDGKCECPGWNGECHTIAHYLDYRVVKGCPGLCNGNGRCITLDLNGHVCVQLGWRGA | 828 |
| Db | 628 | TKDQKCECHSGWNGECHTII-----EGCPGLCNSNGRCITLDQNGHVCVQCPGWRGA | 678 |
| Qy | 829 | GCDTSMETACGDSKONDGDGLVDCMDPDCLQLCHINPLCLGSPNPLDIIQETVPVPSQ | 888 |
| Db | 679 | GCDVAMETLCTDSKDNESDGLIDCMDPDCLQSSCONOPYCRGLPDPODIIISQLSQSPSQ | 738 |
| Qy | 889 | QNLHSFYDRIKFLVGRSTHIIIPGENPFDGHCACVIRQVMTSDGTPLVGVNLSFVNNPL | 948 |
| Db | 739 | QAAXSFYDRISFLTSGDSTHIVGESPFNKSASVIRGQVLTADGTPGLIGVNSFFHYPE | 798 |
| Qy | 949 | FGYTIISQDGSFDLVTNGGSIILPERAPPTIQEHTLWLPDWRFFVWETIIMRHENEI | 1008 |
| Db | 799 | YGYTIITQDGFUDLVANGASLTLVFRSPLTQYHTVWIPMNVFYVMDTLWMEKENDI | 858 |
| Qy | 1009 | PCDLSNFARPNPVVSPSPLTSPASSCAEKGPIVPEIQALQEEISISGCKMRLSYLSRRT | 1068 |
| Db | 859 | PCDLSGFVRPNPIIVSSPLSTPRSSPEDSPIIPETQVLHEETIPGTDLKL SylSSRA | 918 |
| Qy | 1069 | PGYKSVLRIISLTHETIIPNLKWHLVAVRGLRPRKVFAPAAADSLSYFFIWDKTDVYNKV | 1128 |
| Db | 919 | AGYKSVLKITMTQSIIPNLKWHLVAVVGRUFPQWFPASPNAVLYTFIWDKTDAYNKV | 978 |
| Qy | 1129 | FGLSEAFVSGVYEVESCPDLILKEKRTTVTLQGYEIDASKLGWSLDKHALNTQSGILHK | 1188 |
| Db | 979 | YGLSEAVVSGVYEVESCDUFLMEKRTAILQGYELDASNGMGTLDKHHVLDVQNGILYK | 1038 |
| Qy | 1189 | NGNGENFVSOQPPYIGSIMNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDF | 1248 |
| Db | 1039 | NGNGENQISQPPVVPVSSIMNGRRRSISCPSCNQADGNKLLAPVALACGIDGSLYVGDF | 1098 |
| Qy | 1249 | NYTRRIIPSGNVNWIIELRNKDPHSHSPAHYLYLATDPMGSAVFTSDSNSRRVFKIKST | 1308 |
| Db | 1099 | NYVRRIPPSGNVTGVLELRNKDPFHSHSNPAHYLYLATDPTVGLYVSDTWTTRIRYRPSKL | 1158 |
| Qy | 1309 | VVVKDLVKNSEVAVAGTGDQCLPEDDTCRGGGKATEATLNPBGITVDFKGLYFVFDGTM | 1368 |
| Db | 1159 | TGAKDLTKNAEAVAGTGEQCLPPDEARCGDGGKAVEATLMSPGKMAVDKNGLLIYFVDGTM | 1218 |
| Qy | 1369 | IRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDNNV | 1428 |
| Db | 1219 | IRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAINPMDNSIYVLDNNV | 1278 |
| Qy | 1429 | VLOISENHQVRIVAGRPMHCQVPGIDHFLSLSKVAIHATLESATALAVSHNGVLIYIAETDE | 1488 |
| Db | 1279 | VLOITENRQVRIRIAGRPMHCQVPGVE-YPVGKHAVQTTLESATAIAVSYSGLVITYETDE | 1337 |
| Qy | 1489 | KKINIRIQVTTSGEISILVAGAPSCDCKNDANCDSCFGDDGYAKADKLNTPSSILVACDG | 1548 |
| Db | 1338 | KKINIRIQVTTDGEISILVAGIPSCDCKNDANCDQYOSGGGYAKADKILSAPSSILASPDG | 1397 |
| Qy | 1549 | ELYVADLGNIRIRIRKKNKPLNTQNNYELSSPDIQBLYLFTDTTGKHYLTQSLPTGDYLY | 1608 |

Db 2469 PESDLGTLRLTSGKALENGINTVTSQSTTVNGRTRTFADVEMQFALALHVRVYGMWTL 2528
Qy 2685 EKARVLELARAQAVQAWAREOORLAREGEGRAWTEGEKQOVLSTGRVQGVYDGFVL 2744
Db 2529 EKARILEQARALAWAREOORVRDGBEGARLWTEGEKROLLSAGKRVQGVYDGYVL 2588
Qy 2745 VEQYPELSDSANNHFMKQSEMGRR 2769
Db 2589 VEQYPELADSANNIQLRQSEIGRR 2613
RESULT 14
US-09-808-602-81
; Sequence 81, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Hartman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US20020155115A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 81
; LENGTH: 2802
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-808-602-81
Query Match 64.6%; Score 9616.5; DB 3; Length 2802;
Best Local Similarity 61.3%; Pred. No. 0;
Matches 1775; Conservative 411; Mismatches 491; Indels 217; Gaps 27;
Qy 1 MDVKRKPYSLTRR-DAERRYTSSADSEEGAP-QKSYSSSETLKAYDQARLAYGS 58
Db 1 MDIKDRR-HRSLTRGRCCKRYTSSSLDSEDCRVPAQKSYSSSETLKAYGHDRMHYGN 59
Qy 59 RVKDIVPOEAEFCRTGANFTLRELGLEEVTPPHGTLRYTDIGLPQCGYSGMAGSDADME 118
Db 60 RVSDLVHREDEFPQGTNTFLAELGICEPS-PHRSGYCSDIGILHQYSLSTGSDADSD 118
Qy 119 ADTVLSPHVPRLMGRSTRGRSSCLSSRANSNLTLDTEHEN----- 161
Db 119 TEGGMSPEHAIRLWGRGKIKSSRSSGLSSRENSALTLDSDNENKSDSEENDFHTLSEK 178
Qy 162 -----TETDH--- 166
Db 179 DROTSWQOLAETKNSLIRPIPTSSSSSLPSAQLPSSHNPVPSQMPLLDNTSHQIM 238
Qy 167 -----PGQLQNH---ARLRTP-PPPLSHAHTPNQHHAA 197
Db 239 DTNPDEBFSNYSLLRACSGPQQAASSGPNHHSQSLRPLPPPHNHSLS---HHHSSA 295
Qy 198 NSLNRGNFTPRSN---PSRAPTDHSLSGEPAGGAQEPAAHAQENWLLNSNIPLETNRLG 253
Db 296 NSLNRNSLTNRNQIHAPAPAPND--LATTP-----ESVQLQDSWLVNSNVPLETR-- 344
Qy 254 KQPLGLTLDNLNLEMDILGASRHGAYSDGHFLFK-PGGTSPLPCTTSPGYPPLTSSVYS 312
Db 345 -----HFLEKTSSTGTTPLPSSSSPGYPLTSGTVT 374
Qy 313 PPPPLPRSTFARPAFNLKPKSKYCNWKAALSIAVISATIVILLAYFVAMHLFGLNWLH 372

Db 375 PPRLPRNTFSRNAPLKKPKSKYCSWKCAALSAIAAAVLLAILLAYFTAMHLLGLNQWL 434
Qy 373 QWMEQMYEI-----TEDTASSWPVPTDVSLSYPSGGTGLBTPDKGKTGTEGKPPSS 424
Db 435 QADAGHTFNGURPAGAAGAEAGAAPA-----GRG-----PW 467
Qy 425 FPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVIDHPVHLKFNVSIGKAAALVYGRKGL 484
Db 468 VTRNSSIDSGETEVGRKVTQEVPPGVFWRSQIHISQPFKFNISLGKDALFGVYIRRG 527
Qy 485 PPSHTQDFVELLDGRRLLTQEARSLGCTPRQSRGTVPSSSHETGTFQYLDSDGIMHAFY 544
Db 528 PPSHAQYDFMERLDGK-----EKWSVESPRERRSIQTLVQNEAVFVQYLDVGLMHLAFY 582
Qy 545 NDGKESEVVSFLTATJESVDNCPNCGYNGDCISGTCFGLFLGDPDGRASCPCVLCSGN 604
Db 583 NDGKKEVVSFTVILDSVQDCPRNCHGNGECVSGVCHCFPGPHGADCAKACPCVLCSGN 642
Qy 605 GOYMKGRCLCHSGWKGAECDDVPTNQCIDVACSNHGTCTITGTCICNPYKGESCEEVD 664
Db 643 GOYSKGTCLCYSGWKGPEDVPISQCIDPSCGHSGCIEGNCVCSIGYKGENCEEVD 702
Qy 665 PTCSEGVVGRCHCFVCHGNGTNCETPRATCLDQCSGHGTFPLPDTGLCSDPSWTHDC 724
Db 703 PTCNSHGVCVNGECLSPGNGGINCBLPRAQCPCQCSGHGTYLSDTGLCSDPNMMPDC 762
Qy 725 STEICAADCGHGVCGVGTCCBEGMGAACDORACHPRCAEHGTCDRGKCECSPGNWGE 784
Db 763 SVEVCSDCGTHGVCITGGACRCSEGTGACDORVCHPRCTEHTGTXDKGKCEBEGN 822
Qy 785 HCTIAHYLDVRVVKEGCPGLCNGNCRCTLDLNGWHVCQLGWRGAGCDTSMETACGSD 844
Db 823 HCTIGRTTGTETDGGCDLNCNGNCRCTLQNSNQCVQCTGWRGPGCNVAMETSCAD 882
Qy 845 DGDGLVDCMDPCCQLPCHINPLCLGSPNPLDIIOETQVPVQOQNLHSPYDRIFLVGR 904
Db 883 EGDGLVDCVPCCLQSTQNSLLCRGSRDPLDIIQOSH--SGSPA VKSPYDRIFLVGR 940
Qy 905 DSHTHIPGENPDPGHCACVIRGOVMTSDGTPLVGNISFVNNPLFGVTIISROQGS 964
Db 941 DSHTHIPGENPFPNSLVSLRGQVVTGTPLVGNVSVFKYPKYGTITRQDGMFLVA 1000
Qy 965 NGGISILPERAPFITQHTLMLPDRFPFVMTIIMRHEENIPSCDLSNFARPNPVVS 1024
Db 1001 NGSSILTHPERAPFMSQERTVNLWNFSYAMDTLVNKTENSIPSCDLSGFVRPDP 1060
Qy 1025 PSLTSPASCAKBPVPIQALQBEISISGCMRLSYLSRTPGKSVLRISLTHPTI 1084
Db 1061 SSPSTFFSDAPGRNPVTPETQVLHBEIEVPSSIKLIYLSRRTAGYKSLKIMTOS 1120
Qy 1085 PFNLMKVHLMVAVEGRLFRKFAAAPDLSYFTWDTVDVNVOKVFLSEAFVSUYEVES 1144
Db 1121 PLNLIKVHLMVAVEGHFLFKSFLASPLATVTFIWDKTDAYGQKYGVLSDAVSV 1180
Qy 1145 CPDILWEKRTTVLQGYEIDASKLGGWSLDKHALNATQSGILHKGNGENOFVSQPP 1204
Db 1181 CPSLILWEKRTALQGFELDPNLGGWSLDKHLVNVKSGILHKGNGENFLTQPPAV 1240
Qy 1205 SIMNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGFYNYTRIRPPSG 1264
Db 1241 SIMNGRRRSISCPSCNGLAEGNKLAPVALAVIGDGLSFGVDFNYTRIRPPSR 1300
Qy 1265 ELRNKDFRSHSFAHKYLLATDPMGNAFLSDNSRBFVKI KSTVVVKDILVQNSEV 1324
Db 1301 ELRNKDFRSHSFAHKYLLAVDPVSGLSYSDTNSRIYKVSUTGTGLAGNSEV 1360
Qy 1325 GDCLPDDPRCDGGKATEATLTNPRGITVDKFLGYFVDGTMIRRIDONGIISTL 1384
Db 1361 GEQCLPFDEARCGDGKAVDATLMSPRGIADVXYGLMYFVDATMIRKVDQNGI 1420
Qy 1385 NDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYLDNNVVLQISNHOVRI 1444

Db 1421 NDLTAVRPLSCDSSMDVSQVRLEWPTDLAVDPMDNSLYVLENNVILRITENHOVSIAGR 1480
Qy 1445 PWHCOVPGDHFLLSKVAIHTALESATALAVSHNGVLYIAETDEKKINRIQVITTSGEIS 1504
Db 1481 PWHCOVPGID-VLSLSKLAIHSALESASATAISHTGVLYISETDEKKINRLQVITNGEIC 1539
Qy 1505 LVAGAPSGCDCKNDAMDCDFSGDGDYAKDAKNTSSLCVACADGELYVADLGNIRIRPTR 1564
Db 1540 LLAGAASDCCKNDVNCNCYSGDDGYATDAILNSPSSLA VAPDGYIADLGNIRIRAVS 1599
Qy 1565 KXKPFINTQMYELSSPIDOELYLFDTTKHLYTOSLPTG DYLYNFTYTGDDITLITDN 1624
Db 1600 KNRPIILNSFQYEAASPGQEELYVFNADGIHQYTLISLVTGEYLYNFTYSSDNDVTEVMS 1659
Qy 1625 NGMVMVNRDSTCMPLMLVVPDGOVYVWVTMGFNSALKSVTTQGHELAMWTHGNSGLLAT 1684
Db 1660 NGNSLKVRRDASGMPHLLMPDNQIVTLAVGTNGGLKVSTQTLBELGLMNTYNGSGLLAT 1719
Qy 1685 KSNENGWTFYBYDSEFGRLTNTVPTFGQVSSFRSDTSSVHVQVETSSK-DDVTITNLS 1743
Db 1720 KSDGTGWTTFYDHEGRLTNTVPTGVVTSLHREMEKSIITDIENSNRDDDDVTITNLS 1779
Qy 1744 ASGAFYTLQDVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGNKRVTLTP 1803
Db 1780 SVEASYTVVQDVRNSYQLCNGTLRLVMYANGMSISFHSPEHVLAGTVPTTIGRCNISLP 1839
Qy 1804 IDNGLNLVEMRORKEAQGVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRRKFTLRI 1863
Db 1840 MENGLNSIEMRLKEQIKGVTVFGRKLRVHNRNLLSIDYDRNIETEKIYDDHRRKFTLRI 1899
Qy 1864 LYDQAGRPLSLWSPSSRLNGVNTYSPGGYIAGIQIGIMSEMEYDQAGRITRSIFADGKT 1923
Db 1900 IYDQGRPLPLPSSGLAAVNVSPFNGRLAGLORGAMSERDIDKQGRILSMEFADGKV 1959
Qy 1924 WSYTYLEKSMVLLHSQROYIIEFDKNDRLSSVTMPNVARQLETIRSVGYVRNYIQPPE 1983
Db 1960 WSYTYLEKSMVLLQSROYIEFYDSSDRLHAVTMPFSVARHSMSTHTSVGYIRNYNPPE 2019
Qy 1984 GNASVIQDFTEDGHLHLLPYLGTGRVLYKYGKLSKLAETLYDTHKVSFTYDTEAGMLKT 2043
Db 2020 SNASVIFDSDGRLIKTSFLGTGQGVKYGKLSKLSIEVYDSTAVTFGDEITGVLMK 2079
Qy 2044 INLQNEGFTCTIRYQIGPLIDRQIFRTEEGMVNAREFDYNY-DNSFRVTSMQAVINETP 2102
Db 2080 VNLQSGGFCTIRYKIGPLVDKQIVRFPSEEGMVNAREFDYTVHDSNFIASIKPIISETP 2139
Qy 2103 LPIDLYRDDVUSKTEQFGKFGVYIYDINOIITTAWTHTKHFDAYGRMKEVQYEIFRSL 2162
Db 2140 LPVDLYRYDEISGKVEHFGKFGVYIYDINOIITTAWTHLSKHFDTHGRKEVQYEMFRSL 2199
Qy 2163 MYWMTVQYDNMGRVVKELKVGYPYANTTRYSYEYDADGLOQTVSINDKPLWYSYDLNGN 2222
Db 2200 MYWMTVQYDNMGRVTKELKVGYPYANTTRYSYDGDGQLOQSAVANDRPTWYSYDLNGN 2259
Qy 2223 LHLSPGNSARLTPLRYDIRDIRLGLDVQVQKMDGDFLQRGGDIFBYNSAGLLIKAYN 2282
Db 2260 LHLNPGNSVRLMPLRYDLRDIRLGLDIPYKIDDDGFLCQRGSDVFEYNSKGLLTRYN 2319
Qy 2283 RAGSHSVRYRDLGRRVSSKSHSHLOFFYADLTNTKTTHLYNHSSEITSILYDLQ 2342
Db 2320 KANGWNVQYRYDGLGRRASCKNTLGHILQYFYADLHNPTRVTHVYNHSNBSITSILYDLQ 2379
Qy 2343 GHLPAMELSSGDEFYIACDNIGTPLAVFSGTGLMKQILYTAGYGIYMDTNPNFQIIGY 2402
Db 2380 GHLPAMESSGEEYVAGDNTGTPPLAVFSINGLMIKLOQYTAGYGIYDSDPDLQVIGF 2439
Qy 2403 HGGLYDPLTKLVHMGRRDYDLVLAGRWTSFDPHELMKHLSSSNVMPENLYMFKNNNPISNSQ 2462
Db 2440 HGGLYDPLTKLVHFTRDYDLVLAGRWTSFDTVMWKNIGREPA-PENLYMFKSNPNLSNEL 2498
Qy 2463 DIKCFMTDVNSWLLTFGQLHNVIQYKPKPMDAMEPSYELIHTQMTQEWDNKSILGV 2522
Db 2499 DLKNTVTDVKSVMVFGQLSNIIIPGFPRAKMYFVSPPYEL-----TESQACENGOLITGV 2554

Qy 2523 OCEVQKOLKAFVTLERFDOLYGSTITSCQOAPTKK-----PASSGSVFGKGVKALKDGR 2578
Db 2555 QOTTERHNQAFMALE-----QGVISKRLHASIREKAGHWFPATSTPIIGKGMFAVKGR 2608
Qy 2579 VTTOIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPSPSGDLAILGLSGGR 2638
Db 2609 VTTGSIATDDSRKIASVLSAHLEKWHYISGKTHYFVKIGSADSLVTLAMTSGR 2668
Qy 2639 RTLENGVNVTVSQINTVNLNGRTRYTDIOLOYGALCLNTRYG-----TTLDEKARVLELAR 2695
Db 2669 KVLDSGVNVTVSQPTLLINGRTRFRFTNIEFOYSTLLINIRYGLTADTLDEKARVLDQAR 2728
Qy 2696 QRAYRQAWARQOURLREGEGLRAWTEGKQOVLSTGRVQGYDGFVVISVQYPELSDSA 2755
Db 2729 QRALGSWAKEQQKARDGREGSRVWTDGKQOLLNTRGVQGYEGYVLPVPEQYPELADSS 2788
Qy 2756 NNIHFMROQSEMR 2769
Db 2789 SNIQFLRQNEGKR 2802

RESULT 15

US-09-800-198-69
; Sequence 69, Application US/098000198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Cornie AM
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herimann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 2802
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-800-198-69

Query Match 64.6%; Score 9616.5; DB 3; Length 2802;
Best Local Similarity 61.3%; Pred. No. 0;
Matches 1775; Conservative 411; Mismatches 491; Indels 217; Gaps 27;
Qy 1 MDVKERKPYRSLTRRR-DAERRYTSASADSEEGKAP-QKSYSSSETLKAYDQDARLAYGS 58
Db 1 MDIKDRR-HRSLTRGRCGECRVTSLSLSDCKRVPAQKSYSSSETLKAYGHDTRMHYGN 59
Qy 59 RVKDIVPOEAEBCRTCANETLRELGLLEETPPHGTLYRDTIGLPQCGYSGAGSDADME 118
Db 60 RVSDLVHRESDEPQGTNFTLAEGLICEPS-PHRSGYCSGDI GILHQYSLTSGSDADSD 118
Qy 119 ADTVLSPHVRVLRWGRSTRSGRSCSLSSRANSNLTLTDTBHEN----- 161
Db 119 TEGGMSPEAIRLWGRGIKSSRSGSLSSRNSALTITDSNENKNSDEENDPHLSEKLK 178
Qy 162 -----TETDH--- 166
Db 179 DRQTSWOOLAETKNLIRRPPTPTSSSLPSAQLPSSHNPVPVSCOMPLDSDNTHSQIM 238
Qy 167 -----PGQLNH---ARLRTP-PPPLSHAHTPNQOHAASI 197
Db 239 DTNPDEEFPNSYLLRACSGPQQAQSSGSPSNHHSQSLRPLRPPPHNHSLS---HHHSSA 295

| | | | |
|----|------|---|------|
| Db | 2380 | GHLFAMESSSGEEYVVASDNTGTPLAVFSINGLMIKLOQYATAYGEIYYDSNPDFQLVIGF | 2439 |
| Qy | 2403 | HGGLYDPLTKLVHMGRDYYDLAGRWTSPDHELWKHLSSNVMPFNLYMPKNNPISNSQ | 2462 |
| Db | 2440 | HGGLYDPLTKLVHFTQDYDLAGRWTSPDYTWKNI GREPA-PFNLYMFKSNPNLSNEL | 2498 |
| Qy | 2463 | DIKCFMTDVNSWLLTFGFLHNHVI PGYPKPDMDAMEPSYELIHTQMKTOEWDNSKSILGV | 2522 |
| Db | 2499 | DLKNYVTDVKSWLVMFGFQLSNIPGFPRAKMTFVSPPYEL-----TESQACENGQLITGV | 2554 |
| Qy | 2523 | QCEVQKQLKAFVTLERFDQLYGSTITTSQQAPKTKK- ---FASSGSVFGKGVKFKDKGR | 2578 |
| Db | 2555 | QOTTERHNQAFMALE-----GQVISKRLHASIREKAGHWFATSTPIIGKIMFAVKGR | 2608 |
| Qy | 2579 | VTTDIIISVANEDGRRVAAILNHAHYLENLHFTTDGVDTHTYFVKPGPSEGD LAILGLSGGR | 2638 |
| Db | 2609 | VTTGISSIATDDSRKIASVLNSAHYLEKMHYSIEGKDTHTYFVKIGSADSDLVTLAMTSGR | 2668 |
| Qy | 2639 | RTLENGVNVTVSQINTVLNGRTRRYTDIOLQYGALCLNTRYG-- --TTLDEEKARVLELAR | 2695 |
| Db | 2669 | KVLDSGVNVTVSQPTLLINGRTRFTNIEFQYSTLLINIRYGLTADTLDEEKARVLDQAR | 2728 |
| Qy | 2696 | QRAVROAWAREQQRLREGEGLAWTEGEKQQVLTGRVQGYDGFVVISVEQYPELSDSA | 2755 |
| Db | 2729 | QRALGSAWAKEQQKARDGREGSRVWTDGKQQLNTRGVQGYEGYVYLPVEQYPELADSS | 2788 |
| Qy | 2756 | NNIHFMRQSEMGRR | 2769 |
| Db | 2789 | SNIQFLRQNEWGRK | 2802 |

Search completed: December 11, 2005, 05:02:00
Job time : 187 secs

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OM protein - protein search, using sw model

Run on: December 11, 2005, 04:48:57 ; Search time 11 Seconds
(without alignments)
1405.752 Million cell updates/sec

Title: US-10-029-020-14
Perfect score: 14887
Sequence: 1 MDVKERKPYRSLRRRDAER.....ELSDSANNIFHMRQSEWGR 2769

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New:
1: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_PEP.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP.*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_PEP.*
5: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_PEP.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_PEP.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB_PEP.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 14887 | 100.0 | 2769 | 7 | US-11-113-424-14 |
| 2 | 10258 | 68.9 | 2715 | 7 | US-11-096-051-2 |
| 3 | 10227 | 68.7 | 2715 | 7 | US-11-113-424-51 |
| 4 | 10221 | 68.7 | 2721 | 7 | US-11-096-051-10 |
| 5 | 10201 | 68.5 | 2725 | 7 | US-11-096-051-8 |
| 6 | 9584 | 64.4 | 2725 | 7 | US-11-113-424-52 |
| 7 | 9296 | 62.4 | 2376 | 6 | US-11-096-051-4 |
| 8 | 4175.5 | 28.0 | 1094 | 6 | US-10-821-234-1097 |
| 9 | 3979.5 | 26.7 | 1045 | 7 | US-11-113-424-54 |
| 10 | 3854 | 25.9 | 730 | 7 | US-11-113-424-50 |
| 11 | 3804.5 | 25.6 | 2515 | 7 | US-11-113-424-53 |
| 12 | 3276 | 22.0 | 862 | 7 | US-11-096-051-20 |
| 13 | 3270 | 22.0 | 821 | 7 | US-11-096-051-6 |
| 14 | 2418.5 | 16.2 | 607 | 7 | US-11-096-051-14 |
| 15 | 1268.5 | 8.5 | 257 | 7 | US-11-096-051-12 |
| 16 | 1268.5 | 8.5 | 296 | 7 | US-11-096-051-18 |
| 17 | 546 | 3.7 | 214 | 7 | US-11-096-051-16 |
| 18 | 411.5 | 2.8 | 1218 | 7 | US-11-078-735-20 |
| 19 | 404.5 | 2.7 | 1238 | 7 | US-11-078-735-19 |
| 20 | 342 | 2.3 | 723 | 7 | US-11-078-735-17 |
| 21 | 334.5 | 2.2 | 379 | 6 | US-10-131-826A-308 |
| 22 | 334 | 2.2 | 723 | 6 | US-10-131-826A-346 |
| 23 | 323.5 | 2.2 | 685 | 6 | US-10-131-826A-88 |
| 24 | 323.5 | 2.2 | 685 | 7 | US-11-078-735-19 |
| 25 | 316 | 2.1 | 484 | 7 | US-11-078-735-43 |

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|----|-------|-----|------|---|--------------------|-------------------|
| 26 | 293 | 2.0 | 618 | 7 | US-11-078-735-18 | Sequence 18, Appl |
| 27 | 291.5 | 2.0 | 3717 | 6 | US-10-821-234-1076 | Sequence 1076, Ap |
| 28 | 279.5 | 1.9 | 3002 | 6 | US-10-821-234-916 | Sequence 916, App |
| 29 | 278 | 1.9 | 383 | 7 | US-11-147-047-38 | Sequence 38, Appl |
| 30 | 275 | 1.8 | 1400 | 6 | US-10-821-234-1045 | Sequence 1045, Ap |
| 31 | 264 | 1.8 | 369 | 7 | US-11-078-735-38 | Sequence 38, Appl |
| 32 | 261.5 | 1.8 | 3500 | 7 | US-11-085-775-2 | Sequence 2, Appl |
| 33 | 243.5 | 1.6 | 504 | 6 | US-10-999-782-2 | Sequence 48, Appl |
| 34 | 227 | 1.5 | 816 | 7 | US-11-090-439-48 | Sequence 4, Appl |
| 35 | 222 | 1.5 | 336 | 6 | US-10-478-345-4 | Sequence 2, Appl |
| 36 | 216 | 1.5 | 965 | 7 | US-11-113-424-2 | Sequence 6, Appl |
| 37 | 213 | 1.4 | 357 | 6 | US-10-478-345-6 | Sequence 33, Appl |
| 38 | 212 | 1.4 | 331 | 7 | US-11-078-735-33 | Sequence 51, Appl |
| 39 | 212 | 1.4 | 332 | 7 | US-11-078-735-51 | Sequence 35, Appl |
| 40 | 209.5 | 1.4 | 897 | 7 | US-11-137-465-35 | Sequence 58, Appl |
| 41 | 208 | 1.4 | 964 | 7 | US-11-137-465-58 | Sequence 51, Appl |
| 42 | 208 | 1.4 | 965 | 7 | US-11-147-047-51 | Sequence 35, Appl |
| 43 | 205.5 | 1.4 | 961 | 7 | US-11-113-424-35 | Sequence 1016, Ap |
| 44 | 204.5 | 1.4 | 652 | 6 | US-10-821-234-1016 | Sequence 8, Appl |
| 45 | 199.5 | 1.3 | 321 | 6 | US-10-478-345-8 | |

ALIGNMENTS

RESULT 1
US-11-113-424-14
; Sequence 14, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 2769
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-14

Query Match 100.0%; Score 14887; DB 7; Length 2769;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDVKERKPYRSLRRRDAERYTSSADSEEGKAPQKYSSETLKYADQARLAYGSRV 60
Db 1 MDVKERKPYRSLRRRDAERYTSSADSEEGKAPQKYSSETLKYADQARLAYGSRV 60
Qy 61 KDIVPQAEFFCRTGANFTLRELGLEEVTPPHGTYRTDGLPQCGYSMGAGSDADMEAD 120
Db 61 KDIVPQAEFFCRTGANFTLRELGLEEVTPPHGTYRTDGLPQCGYSMGAGSDADMEAD 120

QY 121 TVLSPEHPVRLWGRSTRSSRSCSSRANSNLTLTDTEHENTETDHPGGLQNHARLRTPP 180
DB 121 TVLSPEHPVRLWGRSTRSSRSCSSRANSNLTLTDTEHENTETDHPGGLQNHARLRTPP 180
QY 181 PPLSHAHTPNQHAASINSINLRGNFTPRSNPSPAPTDHSLSGEPAGGAQEPAAHAQENWL 240
DB 181 PPLSHAHTPNQHAASINSINLRGNFTPRSNPSPAPTDHSLSGEPAGGAQEPAAHAQENWL 240
QY 241 LNSNIPLETRNLGKQPFGLTQDNLIEMDILGASRHDGAYSOGHFLFKPQGGTSPFCTTS 300
DB 241 LNSNIPLETRNLGKQPFGLTQDNLIEMDILGASRHDGAYSOGHFLFKPQGGTSPFCTTS 300
QY 301 PGVPLTSSVTYSPPPRPLPRSTFARPAFLKPKSKYCNWKAALSAIVISATLVILLAYF 360
DB 301 PGVPLTSSVTYSPPPRPLPRSTFARPAFLKPKSKYCNWKAALSAIVISATLVILLAYF 360
QY 361 VAMHLFGLNHLQPMQEGMYEITEDTASSWPVPTDVSLYPSGGTGLTDPDRKGKGTTEBK 420
DB 361 VAMHLFGLNHLQPMQEGMYEITEDTASSWPVPTDVSLYPSGGTGLTDPDRKGKGTTEBK 420
QY 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIIDHPVHLKFNVSLSGKAALVGIYG 480
DB 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIIDHPVHLKFNVSLSGKAALVGIYG 480
QY 481 RKGLEPSSHQFDFVELLDGRRLLTOEARSLGTQPSRGTVPPSSHETGFIQYLDGSIWH 540
DB 481 RKGLEPSSHQFDFVELLDGRRLLTOEARSLGTQPSRGTVPPSSHETGFIQYLDGSIWH 540
QY 541 LAFYNDGKESEVVSFLTTAIESVDNCPNSCYNGDCISGTCFCFLGFLGPDGCRASCPVL 600
DB 541 LAFYNDGKESEVVSFLTTAIESVDNCPNSCYNGDCISGTCFCFLGFLGPDGCRASCPVL 600
QY 601 CSGNGQYMKGRCLCHSGWGAECDVPTNQCIIVACSNHGTCITGTICNPGYKGSCEB 660
DB 601 CSGNGQYMKGRCLCHSGWGAECDVPTNQCIIVACSNHGTCITGTICNPGYKGSCEB 660
QY 661 DCMWPTCSGRGVCVRGECHCFVWGNGTNCETPRATCLDQCSGHGTFPLDPTGLCSDPSWT 720
DB 661 DCMWPTCSGRGVCVRGECHCFVWGNGTNCETPRATCLDQCSGHGTFPLDPTGLCSDPSWT 720
QY 721 GHDCSIEICAADCGGHGVCVGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECSPG 780
DB 721 GHDCSIEICAADCGGHGVCVGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECSPG 780
QY 781 WNGHERCTIAHYLDVRVKEGCPGLCHNGHCTLDLNGWHCVCOLGWRGACDTSMBTAGD 840
DB 781 WNGHERCTIAHYLDVRVKEGCPGLCHNGHCTLDLNGWHCVCOLGWRGACDTSMBTAGD 840
QY 841 SKONDGDLVDWDPDCCLOPLCHINPLCLGSPNPLDIIQETQVPVSQONLHSFYDRIKF 900
DB 841 SKONDGDLVDWDPDCCLOPLCHINPLCLGSPNPLDIIQETQVPVSQONLHSFYDRIKF 900
QY 901 LVGRDSTHIIIPGENPPDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTIISRDQGSF 960
DB 901 LVGRDSTHIIIPGENPPDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTIISRDQGSF 960
QY 961 DLVTNGGISIILRFERAPITQEHTLWLWDPRFFWETIIMRHEENEIPSCDLSNFARPN 1020
DB 961 DLVTNGGISIILRFERAPITQEHTLWLWDPRFFWETIIMRHEENEIPSCDLSNFARPN 1020
QY 1021 PVVSPSLTSFASSCAEKGPVPEIQALQEBEISISGCKMRLSYLSRSTPGYKSVLRIISLT 1080
DB 1021 PVVSPSLTSFASSCAEKGPVPEIQALQEBEISISGCKMRLSYLSRSTPGYKSVLRIISLT 1080
QY 1081 HPTIPENLMKVLWMAVEGRLEFRKFAAPADLSYFIWDKTDVYNQKQVFLGSEAFVSYG 1140
DB 1081 HPTIPENLMKVLWMAVEGRLEFRKFAAPADLSYFIWDKTDVYNQKQVFLGSEAFVSYG 1140
QY 1141 EYESCPDLILWEKRTTVLOGYBIDASKLGGWSLDKXHALNQSGLLHKNGENQVFSQOP 1200
DB 1141 EYESCPDLILWEKRTTVLOGYBIDASKLGGWSLDKXHALNQSGLLHKNGENQVFSQOP 1200
QY 1201 PVTGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVVGDFNYIRRIFFPSGNV 1260

DB 1201 PVTGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGFENYIRRIFFPSGNV 1260
QY 1261 TNILELRNKRKOPRSHSPAHKYIYLATDPMGSAVFLSDSNSRRVFKIKSTVVVKDLVKNSEV 1320
DB 1261 TNILELRNKRKOPRSHSPAHKYIYLATDPMGSAVFLSDSNSRRVFKIKSTVVVKDLVKNSEV 1320
QY 1321 VAGTGDOCLPDDPTRCDDGGKATEATLTNPRGIVTDKFGLIYFVDBGTMIRRIDONGIIST 1380
DB 1321 VAGTGDOCLPDDPTRCDDGGKATEATLTNPRGIVTDKFGLIYFVDBGTMIRRIDONGIIST 1380
QY 1381 LLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYLDNNVVLQISENHQRVRI 1440
DB 1381 LLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYLDNNVVLQISENHQRVRI 1440
QY 1441 VAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIQVTTTS 1500
DB 1441 VAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIQVTTTS 1500
QY 1501 GEISLVAGAPSGCDCKNDANCDPFGDDGYAKDAKLANTPBSSLAVCAGELYVADLGNIRI 1560
DB 1501 GEISLVAGAPSGCDCKNDANCDPFGDDGYAKDAKLANTPBSSLAVCAGELYVADLGNIRI 1560
QY 1561 RFIRKNKPFNLTONMYELSSPIDOELYLFDTTGKHLYTQSLPTGDLYLNFYTTGDDGITL 1620
DB 1561 RFIRKNKPFNLTONMYELSSPIDOELYLFDTTGKHLYTQSLPTGDLYLNFYTTGDDGITL 1620
QY 1621 ITDNNGNMNVRRDSTGMPLWLVPDQGVVWVTGNTNSALKSVTTQGHELAMTYHGN 1680
DB 1621 ITDNNGNMNVRRDSTGMPLWLVPDQGVVWVTGNTNSALKSVTTQGHELAMTYHGN 1680
QY 1681 LLATKSNENGWTTTFEYDVSFGRLTNTVTFPTGOVSSFRSDTSSVHVQVETSSKDDVTITT 1740
DB 1681 LLATKSNENGWTTTFEYDVSFGRLTNTVTFPTGOVSSFRSDTSSVHVQVETSSKDDVTITT 1740
QY 1741 NLSASGAFYTLLODQVRNSYVIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVKGKRV 1800
DB 1741 NLSASGAFYTLLODQVRNSYVIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVKGKRV 1800
QY 1801 TLPIDNGLNLVEMVQRKEQARGQVTFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFT 1860
DB 1801 TLPIDNGLNLVEMVQRKEQARGQVTFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFT 1860
QY 1861 LRILLYDOAGPSLWSPSSRLNGVNVTVSPGYTAGIQRGIMSERMEYDQAGRITSRIIFAD 1920
DB 1861 LRILLYDOAGPSLWSPSSRLNGVNVTVSPGYTAGIQRGIMSERMEYDQAGRITSRIIFAD 1920
QY 1921 GKTWSYTYLEKSMVLLLSHRSORQYIFEFDKNDRLSSVTMPNVARQTLTETIRSVMGYRNIYQ 1980
DB 1921 GKTWSYTYLEKSMVLLLSHRSORQYIFEFDKNDRLSSVTMPNVARQTLTETIRSVMGYRNIYQ 1980
QY 1981 PPEGNASVIOQDFTEDGHLLHTFYLGTORRVIYKYGKLSKLAETLYDTTKVSYFTYDETAGM 2040
DB 1981 PPEGNASVIOQDFTEDGHLLHTFYLGTORRVIYKYGKLSKLAETLYDTTKVSYFTYDETAGM 2040
QY 2041 LKTINLQNEGFTCTIRVROIGPLIDROI FRFTEBGMNARFDYNDNSFRVTSMQAVINE 2100
DB 2041 LKTINLQNEGFTCTIRVROIGPLIDROI FRFTEBGMNARFDYNDNSFRVTSMQAVINE 2100
QY 2101 TPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKVEQYEIFR 2160
DB 2101 TPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKVEQYEIFR 2160
QY 2161 SLMTYMTVQYDNMGRVVKELKVGFPYANTTRYSEYDADGOLQTVSINDKPLMRYSDLN 2220
DB 2161 SLMTYMTVQYDNMGRVVKELKVGFPYANTTRYSEYDADGOLQTVSINDKPLMRYSDLN 2220
QY 2221 GNHLHLLSPGNSARLTPLRYDIRDRI TELGDVQYKMDGDFLQRGGDIFEVNSAGLLIKA 2280
DB 2221 GNHLHLLSPGNSARLTPLRYDIRDRI TELGDVQYKMDGDFLQRGGDIFEVNSAGLLIKA 2280
QY 2281 YNRAGSVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSETTSYYD 2340

| | | |
|--|------|--|
| Query Match | | 68.7%; Score 10227; DB 7; Length 2715; |
| Best Local Similarity | | 66.7%; Pred. No. 0; |
| Matches 1864; Conservative 370; Mismatches 457; Indels 102; Gaps 19; | | |
| Qy | 1 | MDVKRPYSLTR--RDABRRYTSSADSEBKAP--OKSYSSSETLKAYDQD--ARLAYG 57 |
| Db | 1 | MDVKRRPYCSLTKSRREKERRYTNSSADNEECRVPTQKSYSSSETLKAFDHDYSLLYG 60 |
| Qy | 58 | SRVKDIPVQAEBCFRTGANFTLRELGLEEVTPPHGTYLRTDGLPCGSGMAGSDADM 117 |
| Db | 61 | NRVKDLVHREADEYTRQGNFTLRQUGVCESATRGVAFCAEMLGPHRGVSIISAGSDADT 120 |
| Qy | 118 | EADTVLSPEHPVLWGRSTRSGRSSCLSSRANSNLTLTDTHEHN---TETDPHGLQNH 174 |
| Db | 121 | ENEAVMSPHARLWGRGVKSGRSSCLSSRSNSALTLTDTHEHNRSDSESEQFSNNPGQP 180 |
| Qy | 175 | RLRTPPPPLSHAHTPNQHHASINSLNRGNFTPRSPNPSPAPTSHLSGEBPAGAQ--- 230 |
| Db | 181 | TLQDPLPP--SHKQHPAQHH--PSITSLNRNSLTNRRNQSPAP-----PAALPAELQTT 229 |
| Qy | 231 | -EPAHQENWLLNSNIPLETNRLGKQFPFLGTLDQNLIEMDILGASRHDGAYSOGHFLFKP 289 |
| Db | 230 | PESVLQDQSVLWGSNVPLESR-----HELFKT 256 |
| Qy | 290 | G-GTSPFLCTTSPGYPLTSTVYSPPPRPLPRSTFAPAPNLKKPSKYCNWKAALSAYV 348 |
| Db | 257 | GTGTPFLFSTATPGYTWASGSVSPPTPLPRNTLSRSAFKFKSSKYCSWRCTALCAVG 316 |
| Qy | 349 | ISATLVILLAYFVAMHLFGLNWHLPQMEGWYE---ITEDTASSWPVPTDVSLYPSGGTG 405 |
| Db | 317 | VSULLAILLSYFTAMHLFGLNWHLQQTENDTFENGKVNST-----VPTNTVSLPSG--- 368 |
| Qy | 406 | LETPDRKGGKTTEGKPSFFPEDSPIDSGEIDVGRASOKIPBCTFWRSQVFIDHPVHLK 465 |
| Db | 369 | -----DNKGCGFTHENNTIDSGELDIGRAIQEVPPGIFWRSOLFIDQPOFLK 417 |
| Qy | 466 | FNVSLGAALVGIYGRKGLPSPHTQFDFVELLDGRRLLTOEARSLEGTQRSGTVPSS 525 |
| Db | 418 | FNTSLQKDALIGVYGRKGLPSPHTQYDFVELLDGSRLLIAREQNLVSEERAGQARSVL 477 |
| Qy | 526 | HETGFIQYLDPSGIWHLAFYNDGKSESVSFLTTAIESVDNCPNCGYNGDCISGTCHCFL 585 |
| Db | 478 | HEAGFIQYLDPSGIWHLAFYNDGNKPEQVSWNTIVIESVWECPRNCHNGECVSGTCHCFP 537 |
| Qy | 586 | GFLGPDGCRASCVPVLCSGNGYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCTGT 645 |
| Db | 538 | GFLGPDGCSRAACPVVLCSGNGQYSGRCLCFSGWKGTEDCVPTTQCIDPQCGGRGICIMG 597 |
| Qy | 646 | CICNPYKGBSCERVDQMDPTCSGRGVCVRGECHCFVGWGTNCETTPRATCLDQCSGHT 705 |
| Db | 598 | CACNSGYKGENCEBADCCLDPGCSNHWGVCIIHGECHCNFGWGSNCEIILKTMCAQCSCGHT 657 |
| Qy | 706 | FLPDTGLSCDPSWTHGDCSIEICAADCGGHGVCGGTCTRCBGMGAACDQACRCHPCA 765 |
| Db | 658 | YLOESGSCDPPNWTGPDSCNEICSVDCSGHGVCMWGSRCSEBEGTGPACNQACRCHPCA 717 |
| Qy | 766 | EHGTCRDKCECSFGWNGEHTCIAHYLDYRVVKECPGLCHNGRGTCLDNGHWCVCOLGW 825 |
| Db | 718 | EHGTCRDKCECSQGWNGEHTCIAHYLDKIVKEGCPGLCNSNGRCTLQDNGHWCVCQPGW 777 |
| Qy | 826 | RGACDTSMETACGSDKNDGDGLVDCMDPCCLOPLCHTNPLCLGSPNPLDIIQETQVP 885 |
| Db | 778 | RGACDVAHMETLCTSDKDNEDGGIUDCMDPCCLLQSSCQNPYCRGLPDPQDIISQSLOT 837 |
| Qy | 886 | VSQNLHSPFYDRIKFLVRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVN 945 |
| Db | 838 | PSQAAKSFYDRIISFLIGSDSTHVLPGESPKNKSLASVIRQVLTADGTPLIGVNVSLFH 897 |
| Qy | 946 | NPLFGYTIRODGSFDLVNCGIISILIRFERAPFITQEHTLWLWDWFFVWETIMHREE 1005 |
| Db | 898 | YSBYGYTITRODGMFDLVANGASLTLVFERSPFLTQYHTWVIWPNVYFYNDTLVLMKKEE 957 |
| Qy | 1006 | NEIFSCDLSNPARPNPVVSPSPLTSFASSCAKEGPIVPEIQALQEEISISCKMKLSYLS 1065 |

| | | |
|----|------|---|
| Db | 958 | NDIPLSCDLSGFRVPSPIIVSSPLSTFFRSPEDSPIIPETQVLHEETTPGTDLKLSYLS 1017 |
| Qy | 1066 | SRTPGVKSVLRISLSTHTPTIPENLMKVHLMVAVEGRLFRKWFAAAPDLSYFYFWDKTDVYN 1125 |
| Db | 1018 | SRAAGYKSVLKITMTQAVIPFNLMKVHLMVAVVGRLFQKWFPPASPNLATFFIWDKTDAYN 1077 |
| Qy | 1126 | QKVFLGSEAFVSVGYEYESCPDLILWEKRTTVLQGYEIDASKLGGWSLDKGHALNTQSGI 1185 |
| Db | 1078 | QKVYGLSEAVSVVGYEYESCLDLTLWEKRTAVLQGYELDASNNGGWTLDKHVLVDQNGI 1137 |
| Qy | 1186 | LHKNGENQFVSQOPPVIGSIMNGRRRISICPSCNGLADGNKLIAPVALTCSDGSLYV 1245 |
| Db | 1138 | LYKNGENQFISQOPPVWSSIMNGRRRISICPSCNGQADGNKLIAPVALACIDGSLYV 1197 |
| Qy | 1246 | GDPNYIRRIIPPSGNVTNILELRNKDFRHSHPAHKYYLATDPMMSGAVFLSDSNSRRVFKI 1305 |
| Db | 1198 | GDPNYIRRIIPPSGNVTSVLELRNKDFRHNSNPAPHYYLATDPTGDLVYSDTWTTRRIYRP 1257 |
| Qy | 1306 | KSTVVVVKLVKXSEVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFLGIYFVD 1365 |
| Db | 1258 | KSLTGAKDLTKNAEVAAGTGEQCLPFDEARCGDGGKAVEATLMSPKGMAIDKNGLIYFVD 1317 |
| Qy | 1366 | GTMIIRIDQNGIISTLLGSDNLTLSARPLSCDSWMDISOVRLEWPTDLAINPMDSNLYVD 1425 |
| Db | 1318 | GTMIKVDQNGIISTLLGSDNLTLSARPLCTDSMHISOVRLEWPTDLAINPMDSNLYVD 1377 |
| Qy | 1426 | NNVLOISNHQVRIIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAE 1485 |
| Db | 1378 | NNVLOITENRQVRIIAGRPMHCQVPGVE--YPVGKHAVQTTLESATAIAVYSGVLVITE 1436 |
| Qy | 1486 | TDEKINRIRQVTTSGEISLVAGAPSGCCKNDANCDCFSGDDGYAKDAKLTNPSSLAVC 1545 |
| Db | 1437 | TDEKINRIRQVTTDGEISLVAGIPSECDKNDANCDCYQSGDGYAKDAKLNAPSSLAAS 1496 |
| Qy | 1546 | AGELYVADLGNIRIRIRKPKPFLATQNMVELUSSPIDOELYLFDTTGKHLIYQSLSPTGD 1605 |
| Db | 1497 | PDGTLIYADLGNIRIRAVSKNKLNSMNFYVASPTDOELYIFDINGTHQYTVSLVTGD 1556 |
| Qy | 1606 | YLYNFYTTGGDITLITDNNGNMNVVRDSTGMLVLVDPDGOVYVWMTGNSALKSVTT 1665 |
| Db | 1557 | YLYNFYSNDNDVATVDNSNGTNRIRRDPRNPRVVRVSPDNQVIMLTICNCLKSMTA 1616 |
| Qy | 1666 | QGHELAMMTYHNGSGLLATKSNENGWTTTFEYDSFGRLTNVTFPTQVSSFRSDTSSVH 1725 |
| Db | 1617 | QGLVLVLYFHNGSGLLATKSDGTWTFDYDSEGLRTNVTFPTGVVTVNLHGMDCAIT 1676 |
| Qy | 1726 | VQVETSSK--DDVTITNLSAGAFYTLLOQVNRNSYIYIADGSLRLLALLANGMEVALQTEP 1784 |
| Db | 1677 | VDIESSREEDVSITSNLSIDSFTYTWQDLANSYQIGYDGLSRIFYASGLDSHQTEP 1736 |
| Qy | 1785 | HLLAGTVNPTVYKGNVTLPIDNGLNLVEMRQKEQAGQVTVFGRRLRVHNRNLLSLD 1844 |
| Db | 1737 | HVLAGTANPTVAKRNMVTLPGENQNLVEMRFRKQKQGVNVEGRKLRVNGRNLSSVDFD 1796 |
| Qy | 1845 | RVTRTEKIYDDHRKFTLRILYDOAGRPSSLWSPSSRLNGVNVTVYSPGYIAGIQGMISER 1904 |
| Db | 1797 | RTTKTEKIYDDHRKFLRLRAYDTSGHPTLWPSKLMANVNTYSSGTQIASIQGTISEK 1856 |
| Qy | 1905 | MEYDQAGRITSRIIFADGKTWSYTYLEKSMVLLLHLSORQYIFEFDKNDRLSSTVMTMVARQ 1964 |
| Db | 1857 | VDYDSQGRIVSVRFADGKTWSYTYLEKSMVLLLHLSORQYIFEYDMWDRLSAITMPSVARH 1916 |
| Qy | 1965 | TLETIRSVGYRNIYQPPENGNASVIODPTEDGHLHTFYLGTGRVRYKYGKLSKLAETL 2024 |
| Db | 1917 | TMQITRISIGYRNIYNPPESNASIIIDYNSBEGLLQTAFLGTSRRVLFKYYRQTRUSEIL 1976 |
| Qy | 2025 | YDTTKYSFTYDETAGMLKTINLQNEGTCTIRYRQIGPLIDROIIFRTEEGMVARPDYN 2084 |
| Db | 1977 | YDSIRVSFTYDETAGVLTQVNLQSDGFICTIRYRQIGPLIDROIIFRSEDEGMVARPDYS 2036 |
| Qy | 2085 | YDNSFRVTSNQAVINETPLPIDLYRDDVSGKTEQFGKFGVIYDINQIITTAWTHTKH 2144 |

Db 2037 YDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQKFGVIYDINQIISTAVMTYTKH 2096
Qy 2145 FPAIGEMKEVOYEIERSLWYMTVOYDNNGRVVKELKGVYANTTRYSYEDADQLOQT 2204
Db 2097 FPAHGRKEIQEYIERSLWYMTVOYDNNGRVTKREIKIGPPANTTKYAYEYDVGQLOQT 2156
Qy 2205 VGINDKPLWRYSDYDNGNLHLSPGNSARLTPLRDIYDRIRLGDVQVQWDEDFLQR 2264
Db 2157 VYLNKIMRWYDNGNLHLNPPSSARLTPLRDLDRIRLGDVQVRLDEDFLQR 2216
Qy 2265 GGDIFEYNSAGLLIKAYNRAGSVRYRYDGLRRVSKSHHLLQFFYADLTNPTKVT 2324
Db 2217 GTEIFEYSKGLLTRVYSSGWTVIYRYDGLRRVSKSLGQHLQFFYADLTVPTRIT 2276
Qy 2325 HLYNHSSEITSLYDLOGLFAMELSSGDEBYIACDNIGTPLAVPSGTGLMIKQILYTA 2384
Db 2277 HLYNHSSEITSLYDLOGLFAMEISSGDEBYIASDNTGTPLAVPSNGLMLKQOTYTA 2336
Qy 2385 YGEIYMDTNPFIIGYHGGLYDPLTKLVHMRDRDYDLGRWTSPOHELMKHLSSNV 2444
Db 2337 YGEIYFDSNVDFQLVGFHGGLYDPLTKLIHGERDYDLAGRWTTPDIEIWKRI-GKDP 2395
Qy 2445 MFFNLYMFKNNPINSODIKCFMTDVNSWLLTFGQLHNVIYPVKPMDAMEPSYBLI 2504
Db 2396 APFNLYMFRNNPNASKIHVDKIYITDVNSWLVTFGHLHNAIPGFPVKFDLTPEPSYBLV 2455
Qy 2505 HTQMKTOEWDNKSILGVQCEYQKOLKAPVTILERFDOLYGSITITSCQAPKTK----- 2558
Db 2456 ----KSQOMEDVPPIFGVQOQVARQAKAFSLSGKMAEV-----QVSRKKGAEOSW 2502
Qy 2559 --FASSGSVFGKGVFALKDGRVTTDIISVANEDGRRVAAIINHAHYLENLHFTIDGVD 2616
Db 2503 LWFATVKSILIGKVMVLAQGRVQVNLVNIANEDCIKVAALNNAFYLENLHFTIEGKDT 2562
Qy 2617 HYFVKGPESGDLAILGSGGRRTLENGVNVTVSQINTVLNQRTRRYTDIQLQYALCIN 2676
Db 2563 HYFIKTTTPESDLGTLRLTSGRKALENGINTVVSQSTTVNQRTRRRFADVENQFALALH 2622
Qy 2677 TRYGTTLDEKARVLELQARAVRQARQORLEBEGELRAWTEGEKQVLSGTVQOG 2736
Db 2623 VRYGTMTLDEKARILEQARALAWAREQORVRDGBEGARLWTEGKROLLSAGVQOG 2682
Qy 2737 YDGFVVISVEQYPELSDSANNIHFMRQSEMGR 2769
Db 2683 YDGYVVLSEVQYPELADSANNIQLRQSEIGR 2715
RESULT 4
US-11-096-051-10
; Sequence 10, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Eitenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 10
; LENGTH: 2721
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-096-051-10
Query Match 68.7%; Score 10221; DB 7; Length 2721;
Best Local Similarity 67.0%; Pred. No. 0;
Matches 1873; Conservative 362; Mismatches 461; Indels 98; Gaps 20;
Qy 1 MDVKERPYRSLTR-RRDAERRRYTSSADSBEGKAP-QKSYSSSETLKYAQDQ-ARLAYG 57
Db 1 MDVKERPYCSLTKSRREKERRYNTSSADNEECRVPTQKSYSSSETLKAPDHDSSRLLYG 60
Qy 58 SRVKDIYVQABAEFCRTGANFTLRELGLBEVTPPHGLTYRTDIGLPGCGYMGAGSDADM 117
Db 61 NRVKDLVHREADEFTQOQNFTLRQLGVCBPATRRGLAFCAEMGLPHRGYISAGSDADT 120
Qy 118 EADTVLSPHVRPLWGRSTSGRSSCLSSRANSNLTLTDTTEHEN---TETHDHPGLQNH 174
Db 121 ENEAVMPEHAMRLWGRGVKSGRSSCLSSRNSALTUTDTEHNKSUSENQPASNOQGS 180
Qy 175 RLRTPPPLGSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDSLSGEPYPAGGAQ---- 230
Db 181 TLQPLPP--SHKQSAQHH-PSITSLNRNSLTNRNQSPAP-----PAALPAELQTT 229
Qy 231 -EPHAQENMLLSNIPETRNLGKQPLGTLQNLITEMDILGASRHDGAYSOGHFLPKP 289
Db 230 PESVQLQDSWVLGSNVPLESR-----HFLPKT 256
Qy 290 G-GTSPFCTTSPCYPLTSSVTYSPPPRPLPRSTFARPAFLKKPKSYCNWKAALSAIV 348
Db 257 GTGTTPLFSTATPYTWASGVSVSPPTPLPRNTLSRSAFKFKSKSTCSWKCTALCAVG 316
Qy 349 ISATLVILLAYFYVAMHLFGLNWLHPMEGQWYE---ITEDTASSWPVPTDVSLYPSGTG 405
Db 317 VSVLLAILLSFYIAMHLFGLNWLQQTENDTFENGKVSNTI-----MPTNVTSLPSG-- 368
Qy 406 LETPDRKGTTEKSPSPFPEDSFIDSGEIDVGRASAKIPPTFWRSFVIDHPVHLK 465
Db 369 -----DNGKLGFTQENNTIDSGELDIGRAIQEIPPIFWRSQLFIDQOPFLK 417
Qy 466 FNVSLGKAALVGIYGRKGLPPSHQTPDFVELLDGRRLLTOEARSLGTPGSRGTVPSS 525
Db 418 FNVSLQKDALIGVYGRKGLPPSHQTYDFVELLDGRLIAREQRLLETERAGRARSVL 477
Qy 526 HETGFIQYLDSGIWHLAFYNDGKSESVSFLLTAIESVDNCPNSCYNGDCISGTHCFL 585
Db 478 HEAGFIQYLDSGIWHLAFYNDGKNAEQVSENTIVIESVVECPRNCHGECVSTCHCFP 537
Qy 586 GFLOPDCGRACPVLCSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCTGT 645
Db 538 GFLGPDCSRACPVLCSGNGQYSGRCLCFSGWKGTEDVPTTQCIDPQCGRGICMGS 597
Qy 646 CIGNPGYKGSCEBVDQMDPTCSGRGVCYVRGECHCFVWGWTNCTETPRATCLDQCSGHT 705
Db 598 CACSSGYKGSCEADDCIDFGCSNHGVCIHGECHCSFGWGSNGCEIILKWCPODCSGHT 657
Qy 706 FLPTDGLCSDPWSWTHGDCSIEICAADCGGHGVCVGTGTCEDGWMGAACDQRAHPRCA 765
Db 658 YLQESSGCTCDPNWTGPDSCNEICSVDCSGSHGCMGTGTCCEGWTGPACNQRAHPRCA 717
Qy 766 EHGTCRKGKCECSPGNWGEHCTTAHYLDRVY-----KEGCPGLCNGRCRTDLNGWHC 819
Db 718 EHGTCRKGKCECSPGNWGEHCTTAHYLDKIVKQIKYKGECPGLCNSNGRCRTDLONGHC 777
Qy 820 VCQLGWRGAGCDTSMETACGDSKNDGDGLVDCMDPDCLQLPLCHINPLCLGSPNLDII 879
Db 778 VCQPGWRGAGCDVAMETLCTDSKDNEDGLIDCMDPDCLQSSQONQPYCEGLFDPQDII 837
Qy 880 QETQVPVVSQQNLHSFYDRIKFLVGRDSTHIIPGSENFDPGGHACVIRQVMTSDGTLVGV 939
Db 838 SOSLQSPSQAAKSFYDRISFLIGSDSTHVIIPGSPENKSLASVIRGOVLTDGTPLIGV 897
Qy 940 NISFVNNPLFGYITISRODGSFDLVNCGISILIFERAPRITQEHITLWLPNDRFVMEIT 999
Db 898 NVSFFHYPEYGYTITRODGMFDLVANGASLTLVFRSPFLTQYHTVMIWNVVFVMDTL 957

| | | | |
|----|------|---|------|
| Db | 1977 | RRQRLSEILLYDSTRVSEFTDETAGVUKTNVLQSDGGFCTIRVRQIOGLIDRQIFRSED | 2036 |
| Qy | 2075 | GMVNAREDYNDSFRVTSMQAVINETPLPIDLYRYDDVDSKTEQFGKFGVIYDINQII | 2134 |
| Db | 2037 | GMVNAREDYSYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYDINQII | 2096 |
| Qy | 2135 | TTAVMTHTKHPDAYGRMKEVQYEIFRSLMTVMTVQYDNMGRRVVKELKGPVYANTTRYSY | 2194 |
| Db | 2097 | STAVMTYTKHFAHGRIKEIQEYEIFRSLMYWITTYDNMGRRVTKREIKGPFAMNTTKYAY | 2156 |
| Qy | 2195 | EYDADGQLOTVSINDKPLWRYSYDLNGLNHLHSPNSARLTPIDYDIDRDIRLGRGDVOYK | 2254 |
| Db | 2157 | EYDVGGLQTVYLNKEKIMWRNYDLNGLNHLNPSNARSRLTPIDYDIDRDIRLGRGDVOYR | 2216 |
| Qy | 2255 | MDEGFLRQGGDITFEYNSAGLLIKAYNAGRSWVRVYDGLGRVRVSSKSHSHLQFFY | 2314 |
| Db | 2217 | LDEGFLRQGGTEIFEYSSKGLLTRVYSKSGWTVIYRYDGLGRVRVSSKTSLGQHLQFFY | 2276 |
| Qy | 2315 | ADLTNPTKVTHLYNHSSEITSLYYDIQGHLFAMELSGGBEFYIACDNIGTPPLAVFSGTG | 2374 |
| Db | 2277 | ADLTYPTRITHVYNHSSEITSLYYDIQGHLFAMEISSGDEFYIASDNTGTGPLAVFSSNG | 2336 |
| Qy | 2375 | LMIKQIILYTAGEIYMDTNPNFOIIIGYHGGLYDPLTKLVHMGRRDYDVLACRWTSDPHE | 2434 |
| Db | 2337 | LMLKQIQYTYAGEIYFDSNIDFQIIVGFHGSLYDPLTKLVHFGERDYDILAGRWTTPDIE | 2396 |
| Qy | 2435 | LWKHLSSNVMPPNLYMFKNPNPISNSODIKCFMTDVNSMLLTGFGOLHNVIPGYPKPDM | 2494 |
| Db | 2397 | IWKRI-GKDPAPPNLYMFRNNPNASKIHDVKDYITDVNSMLVTGFGHLHNAIPGFVPKPF | 2455 |
| Qy | 2495 | DAMEPSYELIHTQMTQEWDNSSKSIIGVQCEVQRQKLAFTVTLERFDLYGSTITSCQAP | 2554 |
| Db | 2456 | DLTEPSYELV-----KSQWDDIPPIFGVQOQVAFQAKAFSLGKWAIEVQ----VSRRRAG | 2507 |
| Qy | 2555 | KTKK---FASGSVFGKVPKALPKDGRVTDDIISVANEDGRVRVAAIINHAHYLENLHFTI | 2611 |
| Db | 2508 | GAQSWLWFATVKSLIGKGVMLAVSQGRVQTNVLNLIANEDCIKVAALVNNAFYLENLHFTI | 2567 |
| Qy | 2612 | DGVUDTHYFVKPGPSEGDLATILGLSGGRITLNGVNVTVSQINTVLNGRTYRTDIOLOYG | 2671 |
| Db | 2568 | EGKDTHYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVVNGKTRRFADVENQFG | 2627 |
| Qy | 2672 | ALCLNTRYGTTLDEKARVLELARQRAVROAWAREQOORLREGEGBLRAWTEGEKQOVLST | 2731 |
| Db | 2628 | ALALHVRYGWLTDDEKARIIEQARQALARAWAREQOORVDRGEEGARLWTEGEKQOLLSA | 2688 |
| Qy | 2732 | GRVQGYDGFVVISVEQYPELSDSANNTHPMRQSEMMGR | 2769 |
| Db | 2688 | GKVOGYDGYVYLYVEQYPELSDSANNIOFROSEIGRR | 2725 |

RESULT 6

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US-11-113-424-52
; Sequence 52, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24

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QY 809 RCTLDNGHCHVCOLGWRGAGCDTSMETACGDSKNDGDGLVDCMDPBCCLQPLCHINPL 868
DB 774 RCTLDQNGHCHVCQGWMSGTCNVVWMLCGNLDNDGDLTDCVDPCCQCSNYCIISPL 833
QY 869 CLGSPNPDLIIQETQVPVSSQNLHSHFYDRIKFLVGRDSTHIIIPGNPFDGGHACVIRQV 928
DB 834 CGSPDPLDLIQSQTLFSQHTSRFLFYDRIKFLGDKSTHVIPEVSPDSRRACVIRQV 893
QY 929 MTSDDGTPLGVNHSFVNNPLFOYTTISRDQSGPDLVTNGISIIILPERAPFITQBHTLWL 988
DB 894 VAIDGTPLGVNHSFLHSHSDYFTTISRDQSGPDLVAIGSIGSVILFDRSPFLPERKTLWL 953
QY 989 PNDRFVFWETIIMRHEENIEPCSDISNPARPNPVSPSLTSSFASCAEKGPVPEIQAL 1048
DB 954 PNMQFIVBKVNRQVRVSDPPSCDISNFIENPILVPSPLTSSFGSCSPERGTVPELQV 1013
QY 1049 QBEISIGCKMRLSYLSRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGRLEKFWFAA 1108
DB 1014 QBEIPIPSFVRLSYLSRTPGYKTLRLTHSTIIPVGMKVHLTVAVEGRLETKWFFA 1073
QY 1109 ADPLSYFYIWDKTVYNQKVFGLSEAFVSUGVEYESCPDLILWEKRTTVLQGEYIDASKL 1168
DB 1074 AINLVYTFANWKTIDYQKVMGLABALNSVGEYETCPDFILWEQRTTVVLQGFEMDASNL 1133
QY 1169 GCMSLDKHHLNIOGILHKGNGENOFVSQPPVIGSTMNGRRRESICPSCNGLADGNK 1228
DB 1134 GWSLUNKHILNPQSGIHKNGENMFISQPPVISTIMNGHQRSVACTNCGPAHNNK 1193
QY 1229 LIAPVALTCGSGSLVYGDVFNIRIFPSPGNVTNILELRNKDFRSHSPAHKYYLATDPM 1288
DB 1194 LPAPVALASGPDGVSVYGVDFNVFRIIPSGNSVSIEL-----STSPAHKYYLAMDPV 1246
QY 1289 SGAVFLSDNSRRVFKISVTVVVKDLVKNSEVAGTGDCQCLPPDTRCGDGGKATEATLT 1348
DB 1247 SEBSYLSDTNTRKVYKLKSLVETKLSKNFEVAGTGDCQCLPPDQSHCGDGRASEASLN 1306
QY 1349 NPRGTTVDKFGILYFVDDGTMIIRIDONGIISTLLGSNDLTSAARPLSCDSVMDISOVLEW 1408
DB 1307 SPRGITTVDKHGFIYFVDDGTMIIRKIDENAVITVIGSNGTSTQPLSCDSGMDITQVRLW 1366
QY 1409 PTDLAINPMDNSLYLDNNVLIQISENHQVRIVAGRPMHCQVPGIDHFLSKVAITHATLE 1468
DB 1367 PTDLAVNPMDNSLYLDNNVLIQISENRRVRIIAGRPICQVPGIDHFLSVKVAIHSLE 1426
QY 1469 SATALAVSHNGVLYIAETDEKINRIQVTTSGEISLVAGAPSGCCKNDANCDCFSGDD 1528
DB 1427 SARAISSVSHSGILFIAETDERKVNRIQVTTNGEYIYIAGAPTDCKIDPNCDCFSGDD 1486
QY 1529 GYAKDAKLTSPSLAVCAGDELYVADLGNIRIRFTRKNKPFNTONMYELASPIDOELYL 1588
DB 1487 GYAKDAKMAKPSLAVSPDGLUYVADLGNVRIITSRQAHLNDNVIYIASPADQELYQ 1546
QY 1589 FDTTGKHLTQSLPTGDLYNFYTTGDDGDTILITDNGNMVNRDSTGMPLWLVPDQ 1648
DB 1547 FTVNGHTLHTLNIITRDVYVNFYNSGDLGAIITSSNGSVHIRDAGMGPLWLVPDQ 1606
QY 1649 VTWVTGNTNSALKSVTTQGHELAMTYHGNISGLATKSNENGWTTTFYIDFGRLTNVT 1708
DB 1607 VYWLTISSNGVLKRVSAQYNALMTYPCNTGLLATKSNENGWTTVYBYDPEGHLTNATF 1666
QY 1709 PTGOVSSPFSDDTSSVHVQVETSSKDDVTITTNLSAGAFYTLLODOVRNSYIYAGDGL 1768
DB 1667 PTGEVSSPFSDDUKTKVELDTNSRNVLMSTNLTAITSIYILKQENTQSTVRNPDGSL 1726
QY 1769 RLLLANGMEVALQTEPHLLAGTVNPTVGKRVNLTLPIDNGLNLAWEVRQORKEARGQVTF 1828
DB 1727 RVTFASGMEIGLSSEPHILAGAVNPTLGKCNISLPGHEANLIEWRQORKEQKNVSAFE 1786
QY 1829 RRLRVHNRNLLSDRFRTRTEKIIDHRKFTLRLIYDQAGPSLWSPSSRLNGVNVTS 1888
DB 1787 RRLRAHNRNLLSIDFHTTRTKIYDDHRKFTLRLIYDQTRPILWSPVSRVNEVNTYS 1846

QY 1889 PGYIAGIQRGIMSRMEYDOAGRITSRIFADKGTWSTYLEKSMVLLLSHQROVIFBFD 1948
DB 1847 PSGLVTFIQRGTWNEKMEYDQSGKILISRTWADGKIWSYTYLEKSMVLLLSHQRRVIFED 1906
QY 1949 KNDRLSSVTPNVARQTLTETIRSUGYVYRNIYQPPEGNASVIQDFTTEGHLHLHTFYLGTGR 2008
DB 1907 QPDCLLSVTPMPSVMRHSJQMLSVGYVYRNIYTPPDSSTSFPIQDYSRDRGLLQTLHLGTGR 1966
QY 2009 RVIYKYKLSKLAETLYDTTKVSEYDGTAGMLKTINLQNEGFTCTIRYROIPLIDROI 2068
DB 1967 RVLKYTKQARLSVLYDTTQVTLTYBESSGVITKIHLMHDDGFCTIRYRTGTPLIGROI 2026
QY 2069 FRFTEEGMVNARFYNDNSFRVTSQMAVINETPLPIDLYRYDDVSGKTEQFGKFGVY 2128
DB 2027 FRFSEGLVNARFYDYSI--NNFRVTSQMAVINETPLPIDLYRYDDVSGRTEQFGKFSVNY 2085
QY 2129 DINQIITTAVMTHTKFDAYGRMKVEQYEIFRSLMYVMYVQYDNNGRVVKKELKVGYPAN 2188
DB 2086 DLNQVITTTVMKHTKIFESANGQVIEQYELKALAYWMTIQYDNGVRMVICDIRGVGDAN 2145
QY 2189 TTRYSEYDADGQLOQTVSINDKPLWRYSDYDLGNLHLLSPGNSARLTPLRYDIRDITRL 2248
DB 2146 ITRYFYDADGQLOQTVSVDNKQWRYSDYDLGNLHLLSHGKSARLTPLRYDLDITRL 2205
QY 2249 GDVQYKDEDFLRQRGDIFEVNSAGLLIKAVNRAGSWSVRYRYDGLGRRVSSKSSH 2308
DB 2206 GEIQYKDEDFLRQRGDIFEVNSAGLLIKAVNRAGSWSVRYRYDGLGRRVSSKSLGQ 2265
QY 2309 HLQFYADLTNPYKTHLYNHSSEITSLYDYDQHLFAMELSSGDEFFYIACDNIGTPLA 2368
DB 2366 HLQFYADLTNPYKTHLYNHSSEITSLYDYDQHLFAMELSSGDEFFYIACDNIGTPLA 2325
QY 2369 VFSCTGLMIKQILYATGEIYMDTNPNFOIIGVHGGLYDPLTKLVHMGRRDYDVLAGR 2428
DB 2326 VFSRGQVIEKILYTPYDGIYDTPDFQVILGHGGLYDPLTKLVHMGRRDYDVLAGR 2385
QY 2429 TSPDHELMKHLSSSNVM--PFNLYMKNNPISNSQDIKCFMTDVSNSMLTFFGQLHNVI 2486
DB 2386 TTPNHHIWKQL--NLPKPFNLYSFENNYPVGKIQVAKYTTDIRSMLELFGQLHNVL 2442
QY 2487 PGYKPKMDMAMPSEYELIHTQMTQWEDNSKSLGVQCEVQKQKAFVTLRPFQLYGST 2546
DB 2443 PGFPKPLENLELYELRLQTKTQWEDPGKTIILGIQCELQKQLRNFISLDQLPMTPRYN 2502
QY 2547 ITSQQAQPKTKFASCSGVRGKVPKALKQGRVTTDIISVANEDGRVAAITLNAHYLEN 2606
DB 2503 DGRCLGGKQPRFAAVSPVFGKIKFAIKDQIVTADIIGVANEDSRRLAAILNNAHYLEN 2562
QY 2607 LHFTIDGVDTHYFVKPGPSEGDAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRTYDI 2666
DB 2563 LHFTIEGRDTHYFIKLSLEEDLVLIQNTGRRILENGVNVTVSQMTSVLNGRTRRPADI 2622
QY 2667 QLOVGAICLNTRYGTTTDESKARVLELARAQAVQAWARQOORLREGEGLRANTEBQK 2726
DB 2623 QLOHGALCFNIRYTTTVEEKNHVLEIARQAVQAQWTKQORLQOEEGIRAWTEBQK 2682
QY 2727 QVLTSGVQVQDGPVLSVEQYPELSDSANNIHPMROSEMR 2769
DB 2683 QLLSTGRVQVQDGYFVLSVSQYLELSDSANNIHPMROSEIGRR 2725

RESULT 7

US-11-096-051-4
; Sequence 4, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967

; CURRENT APPLICATION NUMBER: US/11/096.051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 4
; LENGTH: 2376
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-096-051-4

Query Match 62.4%; Score 9296; DB 7; Length 2376;
Best Local Similarity 69.6%; Pred. No. 0;
Matches 1673; Conservative 317; Mismatches 379; Indels 36; Gaps 9;

Qy 372 LQMEGQMYE---ITERTASWPVPTDVSLYPSGGTGLETPDRKGKTTTEGKPSFFPED 428
Db 1 LQOTENDTFENGKVNST-----MPTNTVSLPSG-----DNKLGGFQEN 41

Qy 429 SFIDSGBIDVGRASQKIPGCTFWRISOVFIDHPVHLKFNVSLSGKAALVGIYGRKGLPPSH 488
Db 42 NTIDSGELDTGRRAIQIIPGIFWRSOLFIDQPOFLKFNISLQKDALIGYGRKGLPPSH 101

Qy 489 TQDFVBLDGRRLLTQARSLEGTQRSRGTVPPSPSHETGFTQYLDGSIWHIAFYNDGK 548
Db 102 TQDFVBLDGRRLIAREQSRSLLETERAGQARSVSLHEAGFIQYLDGSIWHIAFYNDGK 161

Qy 549 ESEVVSFLTAIESVDNCPNCGNGDCISGTCFLGFLGPGDCGRASCPVLCSGNGQYM 608
Db 162 NAEQVSNTIVIESVVCPRNCHNGBCVSGTCHCFPGFLGPGDCSRAACPVLCSGNGQYS 221

Qy 609 KGRCLCHSGWKAGCDVPTQCIDVACSNHGTCTGTICINPGYKGBSCBEVDCMDPTCS 668
Db 222 KGRCLCFSGWKGTEDVPTTQCIDPCGGRGICIMGSCACNSGYKGBSCBEADCIDPGCS 281

Qy 669 GRGVCVGECHCFVWGWTNCETPRATCLDQCSGHGTFLEPDTGLCSDDPSWTGHDCSI 728
Db 282 NHGVCIHGECHCSPGWGSNCEILKTCPCDQCSGHGTYLQESGSCCTCDPNWTPGDCSNEI 341

Qy 729 CAADCGHGVCGTCTCEDGWMGAAACDORACHPRCAEHGTCRDGKCECSPGNNGEHTI 788
Db 342 CSVDGSHGVCMGGTCTCEGWTGPACNQRAHPRCAEHGTCRDGKCECSPGNNGEHTI 401

Qy 789 AHYLDVVYKEGCPGLCHNGRCTLDLNGWHCVCOLGWRGAGCDTSMETACDSKDNBDGD 848
Db 402 AHYLDKIVKEGCPGLCHNSGRCTLQDQNGWHCVQCPGHRGAGCDVAMETLCTDSKDNBDGD 461

Qy 849 LVDCMDPDCLQLCHINPLCLGSPNPLDIIFQETQVPVSQNLHSHFYDRIKFLVGRDSTH 908
Db 462 LIDCMDPDCLQLSSCONQPCRGFLPDQDIISQSLQSPSOQAASFYDRISFLIGSDSTH 521

Qy 909 IIPENFPDGHACHVIRGOWMTSGTFLGVNWFVFNPLFGYTIISQDQSGFDLYTNGGI 968
Db 522 VIPGESPFNKLASVIRGOVLTAQDTPLIGVNVSFHYPEYGYTITRQDGMFDLVANGGA 581

Qy 969 SIILRFRAPPTIQTHTLWLPWDRFFVYMETIIMRHEENETPSCDLSNFPARNPNVVSPL 1028
Db 582 SLTLVFERSPLTQYHVIWPNVYVYNDTLVMKKEENDIPSCDLSGFVRPNPIIVSSPL 641

Qy 1029 TSPASSCAEKGPVPEIQALQEEISISGCKMRLSYLSRTPGYKSVLRLISLTHPTIPFN 1088
Db 642 STFFRSSPEDSPIPETQVLHEETIIPGTDLKLKSYLSRAAGYKSVLKITWTQSIIPFN 701

Qy 1089 MKVHLMVAVEGRLLFRKFAAPDLISYFINDKTDYVQKVPGLSEAFVSQVGEYESCPDL 1148
Db 702 MKVHLMVAVGRLLFKQWFPASPPLAYTFIWDKTDAYNKVYGLSEAVVSQVGEYESCLDL 761

Qy 1149 ILWEKRTTVLQGEIDASKLGWSLIDKHHALNIQSGILHKGNGENQFVSQPPVIGSIMG 1208

Db 762 TLWEKRTAILQGYELDASNMGWGLDKRHVLDVQNGILYKNGENQFISQQPPVSSIMG 821
Qy 1209 NGRRRSISCPSCNGLADGNKLLAPVALTCGSDGLSVVGFNYIRRIIPPSSGNVTNILELRN 1268
Db 822 NGRRRSISCPSCNQGADGNKLLAPVALACIGDGLSVVGFNYVRRIPPSSGNVTSVLELRN 881
Qy 1269 KDFRHSHPAHKYLLATDPMGSAVFLSDSNSRRVFKIKSTVVVKDLVKQSEVVAGTGDQC 1328
Db 882 KDFRHSNPAHRYLLATDPTVGDLYVSDTNTTRRIYRPSKSLTGAKDLTKQAEVVAGTGEQC 941
Qy 1329 LPDPTRCDDGGKATEATLTNPRGITVDKFGLLIYFVDGTMIRIRIDONGIISTILGSDNLT 1388
Db 942 LPDEARCGDGGKAVEATLMSPKGMAVDKNGLIYFVDGTMIRKRVQDQNGIISTILGSDNLT 1001
Qy 1389 SARPLSCDSVMDISOVRLEWPTDLAINPMDNSLYLVLDNNVLOISNHOVRIYVAGRPMHC 1448
Db 1002 SARPLTCDTSMHLSQVRLEWPTDLAINPMDNSLYLVLDNNVLOITENRQVRIAGRPMHC 1061
Qy 1449 QVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIQOVTTSGEISLVAG 1508
Db 1062 QVPGVE-YPVGKHAVQTTLLESATAIAVSYSGVLYITETDEKKINRIQOVTTDGEISLVAG 1120
Qy 1509 APGCDCKNDANCDPFGDDGYAKADAKLNTPPSLAVCAAGELYVADLGNIRIRIRKPK 1568
Db 1121 IPSECDCKNDANCDPFGDDGYAKADAKLAPSSSLAASPDTGLYIADLGNIRIRIRAVSKPK 1180
Qy 1569 FLNTQNMVELSPIDOEYLFDTTGKHLTYTQSLPTGDLVNFYTGDDTLTLDNNGNM 1628
Db 1181 LLNSMNFYEVASPTDQELYIFDINGTHQYTVSLVTGDLVNFYSNDNDITAVTDSNGT 1240
Qy 1629 VNVRRDSTGMPLVWVDPGQVYVMTGNSALKSVTTQGHHELAMTYVHGNSGLLATKSNE 1688
Db 1241 LRIRRDPNRMPVRVSPDNQVIMLTIGTGCLSKSMTAQGLELVLTFTVHGNSGLLATKSDE 1300
Qy 1689 NGWTTYEYDPSFORLTNVTPTQCVSSFRSDTSSVHVQVETSSK-DDVTITNLSASGA 1747
Db 1301 TGWTTTFDYDSEGLRNTVPTGVTNHLGMDKAITVDIESSREEDSVITSNLSIDS 1360
Qy 1748 FYTLLODOVRNSVYIGADGSLRLLLANGMEVALQTPHLLAGTVNPTVGRNVTLPTDNG 1807
Db 1361 FYTMVQDQLRNSYQIYGVGSLRIIYASGLDSHYQTEPHVLGAGTANPTVAKRNTLPENG 1420
Qy 1808 LNLVEVRQRKEQARGQVTVFGRRLRVHNRLLSLDFDRVTRTEKIYDDHKKFLRLIYDQ 1867
Db 1421 QNLVEVRFRKEQAQGVNVFGRKLVNGRNLLSVDFTTKTEKIYDDHKKFLRLIAYDT 1480
Qy 1868 AGRPSLWSPSSRLNGVNVTVSPGYIAGIQRGIMSRMEYDQAGRITSRIFADGKTWSYT 1927
Db 1481 SCHPTLWLPSSKLMAVNVTVSYSTGQIASIQRGTTSEKVDYDQGGRIVSRVFADGKTWSYT 1540
Qy 1928 YLEKSMVLLHLSORQYIFEDKNDRLSSVTMPNVARQTLTETIRSVGYRNIYOPPEGNAS 1987
Db 1541 YLEKSMVLLHLSORQYIFEYDMMDRLSIAITMPSVARHTMQTIRSIGYRNIYOPPEGNAS 1600
Qy 1988 VIQDFTEDGHLLHTFVLGTGRRVYIKYKLSKLAETLYDTTKVSFTYDETAGMLKTINLQ 2047
Db 1601 IITDYNEEGLLLQTAFLGTSRRVLKYRQRLSEILYDSTRVSVFTYDETAGVLKTVNLQ 1660
Qy 2048 NEGFTCTIRYQIGPLIDRQIFRFTBEGMVNARFDYNDNSFRVTSNQAVINETPLPIDL 2107
Db 1661 SDGFICTIRYQIGPLIDRQIFRSEDGMVNRFDYSYDNSFRVTSNQAVINETPLPIDL 1720
Qy 2108 YRVDVDSGKTEQKGVVYVDINQIITTAAMTHTKHFDAYGKMEQVQYEIFRSLMWMT 2167
Db 1721 YQFDDISGKVEQKGVVYVDINQIISTAVMTYTKHFDAGHRIKEIQYEIFRSLMTWIT 1780
Qy 2168 VOYDNNGRVVKELKGVPAVNTTYSVEYDADQLOQTVSINDKPLWYSYDLNGLHLLS 2227
Db 1781 IQYDNNGRVTKRIKIGFPANTTKYAYEYDQLOQTVLYLNEKIMRYNYDLNGLHLN 1840
Qy 2228 PGNSARLTPLURYDIRITRLGLDVQVQYMDDEGFLRQRGDIFEYNSAGLLIKAYNRAGSW 2287

```
Db 1841 PMSARLTPLRYDLDRITRLDGDVQVRLDEDDGFLRQGRTEIFEYSSKGLLTRVYSGSGW 1900
Qy 2288 SVRYRYDGLGRVSSKSSHLOPFYADLTNPTKVTHLYNHSSEITSLYYDLQGLHPA 2347
Db 1901 TWIYRYDGLGRVSSKSTSLGQHLQFPYADLTPTTRITHVYNHSSSEITSLYYDLQGLHPA 1960
Qy 2348 MELSSGDEFYIACDNIPTGLAVFSGTGLMIKQILYATYGEIYMDTNPFPQIIIGYHGGLY 2407
Db 1961 MEISSGDEFYIASDNTGTGLAVFSSNGLMKQIQYATYGEIYFDSNIDPQLVIGHGGLY 2020
Qy 2408 DPLTKLVHMGRRDYDVLGRWTSPOHELMKHLSSSNVMPFNLYMPKNNPISNSODIKCF 2467
Db 2021 DPLTKLIHFGERDYDILAGRWTTPDIEIWKRI-GKDPAPFNLYMPFRNNPASKIHDVKDY 2079
Qy 2468 MTDVNSWLLTFQQLHNVTLPYKPKDMDAMEPSYELIHTOMKTOEWDNSKSTLGVQCVQ 2527
Db 2080 ITDVNSWLVTFGFLHNAIPGFPVPKFDUTEPSYELV----KSQWDDIIPPIFGVQQVA 2135
Qy 2528 KQKAFVTLERFDQLYGSTITSQOAPTKK---FASSGSVFGKVKFALKDGRVTTDII 2584
Db 2136 RQAKAPLSLGKMAEQ---VSRRRAGGAQSMLWFATVKSLLIGKGMVLAVSQGRVQTNVL 2191
Qy 2585 SVANEDGRVAAILNHAHYLENLHFTIDGVTHYFKGCPSEGDALILSGGRTLNG 2644
Db 2192 NIANEDCIKVAALVNAFYLENLHFTIEGKOTHYFIKTTTPESDGLTLRTSGRKALENG 2251
Qy 2645 VNVTVSQINTVLNGRTRRTDIOLOYGALCLNTRYGTTLDEBKARVLELARQAVROAWA 2704
Db 2252 INVTVSQSTTVNGRTRRFADVEMQFGALAHVRYGMTLDEBKARILQARQALARAWA 2311
Qy 2705 RQQRLEGEGLRATWEGEKKQVLSTGRVQGYGFFVISVEQYPELSDSANNIHFMRQS 2764
Db 2312 RQQRVRDGEGLRATWEGEKKQLLSAGKVQGYDGYVLSVEQYPELADSANNIOFLRQS 2371
Qy 2765 EMGR 2769
Db 2372 EIGRR 2376

RESULT 8
US-10-821-234-1097
; Sequence 1097, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1097
; LENGTH: 1094
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1097

Query Match 28.0%; Score 4175.5; DB 6; Length 1094;
Best Local Similarity 69.3%; Pred. No. 2,3e-262;
Matches 764; Conservative 170; Mismatches 155; Indels 13; Gaps 5;

Qy 1672 MMTYHGNSGLLATKSNENGWTTFFYDYSFGRLTNNVTFTPTGVSSFRSDTSVHVQVETS 1731
Db 2 LPTYHGNSGLLATKSDETGTTTFFDYDSEGRLTNNVTFTPTGVVNLHLGMDKAITVDIESS 61

Qy 1732 SK-DDVTTITNLSAGAFYLLQDQVRNSYYIGADGSRLLLANGMEVALQTEPHLLAGT 1790
Db 62 SREEDVTSITNLSIDSFTYMWQDLRNSYQIGYDGSRLIYYASGLDSHYQTEPHVLGAT 121
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RESULT 9

US-11-113-424-54

; Sequence 54, Application US/11113424

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Qy 1791 VNPVGRKRVNTPIDNGLNLVEMRQREQARQOVTVFGRRRLVRHNRNLLSLDFQVTRTE 1850
Db 122 ANPTVAKRNWTLPEQENQNLVEMRFRKAEQAGKQVNVFGRKLRVNGRNLSSVDFPRTYKTE 181
Qy 1851 KIYDHRKFTLRILLYDQAGRPSSLWSPSSRLNGVNVTVSPGYIAGIQGINSMERMEYDOA 1910
Db 182 KIYDHRKFTLRILAYDTSGHPTLWLPSSKLMVNVTVSYSTGQIASIQRGTTSEKVDYDQ 241
Qy 1911 GRITSRIFADCKTWSYTYLEKSMVLLLSHQRYIFEDKNDRLSSVTMPNVAROTLEIR 1970
Db 242 GRIYSRVFADCKTWSYTYLEKSMVLLLSHQRYIFEYDMMDLRLSAITMPSVARHTMQTIR 301
Qy 1971 SVGYRNIYOPPEGNASVIOFTEDGHLLHTFYLGTRRVYKYKGLSKLAETLYDTTKV 2030
Db 302 SIGYRNIYNPESNASIITDNEEGLLQTAFLGTSRRVLFKYRQTRLEIYLIDSTRV 361
Qy 2031 SFTYDETAGMLKTINLQNEGTCTIRYRQIGLPLDRQIFRTEEGMVNARPDYNDNSFR 2090
Db 362 SFTYDETAGMLKTINLQSDGFICTIRYRQIGLPLDRQIFRPEDEGMVNARFDYSDNSFR 421
Qy 2091 VTSQAVINETPLPIDLYRVDVSGKTEQFQKGVYVDINOIITTAVMTHTKHFDAYGR 2150
Db 422 VTSQGVINETPLPIDLYQFDDISGKVEQFQKGVYIYDINOIISTAVMTYTKHFDAGHR 481
Qy 2151 MKEQYEIFRSLMYMMTVQYDNNMGRVVVKELKVGPYANTTRYSEYDADGQLOQTVSINDK 2210
Db 482 IKEQYEIFRSLMYWITIYQDNNMGRVTKREIKGFPANTTKYAYEYDVGQLOQTVLYNEK 541
Qy 2211 PLMRYSYDLNGLNHLSPGNSARLTPLRYDIRDIRITLGDVQYKMDDEGFLRQGGDIFE 2270
Db 542 IMWRYNYDLNGLNHLNPSNSARLTPLRYDLDRITRLGDVQYRLDEDDGFLRQGTIFE 601
Qy 2271 YNSAGLILKAYNRAGSVSYRYVDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHS 2330
Db 602 YSSKGLLTRVYSGSGWTVIYRYVDGLGRRVSSKSTSLQHLQFFYADLTPTTRITHVYNHS 661
Qy 2331 SSEITSLYDLQGLHPAMELSSGDEFYIACDNIPTGLAVFSGTGLMIKQILYATYGEIYM 2390
Db 662 SSEITSLYDLQGLHPAMEISSGDEFYIADNTGTPLAVFSSNGLMKQIQYATYGEIYP 721
Qy 2391 DTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLGRWTSPOHELMKHLSSSNVMPFNLY 2450
Db 722 DSNIDFQLVIGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDIEIWKRI-GKDPAPFNLY 780
Qy 2451 MFKNPNPISNSODIKCFMTDVNSWLLTFGQLHNVPYKPKDMDAMEPSVELIHTOMKT 2510
Db 781 MFRNNPASKIHDVKDYITDVNSWLVTFGFLHNAIPGFPVPKFDLTPSPSYELV----KS 836
Qy 2511 QEWDNKSILGVQCEVQOKLQKAFVTLERFPDQLYGSTITSQOAPTKK---FASSGSVFG 2567
Db 837 QOWDDIIPPIFGVQOQVARQAKAFSLGKMAEQ---VSRRRAGGAQSMLWFATVKSILG 892
Qy 2568 KGVKFAKDGRTVTDIIISVANEDGRVAAAILNHAHYLENLHFTIDGVTHYFKGPGSEB 2627
Db 893 KGVMLAVSQGRVOTNVLNANEDCIVAAALNNAFYLENLHFTIEGKOTHYFIKTTTPES 952
Qy 2628 DLATILGSGGRRRTLENGVNVTVSQINTVLNGRTRRTYDIOLOYGALCLNTRYGTTLDEEK 2687
Db 953 DLGTLRLTSGRKALENGINVTYVQSSTTVNGRTRRFADVEMQFGALAHVRYGMTLDEEK 1012
Qy 2688 ARVLELARQAVRQAWAREQORLREGEGLRAMTEGSKQOVLSTGRVQGVDFGFVISVEQ 2747
Db 1013 ARILEQARQALARAWAREQORVRDGEGARLWTEGKRLQLLSAGKVQGYDGYVLSVEQ 1072
Qy 2748 YPELSDSANNIHFMRQSEMGRR 2769
Db 1073 YPELADSANNIOFLRQSEIGRR 1094
```

Publication No. US20050260713A1
GENERAL INFORMATION:
APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/311,590
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/307,506
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/322,358
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/288,153
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 54
LENGTH: 1045
TYPE: PR1
ORGANISM: Homo sapiens
US-11-113-424-54

Query Match 26.7%; Score 3979.5; DB 7; Length 1045;
Best Local Similarity 69.2%; Pred. No. 1e-249;
Matches 729; Conservative 164; Mismatches 147; Indels 13; Gaps 5;

QY 1721 DSSVHVQVETSSK-DDYVITITNLSASGAFYTLQDOVRNYSYIGADGSLRLLLLANGMEVA 1779
DB 2 DKAITVDIESSEEDYSITNSLSDISFYTMVDQDQURNYSQYGDGSLRIIYASGLDUSH 61
QY 1780 LQTEPHLLAGTNPVTGKRNVTLPIDNGLNLVWRQKEAQGVTVFGRRLRVHRNLL 1839
DB 62 YQIEPHVLGANTVAKRNWTLPGENGQNLVWRFRKEAQGVTVFGRKLAVNGRNL 121
QY 1840 SLDFDVRTRTEKIYDDHRKFLRLIYDQAGRPSLWSPSSRLNGVNVYISGGYIAGIQRG 1899
DB 122 SVDPDRATTKTEKIYDDHRKFLRLIYDTSGHPTLWLPSSKLMVAVNVYISGTQIASIQRG 181
QY 1900 IMSEMEVDQAGRTSRIFADGKTWSYTYLEKSMVLLLSHORQYIPEFDKNDRLSSVTMP 1959
DB 182 TTSEKVDYDGGGRIVSRVFDGKTWSYTYLEKSMVLLLSHORQYIPEYDMDRLSALTMP 241
QY 1960 NVARQTLTTRSVGYRNIPQPEGNASVTQDFTEDGHLHLHTFYLGTRGRVIVYKGLSK 2019
DB 242 SVARHTWQTRISIGYRNIPPNPSNASIITDYNBEGLLQTAFLGTSRRLVFKYRQTR 301
QY 2020 LAETLYDTTKVSFTYDETAGMLKTNLQNEGFTCTIRYQIGPLIDRQIFRFTPEGMVNA 2079
DB 302 LSEILYDSTRVSFTYDETAGVLKTNVLSQDGFICTIRYQIGPLIDRQIFRFSBDGMVNA 361
QY 2080 RFDYNYNSFRVTSQMAVINETPLPIDLYRYDDVSGKTEQKGVYVYDINOIITAVM 2139
DB 362 RFDYSYNSFRVTSQMGVINETPLPIDLYQDSDISGKVEQKGVYVYDINOIITAVM 421
QY 2140 THTKHFDAYGRMKVQVEIFRSLMYMTVQDNNGRVVKKELKVGVPANTTRYSVEYDAD 2199
DB 422 YTKHFDAGRIKIQVEIFRSLMYWITIQDNNGRVTKEIKIGPANTTKYAYEYDAD 481
QY 2200 GQLQTVSINDKPLWRYSDYDNLGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMBEDG 2259
DB 482 GQLQTVYVINEKIMRWRYNDYDNLGNLHLLNPSNSARLTPLRYDLRDRITRLGDVQYRLDEG 541

QY 2260 FLRQGGDIFEYNSAGLLIKAYNRAGSVSVRYDGLGRVRSKSSSHHLOFFYADLTN 2319
DB 542 FLRQGTETFEYSSKGLTRVYSKSGMTVIYRYDGLGRVRSKTSGLQHLQFFYADLT 601
QY 2320 PTKVTHLYNHSSEITSLYDLOQHLFAMELSSGDEFFIACNIGTPLAVFSGTGLMIKQ 2379
DB 602 PRITHVYHNSSEITSLYDLOQHLFAMEISGDEFFIASDNTGTPPLAVFSSNGLMLKQ 661
QY 2380 ILYTAYGEIYMDTNPFIIGYHGLGYDPLTKLVHMGRRDYDVLAGRWTSPDHEWLKHL 2439
DB 662 IQYTAYGEIYFDSNIDFQLVIGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDIEIWKRI 721
QY 2440 SSSNVMPNLVYMPKNNPISNSQDKCFMTDYNLSMLTTFGFLHNVIPGYPKPDMAMEP 2499
DB 722 -GKDPAPFNLYMFRNNPASKIHDVKDYITDYNLSMLTTFGFLHNAIPGFPVPKFDLTP 780
QY 2500 SYELIHTQMTQBDWNSKSIILGVQCEVOKLAFVTLERFDOLYGSTITSQOAPTKK- 2558
DB 781 SYELV----KSQOMDDIPPIFGVQOQVQARQAKAFISLGMKAEVQ-----VSRRRAGGAQSW 832
QY 2559 --FASGSGVFGKGVKFPALDKGRVTTDIIISVANEDGRRVAAIILNHAHYLENLHFTIDGVD 2616
DB 833 LMFATVYKSLIGKGVMLAVSQGRVQTNVNLAINANEDCIKVAVALNNAFYLENLHFTIEGKDT 892
QY 2617 HYFVKPGPSEGLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRYTDIQLQYGALCLN 2676
DB 893 HYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVVNGRTRRFADVMQFGALALH 952
QY 2677 TRYGTTLDEKARVLELORAVROQAWREOQRLREGESGLRAWTGEKQOVLSTGRVQ 2736
DB 953 VRYGWTLDDEKARILEQARALARAWREOQVRDGEGBGARLWTEGKQKQLLSAGKVQ 1012
QY 2737 YDGFVVISVEQYPELSDSANNIHFMRQSEMGRR 2769
DB 1013 YDGFVVISVEQYPELSDSANNIHFMRQSEIGRR 1045

RESULT 10
US-11-113-424-50
Sequence 50, Application US/11113424
Publication No. US20050260713A1
GENERAL INFORMATION:
APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/311,590
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/307,506
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/322,358
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/288,153
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 730
TYPE: PR1
ORGANISM: Homo sapiens
US-11-113-424-50


```
Query Match      25.9%; Score 3854; DB 7; Length 730;
Best Local Similarity 99.7%; Pred. No. 7.8e-242;
Matches 728; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2040 MLKTLNLQNEGTCTIRYRQIGPLDRQIFRTEEGMNARFDYNDNSFRVTSMQAVIN 2099
DB 1 MLKTLNLQNEGTCTIRYRQIGPLDRQIFRTEEGMNARFDYNDNSFRVTSMQAVIN 60

QY 2100 ETPFLIDLYRYDDVSGKTEQFKFVIYYDINQIITTAVMTHKHFDAYGRMKVQYEIF 2159
DB 61 ETPFLIDLYRYDDVSGKTEQFKFVIYYDINQIITTAVMTHKHFDAYGRMKVQYEIF 120

QY 2160 RSLMYMTVOYDNMGRVVKELKVGPNANTTRYSEYDADGLOLQTVSINDKPLWYSYDL 2219
DB 121 RSLMYMTVOYDNMGRVVKELKVGPNANTTRYSEYDADGLOLQTVSINDKPLWYSYDL 180

QY 2220 NGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEGFLRQGGDIFEYNSAGLLIK 2279
DB 181 NGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEGFLRQGGDIFEYNSAGLLIK 240

QY 2280 AYNRAGMSVRYRVDGLGRRVSSKSSHHLQFFVADLTNPTKVTHLYNHSSEITSLYY 2339
DB 241 AYNRAGMSVRYRVDGLGRRVSSKSSHHLQFFVADLTNPTKVTHLYNHSSEITSLYY 300

QY 2340 DLQGHFLAMELSSGDEFYIACDNICTPLAVSGTGLMIKQILYTAIGEYIMDTNPNFQII 2399
DB 301 DLQGHFLAMELSSGDEFYIACDNICTPLAVSGTGLMIKQILYTAIGEYIMDTNPNFQII 360

QY 2400 IGYHGLYDPLTKLVHMGRRDYDLVLAGRWTSFDPHELWKHLSSSNVMPFNLYMKNNNPIS 2459
DB 361 IGYHGLYDPLTKLVHMGRRDYDLVLAGRWTSFDPHELWKHLSSSNVMPFNLYMKNNNPIS 420

QY 2460 NSODIKCFMTDVSMLLTFGQLHNVIPGYPKPDMAMEPSYELIHTQMKTOEWDNSKSI 2519
DB 421 NSODIKCFMTDVSMLLTFGQLHNVIPGYPKPDMAMEPSYELIHTQMKTOEWDNSKSI 480

QY 2520 LGVQCEVQKQAFVTLERFDOLYGSTITSCQAPKTKKFASSGVGKVFALKDGRV 2579
DB 481 LGVQCEVQKQAFVTLERFDOLYGSTITSCQAPKTKKFASSGVGKVFALKDGRV 540

QY 2580 TTDTISVANEDGRRVAAIILNHAHYLENLHFTIDGVDTYFVKPGPSEGDALTLGLSGRR 2639
DB 541 TTDTISVANEDGRRVAAIILNHAHYLENLHFTIDGVDTYFVKPGPSEGDALTLGLSGRR 600

QY 2640 TLENGVNVTVSINTVLNGRTRYTDIQLQYCALCLNTRYGTTLDEEKARVLELARQAV 2699
DB 601 TLENGVNVTVSINTVLNGRTRYTDIQLQYCALCLNTRYGTTLDEEKARVLELARQAV 660

QY 2700 ROAWAREOORLREGBEGLRAWTEGKQOVLSTGRVQYDGFVISEQYPELSDSANNIH 2759
DB 661 ROAWAREOORLREGBEGLRAWTEGKQOVLSTGRVQYDGFVISEQYPELSDSANNIH 720

QY 2760 FMRQEMGRR 2769
DB 721 FMRQEMGRR 730
```

```
RESULT 11
US-11-113-424-53
; Sequence 53, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
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; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 2515
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-11-113-424-53

Query Match      25.6%; Score 3804.5; DB 7; Length 2515;
Best Local Similarity 33.2%; Pred. No. 8.1e-238;
Matches 818; Conservative 497; Mismatches 969; Indels 181; Gaps 54;

QY 384 EDTASSWPVPTDVSYPGGTGLETPDRKKGKGTTEGKPSFFPDSFIDSGEIDVGRAS 443
DB 131 EATSSAATSSQSLSLTLSLSSLANANGGARTF---PARSFPPDG-TTFQOITLGOKLT 186

QY 444 QKIPPTFWRSQVFIHPVHLKFNVLGKAALVGIYGRKGLPPSHTPQDFVELLDGRRLL 503
DB 187 KEIQSYVNMWQFYQSEPAVVKFDYTPRGASIGVYGRNALPHTHTQVHFKEVLSGFSAS 246

QY 504 TOEARS--LEGTPRQSGTVPPSSSHETGFTQYLDGSGIWHLAFYN-DGKESVWVFLTTAI 560
DB 247 TRTARAHLSTREVTRE-----YMEPGHMFVSLYNDGQVQELTFFAAVAE 292

QY 561 ESVNCPNSCVNGDCISGTCFCLFLPLGPCGRASCPVLCSGNGQYMKGRCLCHSGWK 620
DB 293 DMTQNCPNCSGNCQCLLGHQCQNPFGGDDCSSEVCPVLCISOHGEYTNCEICNPGWK 352

QY 621 AECVPTNQCIDVACSNHGTCTITCTICNPQYKESGEEVDCMDPTCSGRGVVGRGCHC 680
DB 353 KECSLRHDECEVADCSGHGHCVCQCMRGYKGFCEEVDCPHPCNSGHHGFCADGTCIC 412

QY 681 FVHGHTNCET---PRATCLDQCSGHGTFLPDTGLCSDPSPMTGDCSIEICAADCGHG 737
DB 413 KKGWKGPDCAITMDQDALQCLPDCSGHGTFLDPTCTCEAKWSGGDCSKELCDLDCGQHG 472

QY 738 VCVGTGTCRCEDGMMGAACDQRAHCPRAEHGTCRDGKCECSPGWNGEHCTIAHYLDYVK 797
DB 473 RCEGDACADPEWGEVYCNTRFLCDVRCNEHQCKNGTCLCVTGNNGKHTI----- 523

QY 798 EGCPLCNGNGRCTLDLNG-WHCYCOLGWRGAGCDTSMETACGDSKONDGDLVDCMDPD 856
DB 524 EGCNPSACAGHCQCRVSGEGWECRCYEGWDGPDGIALELNCGDSKONDGDLVDCDEPE 583

QY 857 CCLQPLCHINPLCLGSPNPLDIIQETQVPVSQQLNHSFYDRIKELVGRDSTHILPGENPF 916
DB 584 CCASHVCKTSQLCVSAKPIDVLLRKQPPAITA---SFFERMKFLIDESSLQNYAKLTFF 640

QY 917 DGHGACVIRGOVMTSDGTFPLVGNISFVNPNLFGVTISRODQSGFDLVNNGISILRPER 976
DB 641 NESSAVIRGRVVISLGMGLVGRVVS-TTTLLEGFTLTRDDGWDPLMWNGGAVTLQFGR 699

QY 977 APFTIQEHTLWLPDRFFVMEIIMRHEEN-----IPSCDLNFAFNPNVPSPSPTS 1030
DB 700 APPRQSRIVQVPWNEVVIIDLVMNSMSEKGLAVTTTHTCTFAHDYDLKMPVVLASWKHG 759

QY 1031 PASSCAEKGPVPEIQALQOEISISGCKWRILSYSSRTPGYKSVLRISLTHTPTIPFNLMK 1090
DB 760 FQGACPDRSAILAESQVIESLQIPGTGLNLVYHSSRAAGYLSTIKLQLTDPDVIPTSL 819

QY 1091 VHLMAVEGRLFRKFAAAPDLSYVFFIWDKTDVYNQKVFGLSEAFVSVGYEYESCPDLIL 1150
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Db 820 IHLRITTEGILFERIFADPGIKFTYAMNRLNIYRQRYVGTAVVKVGYQYTDCTD-IV 878
Qy 1151 WEKRTTVLOYEYDASLKGWSLDKHALNIQSGILHKGNGENOFVSOQPPVIGSGTNG 1210
Db 879 WDQTKLSGHDMSISEVGNWJDIHRYHNFHEGILQKGDGSIYLRNKPRIILITMTMG 938
Qy 1211 RRSISPCSCNGGLADGNKLLAPALTCGSDGSLVYVGFNFIIRIFPSGNTNILELRNKD 1270
Db 939 HQPLEPCDCGQATKORLLAPVALAAPGSLFVGFDPNFIIRIMTDSIRTVVKL---- 994
Qy 1271 FRHSHSPAHYYLATDPMGAVFLSDNSRRVFKISVTVVYKOLVKNSEVAVGTGQCLP 1330
Db 995 --NATRVSYRYHMAISPLDGTLYVSDPESHQIIRVRDNDYSQPELNWEAVVSGERCLP 1052
Qy 1331 FDDTRCGDGKATYATLTPRGITVDKFLIYFVDTGTMIRIDONGIISTLLGSNDLTS 1390
Db 1053 GDEAHCDCGALAKDAKLAYKGAISAISDNILYFADGTNIRMDRDGIVSTLIGNHMKSH 1112
Qy 1391 -RPLSCDSVMDISQVRLWPTDLAINPMDNSLYVLNNVLOIASEHQVIRIVAGRPCHQ 1449
Db 1113 WKPIPCSGTKLEMHRLRWTELAVSPMDNLHIIDHMLRMTPDGRVAVISGRPLHCA 1172
Qy 1450 VPGIDHLLSKVAITHATESATALAVSHNGVLYIAETDEKINRIRQVTTSGEISLVGA 1509
Db 1173 TASTAYD--TDLATHALVMPQSTAFGLGELYVAESDSQIRNVRVIGTDGRIAPPAGA 1230
Qy 1510 PSGCDKNDANCDCFSGDGDAKADKANTPSSSLAVCADGELYVADNLGNIRIRKKNKP 1569
Db 1231 ESKNCNL-ERGCDCFEAHLATSAKENTIAALAVTPDSDHIAADQANYRIRSVMSIPE 1289
Qy 1570 LNTQMYELASPIDQELVFDTKSHLYTOSLPTGDLYLNFTY---TGDGDIITLTDNNG 1626
Db 1290 ASPSEVEIYAPDMQEIYIIFNRFGQVSTRNILTGETTYVFTYVNTNSKLSVTVDAG 1349
Qy 1627 MNVNRDSTGCMPLMLVVPDQVYVWTGNSALKSVTTQGHELAMMTYHGNSSGLATKS 1686
Db 1350 NKVFLLRDYSQVNSIENTKGKCLRWTRMKMLHELSTPDNVTYVYEHGPTGLLRKTL 1409
Qy 1687 NENGWTTFYEDSFRGRTNVTFTPGQVSSFRSDTD-SSVHVQVETSKDDVTTITNLSAS 1745
Db 1410 DSTGRSVYVNYDEFRGLTSAVTPTRVIELSFSLSVRGAQVKVSENAQKEM----SLLIQ 1465
Qy 1746 GAFVTLQDQVRNSYVYGADSLRLLLANGMEVALQTEPHLLAGTAVNPTVG-----KR 1798
Db 1466 GATVIVRNGAESRTTDMGDSTTSITPWGHNQMEVAPYIILABQSPLLGSSYPVPAKQ 1525
Qy 1799 NVTLPIDNGLMLVEWR-----ORKEQARG---QVTFGRRLRVHNRNLLSLDFDRV 1846
Db 1526 RTEIAGDLA-NRFWRVYFVRQQPLQAGKQSKGPPRPVTEVGRKLRVNGDNVLTLEYDRE 1584
Qy 1847 TRTEKIYDDHRKFTLRILYDQAGRPSPWSPSRLNG-----VNVYSPGGYIAGIQRIMS 1902
Db 1585 TQSVVMVMDKQELLNVYDRTSPISFRPOS---GDYAVYDLEYDRFGRILSVSKWGVLO 1641
Qy 1903 ERMEYDQAGRITSIPADGKTWSTYLEK--SMVLLHLSORQ--YIPEFDKNDELSSVTM 1958
Db 1642 EAYSFDRNGRNLNEIKYGDGSTMVYAFKDMFGSLPKVTTPRRSDYLLQYDDAGALQSLTT 1701
Qy 1959 P--NVARQTLTIRSVGYRNIYOPPEGNASVIOQFTEDGHLHFTFLGTGRRYIYKYG 2016
Db 1702 PRGHIHAFSLQT--SLGFFKYQYSPINRHPFELYNDEGQILAKIHPHQSGKVAFVHDT 1759
Qy 2017 LSKLAETLYDTTKVSYFVDETAGMLKTINLQNEGFTCTIRYQGLIDRQIFRP-TEEG 2075
Db 1760 AGRLETLIAGLSSHTYTDTTSLVKSVEQPEGFELRRFPKYHAGILKDEKLRFGSKNS 1819
Qy 2076 MVNARFDYNDNSFRVTSMAVINETPLPIDLYEYDDVSGKTEQFGKGVYIYDI----N 2131
Db 1820 LASARYKYAYDGNARLNGIENAIIDKELPTTRYKYSQNLGQLE-----VVQDLKLTNRN 1872
Qy 2132 QIITTAVMTHTKHF-----DAYGRMKEVQVEIFRSIMYMWTVQYDNNMGRVVKELKVG 2185

Db 1873 AFNRTVQDSAKQFFAIVDYDQHGVRKSVLMNVKNIDVFRLELDYDLNRIRKSKQKTFG- 1931
Qy 2186 YANTTRYSEYDADGO-LQTVSINDKPLMRYSYDLNGN-LHLISPGNSARLTLPLRYDIRD 2243
Db 1932 -RSTAFDKINYNADGHVVEVLGTNN---WKYLPDENGNTVGVVDQGEKEN---LGVDIGD 1984
Qy 2244 RITRLGDVQY-KWDEGFLRQGGDIFEYNSAGLLIKAYNRA--GSNSVRYRVDGLGRRV 2300
Db 1985 RVIKVGDFVFNNDARGFVVVGEQKYRYNNRQOLIHSFERERFQSW---YYVDDRSRLV 2041
Qy 2301 SKSSSHSHLOFPYADLTNPTKVTHLYNHSSEITSLYVDLQGLQFAMELSSGDEFVIAC 2360
Db 2042 AMHNDKNGTQYYANPRTHLVHFPKISMTKMLFYDDRMKLTALE-HEDQRIYVAT 2100
Qy 2361 DNIGTPLAVFSGTGLMIKQILYTAIGEIVMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRD 2420
Db 2101 DQNGSPLAFDQNGSIVKEMKRTPFGRILIKDTKPEFFVPIDFHGGLIDPHTKLVTYEQ 2160
Qy 2421 YDVLAGRWTSPDHLMKHLSSSNVMPFN--LYMFKNNPISNSQDIKCFMTDVSMLLTF 2478
Db 2161 YDPHVQWMTF--LWETLATEMSHPTDVFYIYRHNNDPI-NPNKPNQYMLDLSMLQLF 2216
Qy 2479 GFOLHNVIPOYKPDMDAMEPSYELIHTQMKTOEWDSKS-----ILGVOCEVOKQLK 2531
Db 2217 GYDLNN-----MQSSRYTKLAQYTPQASIKSNTLAPDFGVISGLECIVEK--- 2261
Qy 2532 AFVTLERFDQYGTSTTSCQAPKTKKFASSGS---VFGKGVKFKOGRVTTDIISVA 2587
Db 2262 ---TSKFSDFDVPKPLKTEPKRMNLPRVYRGRVFGEGVLLSRIGBALVSVDGS 2318
Qy 2588 N---EDGRRVAAIILNHAHYLENLHFTIDGVDTHYFVKPGPSEGDAILGSGGRRTLENG 2644
Db 2319 NSVVQD--VSSVFNNSYFLD-LHFSIHQDQVYFVK---DNVLKLRDNDNEELRLGGM 2371
Qy 2645 VNVTVSQINTVLNGRTRRYTDIOQYKALCLNTRYGTTLDEEKARVLELQARVQAWA 2704
Db 2372 FNSTHEISDHGSSAAK---ELRLHGPDVVIKYGVDPEQERHRLKHAHKRAVERAWE 2428
Qy 2705 REOQRLREGEGLRAWTEGEGKQOVLSTGRVQGVDPFVISEQVPELSDSANNIHFMRQS 2764
Db 2429 LEKQLVAAGFQGGDMDTEEBEKLQVHGVQDVGWNGDIDHSHKYPQLADDPGNVAFORDA 2488
Qy 2765 EMGRR 2769
Db 2489 KRKR 2493
RESULT 12
US-11-096-051-20
; Sequence 20, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Eitenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 20
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Homo sapiens

QY 1086 FNLKMHLMVAVBGRFRKWFAPAAPDLSYFFIWDKTDVYNQKVFGLSEAFVSXGYEYESC 1145
Db 702 FNLKMHLMVAVBGRFRKWFAPAAPDLSYFFIWDKTDVYNQKVFGLSEAFVSXGYEYESC 761
QY 1146 PDILWEKRTTVLQGYEIDASKLGGWSLKDGHALNTOSGLLHKNGENGFVSQOPPVIGS 1205
Db 762 LDILTWEKRTAILQGYELDASNMGWTLDKHVLVDQNGILYKNGENGFISQOPPVWS 821

RESULT 14
US-11-096-051-14
; Sequence 14, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 14
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-051-14

Query Match 16.2%; Score 2418.5; DB 7; Length 607;
Best Local Similarity 70.8%; Pred. No. 4.1e-149;
Matches 435; Conservative 81; Mismatches 91; Indels 7; Gaps 1;

QY 813 DLNGHVCVCLGWRGACDTSMTACGDSKXNDGDGLVDCMDPCCQLQPLCHINPLCLGS 872
Db 1 DQNGHVCVCLGWRGACDTSMTACGDSKXNDGDGLVDCMDPCCQLQPLCHINPLCLGS 60

QY 873 PNPLDIQETQVPVVSQNLHFSYDRIFKLVGRDSTHIIPOENPFDDGHACVIRQWNTSD 932
Db 61 PDQDIISQSLQSPSQAAKSFYDRISFLIGSDSTHVPGESPFNKSLASVIRGQVLTAD 120

QY 933 GTPLVGNISFVNPLFGYITISRODGSFDLVTTGGISIIILFRAPFIQEHTLWLPWDR 992
Db 121 GTPLVGNISFVNPLFGYITISRODGSFDLVTTGGISIIILFRAPFIQEHTLWLPWDR 180

QY 993 FFWMETIIMHEHNEIPSCDLSPARPNPVVSPSLTSPASSCAEKGPVPEIQALQEEI 1052
Db 181 FYWMDTLVKKKEENIPSCDLSPARPNPVVSPSLTSPASSCAEKGPVPEIQALQEEI 240

QY 1053 SISCKMRLSYLSRTPGYKSVLRISLTHPTIPNLMKVHLMVAVGRLFRKWFAPAAPDL 1112
Db 241 TIPGTDLKLSSRAAGYKSVLKITWTQSIIPNLMKVHLMVAVGRLFRKWFAPAAPDL 300

QY 1113 SYFPIWKTVDYNNQKVFGLSEAFVSXGYEYESCDPDLILWEKRTTVLQGYEIDASKLGGWS 1172
Db 301 AYTFPIWKTVDYNNQKVFGLSEAFVSXGYEYESCDPDLILWEKRTTVLQGYEIDASKLGGWS 360

QY 1173 LDKHHLNIOGILHKGNGENQFVSQOPPVIGSTMGNGRRRSISCPSCNGLADGNKLLAP 1232
Db 361 LDKHHLNIOGILHKGNGENQFVSQOPPVIGSTMGNGRRRSISCPSCNGLADGNKLLAP 420

QY 1233 VALTCGSDGSLYVGDFNYIRRIFFPSGNVNTWILELRNKDFRHSHPAHKYIYLATDPMGAV 1292
Db 421 VALACGIDGSLYVGDFNYIRRIFFPSGNVNTWILELRNKDFRHSHPAHKYIYLATDPMGAV 473

QY 1293 FLSDNSRRVFKIKSTVVVKDLVKNSEVVAGTGDQCLPDDTRCGDGGKATATLTNPRG 1352
Db 474 VYSDNTNTRIRYRPKSLTGAKDLTKNAEVVAGTGEQCLPDEARCGDGGKAVEATLMSPGK 533

QY 1353 ITVDKFEGLIYFVDCGTMIIRIDONGIISTLLGSNDLTSARPLSCDSVMDISOVRLEWPTDL 1412
Db 534 MAVDKNGLIYFVDCGTMIIRIDONGIISTLLGSNDLTSARPLSCDSVMDISOVRLEWPTDL 593

QY 1413 AINPMDNSLYVLDN 1426
Db 594 AINPMDNSLYVLDN 607

RESULT 15
US-11-096-051-12
; Sequence 12, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 12
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-051-12

Query Match 8.5%; Score 1268.5; DB 7; Length 257;
Best Local Similarity 74.4%; Pred. No. 2.6e-75;
Matches 198; Conservative 19; Mismatches 40; Indels 9; Gaps 1;

QY 566 CPNSVCYNGDCISGTCCHCFGLPGDPCGRASCPLVLCSGNGQYMKGRCLCHSGWKGAECNV 625
Db 1 CPNCHNGNCEVSGTCHCFGLPGDPCGRASCPLVLCSGNGQYMKGRCLCHSGWKGAECNV 60

QY 626 PTNQCIDVACSNHGTCTITGTCICNPQYKGESCEEVDCMDPTCGSRGVGVRGECHCFVGMG 685
Db 61 PTQCIDVACSNHGTCTITGTCICNPQYKGESCEEVDCMDPTCGSRGVGVRGECHCFVGMG 120

QY 686 GTNCETPRATCLDQCDSGHGTFLPDTGLCSCDPSWTGHDCSIIFCAADCCGHHGVVCGGTCT 745
Db 121 GSNCEILTKMCPDQCSGHGTFLPDTGLCSCDPSWTGHDCSIIFCAADCCGHHGVVCGGTCT 180

QY 746 CEDGWMGAACDORACHPRCAEHGTCDRGKCECSPHNGEHCITIAHYLDRVVKEGCGCLCN 805
Db 181 CEGWMTGPACNORACHPRCAEHGTCDRGKCECSPHNGEHCITIAHYLDRVVKEGCGCLCN 231

QY 806 GNGRCITLDLNGHVCVCLGWRGACD 831
Db 232 SNGRCITLDLNGHVCVCLGWRGACD 257

Search completed: December 11, 2005, 05:02:05
Job time : 28 secs

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OM protein - protein search, using sw model

Run on: December 11, 2005, 04:40:53 ; Search time 48 Seconds
(without alignments)

4769.353 Million cell updates/sec

Title: US-10-029-020-14

Perfect score: 14887

Sequence: 1 MDVKERKPYRSLRRDAER.....ELSDSANNHFMQSEMGRR 2769

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 2989 | 20.1 | 768 | 2 | US-08-891-845-2 |
| 2 | 2989 | 20.1 | 768 | 2 | US-09-514-573-2 |
| 3 | 2989 | 20.1 | 768 | 2 | US-10-290-578-2 |
| 4 | 2982 | 20.0 | 560 | 2 | US-08-891-845-4 |
| 5 | 2982 | 20.0 | 560 | 2 | US-09-514-573-4 |
| 6 | 2982 | 20.0 | 560 | 2 | US-10-290-578-4 |
| 7 | 1575 | 10.6 | 501 | 2 | US-08-891-845-10 |
| 8 | 1575 | 10.6 | 501 | 2 | US-09-514-573-10 |
| 9 | 1575 | 10.6 | 501 | 2 | US-10-290-578-10 |
| 10 | 649.5 | 4.4 | 2200 | 2 | US-09-796-575-2 |
| 11 | 648.5 | 4.4 | 2199 | 2 | US-08-793-273C-2 |
| 12 | 648.5 | 4.4 | 2199 | 4 | PCT-US95-11684-2 |
| 13 | 641 | 4.3 | 1810 | 2 | US-08-793-273C-4 |
| 14 | 641 | 4.3 | 1810 | 4 | PCT-US95-11684-4 |
| 15 | 585 | 3.9 | 2254 | 2 | US-09-949-016-9270 |
| 16 | 440 | 3.0 | 2471 | 1 | US-08-185-432-16 |
| 17 | 440 | 3.0 | 2471 | 1 | US-08-083-590A-19 |
| 18 | 440 | 3.0 | 2471 | 2 | US-08-532-384-19 |
| 19 | 440 | 3.0 | 2471 | 2 | US-08-899-232-1 |
| 20 | 440 | 3.0 | 2471 | 2 | US-09-121-457-1 |
| 21 | 438.5 | 2.9 | 2703 | 1 | US-08-185-432-19 |
| 22 | 438.5 | 2.9 | 2703 | 2 | US-08-899-232-4 |
| 23 | 438.5 | 2.9 | 2703 | 2 | US-09-121-457-4 |
| 24 | 429 | 2.9 | 2523 | 1 | US-08-185-432-18 |
| 25 | 429 | 2.9 | 2523 | 1 | US-08-899-232-3 |
| 26 | 429 | 2.9 | 2523 | 2 | US-09-121-457-3 |
| 27 | 428 | 2.9 | 2556 | 1 | US-08-083-590A-20 |

| | | | | | | |
|----|-------|-----|------|---|-------------------|-------------------|
| 28 | 428 | 2.9 | 2556 | 2 | US-08-532-384-20 | Sequence 20, Appl |
| 29 | 425 | 2.9 | 494 | 2 | US-09-949-002-373 | Sequence 373, App |
| 30 | 425 | 2.9 | 574 | 2 | US-09-949-002-497 | Sequence 497, App |
| 31 | 423 | 2.8 | 1193 | 1 | US-08-400-159-10 | Sequence 10, Appl |
| 32 | 423 | 2.8 | 1193 | 2 | US-08-611-729A-10 | Sequence 10, Appl |
| 33 | 423 | 2.8 | 1193 | 2 | US-09-195-524-10 | Sequence 10, Appl |
| 34 | 423 | 2.8 | 1193 | 2 | US-09-310-685-8 | Sequence 8, Appl |
| 35 | 419.5 | 2.8 | 1219 | 2 | US-08-882-046-5 | Sequence 5, Appl |
| 36 | 419.5 | 2.8 | 1219 | 2 | US-09-566-047-5 | Sequence 6, Appl |
| 37 | 411.5 | 2.8 | 1036 | 2 | US-09-068-740A-6 | Sequence 18, Appl |
| 38 | 411.5 | 2.8 | 1067 | 2 | US-09-579-536C-18 | Sequence 7, Appl |
| 39 | 411.5 | 2.8 | 1187 | 2 | US-09-068-740A-7 | Sequence 1, Appl |
| 40 | 411.5 | 2.8 | 1208 | 2 | US-09-199-865-1 | Sequence 1, Appl |
| 41 | 411.5 | 2.8 | 1208 | 2 | US-10-213-329-1 | Sequence 2, Appl |
| 42 | 411.5 | 2.8 | 1218 | 2 | US-08-882-046-2 | Sequence 11, Appl |
| 43 | 411.5 | 2.8 | 1218 | 2 | US-09-068-740A-11 | Sequence 2, Appl |
| 44 | 411.5 | 2.8 | 1218 | 2 | US-09-566-047-2 | Sequence 85, Appl |
| 45 | 411.5 | 2.8 | 1218 | 2 | US-09-917-254-85 | |

ALIGNMENTS

RESULT 1
US-08-891-845-2
; Sequence 2, Application US/08891845
; Patent No. 6096873
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Sliwowski, Mark
; TITLE OF INVENTION: Gamma-Herogulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-891-845-2

Query Match 20.1%; Score 2989; DB 2; Length 768;
Best Local Similarity 76.5%; Pred. No. 9.8e-215;
Matches 598; Conservative 22; Mismatches 84; Indels 78; Gaps 10;
Qy 1 MDVKERKPYRSLRRDAERYYSSSSADSEKAPQKYSSTLKA YDQDARLAYGSRV 60
Db 1 MDVKERKPYRSLRRDAERYYSSSSADSEKAPQKYSSTLKA YDQDARLAYGSRV 60

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QY 61 KDI VQEAEEFCRTGANFTLRELGLLEEVTPPHGTLRYTDIGLPGCGYSGAGSDADMEAD 120
DB 61 KDI VQEAEEFCRTGANFTLRELGLLEEVTPPHGTLRYTDIGLPHCGYSGAGSDADMEAD 120
QY 121 TVLSPEHPVRLWGRSTRSGRSCSSRANSNLTLDTEHENTETDHPGGLQNHARLRTPP 180
DB 121 TVLSPEHPVRLWGRSTRSGRSCSSRANSNLTLDTEHENTETDHPGGLQNHARLRTPP 180
QY 181 PPLSHAHTPNQHAASINSNLRGNFTPRSNPSPAPTDHSLGSEPPAGGAQPAHAQENWL 240
DB 181 PPLSHAHTPNQHAASINSNLRGNFTPRSNPSPAPTDHSLGSEPPAGGAQPAHAQENWL 240
QY 241 LNSNIPLETNRNLGKQPFGLTQDNLIEMDILGASRHDGAYSDGHFLFKPGGTSPLFCTTS 300
DB 241 LNSNIPLETNRNLGKQPFGLTQDNLIEMDILGASRHDGAYSDGHFLFKPGGTSPLFCTTS 300
QY 301 PGYPLTSTVYSPPPRPLPRSTFARPAFLNKKPSKYNWKAALSAIVISATLVILLAYF 360
DB 301 PGYPLTSTVYSPPPRPLPRSTFARPAFLNKKPSKYNWKAALSAIVISATLVILLAYF 360
QY 361 VAMHLFGLNHLQPMQMEQYEITDASSWPVPTDVSILYPSGGTGLETPDRKGKGTTEGK 420
DB 361 VAMHLFGLNHLQPMQMEQYEITDASSWPVPTDVSILYPSGGTGLETPDRKGKGTTEGK 420
QY 421 PSSFPPEDSFIDSGEIDVGRRASOKIPPGTFRWSQVFDHPVHLKFNYSLGKAAVLGIY 480
DB 421 PSSFPPEDSFIDSGEIDVGRRASOKIPPGTFRWSQVFDHPVHLKFNYSLGKAAVLGIY 480
QY 481 RKGLPPSHTOFDFVELLDGRELITQEARSLGSTRQSRGTVPSPSSHETGFTQYLDSGIWH 540
DB 481 RKGLPPSHTOFDFVELLDGRELITQEARSLGSTRQSRGTVPSPSSHETGFTQYLDSGIWH 540
QY 541 LAFYNDGKESEVVSFLTTAI-----ESVDNCPNCGNGD-----CISGTCCHCFLGFL----- 588
DB 541 LAFYNDGKESEVVSFLTTAI-----ESVDNCPNCGNGD-----CISGTCCHCFLGFL----- 588
QY 589 GPDCCRASCP-----VLCSGNGQYMKGRCLCHSGWKGAECVPTNQ 630
DB 589 GPDCCRASCP-----VLCSGNGQYMKGRCLCHSGWKGAECVPTNQ 630
QY 601 GNLNRKNKPNQIKQKPKGKSELINAKSLADSGEYM-----CRVISKLG 646
DB 601 GNLNRKNKPNQIKQKPKGKSELINAKSLADSGEYM-----CRVISKLG 646
QY 631 IDVACSNHGTCTGTGTCINPGYKGSCEBDCMDPTCSGRGVGVVGECHCFVWGNTNCE 690
DB 631 IDVACSNHGTCTGTGTCINPGYKGSCEBDCMDPTCSGRGVGVVGECHCFVWGNTNCE 690
QY 647 NDSASAN-----ITIV-----ESNEIITCMPASTEGAYVSSSPRISVSTEGANTS 693
DB 647 NDSASAN-----ITIV-----ESNEIITCMPASTEGAYVSSSPRISVSTEGANTS 693
QY 691 TPRAT-----CLDQ-----CSHGTF-----PDTGLCSDPSWTHGDCSIBIC 729
DB 691 TPRAT-----CLDQ-----CSHGTF-----PDTGLCSDPSWTHGDCSIBIC 729
QY 694 SSTSTSTGTGTHLVKCAEKEKTCVNGGECFVMDLSNPSRYLCKCPNEFTGDRQNTVM 753
DB 694 SSTSTSTGTGTHLVKCAEKEKTCVNGGECFVMDLSNPSRYLCKCPNEFTGDRQNTVM 753
QY 730 AA 731
DB 754 AS 755
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RESULT 2

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US-09-514-573-2
; Sequence 2, Application US/09514573
; Patent No. 6500941
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Sliwowski, Mark
; TITLE OF INVENTION: Gamma-Herregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/514, 573
; FILING DATE: 28 FEB 2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/891845
; FILING DATE: 10 JULY 1997
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40, 378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-514-573-2
```

Query Match 20.1%; Score 2989; DB 2; Length 768;
Best Local Similarity 76.5%; Pred. No. 9.8e-215;
Matches 598; Conservative 22; Mismatches 84; Indels 78; Gaps 10;

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QY 1 MDVKERPYRSLTRRRDAERRYTSADSEBKAPOKSYSSSETLKAYDQDARLAYGSRV 60
DB 1 MDVKERPYRSLTRRRDAERRYTSADSEBKAPOKSYSSSETLKAYDQDARLAYGSRV 60
QY 61 KDI VQEAEEFCRTGANFTLRELGLLEEVTPPHGTLRYTDIGLPGCGYSGAGSDADMEAD 120
DB 61 KDI VQEAEEFCRTGANFTLRELGLLEEVTPPHGTLRYTDIGLPGCGYSGAGSDADMEAD 120
QY 121 TVLSPEHPVRLWGRSTRSGRSCSSRANSNLTLDTEHENTETDHPGGLQNHARLRTPP 180
DB 121 TVLSPEHPVRLWGRSTRSGRSCSSRANSNLTLDTEHENTETDHPGGLQNHARLRTPP 180
QY 181 PPLSHAHTPNQHAASINSNLRGNFTPRSNPSPAPTDHSLGSEPPAGGAQPAHAQENWL 240
DB 181 PPLSHAHTPNQHAASINSNLRGNFTPRSNPSPAPTDHSLGSEPPAGGAQPAHAQENWL 240
QY 241 LNSNIPLETNRNLGKQPFGLTQDNLIEMDILGASRHDGAYSDGHFLFKPGGTSPLFCTTS 300
DB 241 LNSNIPLETNRNLGKQPFGLTQDNLIEMDILGASRHDGAYSDGHFLFKPGGTSPLFCTTS 300
QY 301 PGYPLTSTVYSPPPRPLPRSTFARPAFLNKKPSKYNWKAALSAIVISATLVILLAYF 360
DB 301 PGYPLTSTVYSPPPRPLPRSTFARPAFLNKKPSKYNWKAALSAIVISATLVILLAYF 360
QY 361 VAMHLFGLNHLQPMQMEQYEITDASSWPVPTDVSILYPSGGTGLETPDRKGKGTTEGK 420
DB 361 VAMHLFGLNHLQPMQMEQYEITDASSWPVPTDVSILYPSGGTGLETPDRKGKGTTEGK 420
QY 421 PSSFPPEDSFIDSGEIDVGRRASOKIPPGTFRWSQVFDHPVHLKFNYSLGKAAVLGIY 480
DB 421 PSSFPPEDSFIDSGEIDVGRRASOKIPPGTFRWSQVFDHPVHLKFNYSLGKAAVLGIY 480
QY 481 RKGLPPSHTOFDFVELLDGRELITQEARSLGSTRQSRGTVPSPSSHETGFTQYLDSGIWH 540
DB 481 RKGLPPSHTOFDFVELLDGRELITQEARSLGSTRQSRGTVPSPSSHETGFTQYLDSGIWH 540
QY 541 LAFYNDGKESEVVSFLTTAI-----ESVDNCPNCGNGD-----CISGTCCHCFLGFL----- 588
DB 541 LAFYNDGKESEVVSFLTTAI-----ESVDNCPNCGNGD-----CISGTCCHCFLGFL----- 588
QY 589 GPDCCRASCP-----VLCSGNGQYMKGRCLCHSGWKGAECVPTNQ 630
DB 589 GPDCCRASCP-----VLCSGNGQYMKGRCLCHSGWKGAECVPTNQ 630
QY 601 GNLNRKNKPNQIKQKPKGKSELINAKSLADSGEYM-----CRVISKLG 646
DB 601 GNLNRKNKPNQIKQKPKGKSELINAKSLADSGEYM-----CRVISKLG 646
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Qy 631 IDVACSNHGTCTGTCTICNPGYKGCSECEVDMDPTCSGRGVCVRGECHECFVGMGCTNCE 690
Db 647 NDSASAN-----ITIV-----ESNEIITGMPASTEGAYVSESPIRISVSTEGANTS 693
Qy 691 TPRAT-----CLDQ-----CSGHGTFL-----PDTGLCSDPDSMTGHDSCIEIC 729
Db 694 SSTSTSTGTGSHLVKCAEKEKTEFCVNGGECFVMKDLNSPRLCKCPNEFTGDRCCQNYVM 753
Qy 730 AA 731
Db 754 AS 755

RESULT 3

US-10-290-578-2
; Sequence 2, Application US/10290578
; Patent No. 6916624
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; TITLE OF INVENTION: Gamma-Heregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/290,578
; FILING DATE: 08-No. 6916624-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/021640
; FILING DATE: 12-Jul-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-290-578-2

Query Match 20.1%; Score 2989; DB 2; Length 768;
Best Local Similarity 76.5%; Pred. No. 9.8e-215; Indels 78; Gaps 10;
Matches 598; Conservative 22; Mismatches 84;

Qy 1 MDVKERPYSLTRRRDAERRYSSSSADSEEGKAPQKYSSETLTKAYDQDARLAYGSRV 60
Db 1 MDVKERPYSLTRRRDAERRYSSSSADSEEGKAPQKYSSETLTKAYDQDARLAYGSRV 60
Qy 61 KDIVPQAEBCFRTGANFTLRELGLEEVTPPHGTLTYRTDGLPCGYSMGAGSDADMEAD 120
Db 61 KDIVPQAEBCFRTGANFTLRELGLEEVTPPHGTLTYRTDGLPCGYSMGAGSDADMEAD 120
Qy 121 TVLSPEHPVRLWGRSTRSGRSSLSSRANSNLITDTEHENTETDHPGGLQNHARLTTP 180

Db 121 TVLSPEHPVRLWGRSTRSGRSSLSSRANSNLITDTEHENTETDHPGGLQNHARLTTP 180
Qy 181 PPLSHAHTNQHAASINSLNNGNFTPRSNPSPAPTQDHSLSGSEPPAGGAQEPAAHQAENWL 240
Db 181 PPLSHAHTNQHAASINSLNNGNFTPRSNPSPAPTQDHSLSGSEPPAGGAQEPAAHQAENWL 240
Qy 241 LNSNIPLERNLGKOPFLGTLQDNLIEMDILGASRHDGAYS DGHFLFKPGGTSPLFCTTS 300
Db 241 LNSNIPLERNLGKOPFLGTLQDNLIEMDILGASRHDGAYS DGHFLFKPGGTSPLFCTTS 300
Qy 301 PGYPLTSSVYSPPPRPLPRSTFARPAFNLKPKSKYCNWKCAALSIAIVISATLVIILAYF 360
Db 301 PGYPLTSSVYSPPPRPLPRSTFARPAFNLKPKSKYCNWKCAALSIAIVISATLVIILAYF 360
Qy 361 VAMHLFGLNHLQPMEGOMYEITETDASSWPVPTDVSLYPSGGTGLTETDPRKKGTEGK 420
Db 361 VAMHLFGLNHLQPMEGOMYEITETDASSWPVPTDVSLYPSGGTGLTETDPRKKGTEGK 420
Qy 421 PSFPPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIIDHPVHLKFNVLGKAALVGIYG 480
Db 421 PSFPPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIIDHPVHLKFNVLGKAALVGIYG 480
Qy 481 RKGLPPSHQTQDFVELLDGRRLLTQBARSLGTPPROSGRTVPPSSHETGFIQYLDGSIWH 540
Db 481 RKGLPPSHQTQDFVELLDGRRLLTQBARSLGTPPROSGRTVPPSSHETGFIQYLDGSIWH 540
Qy 541 LAFYNDGKESVVSFLTTAI---ESVDNCPSCYNGND---CISGTCHCFGLF--- 588
Db 541 LAFYNDGKESVVSFLTTAI---ESVDNCPSCYNGND---CISGTCHCFGLF--- 588
Qy 589 GPDGGRASCP-----VLCGNGQYMKRGKCLCHSGWGAECDDVPTNQC 630
Db 601 GNELNKKNKPNKIQKPKGSELRLINKASLADSGEYM-----CKVISKLG 646
Qy 631 IDVACSNHGTCTGTCTICNPGYKGCSECEVDMDPTCSGRGVCVRGECHECFVGMGCTNCE 690
Db 647 NDSASAN-----ITIV-----ESNEIITGMPASTEGAYVSESPIRISVSTEGANTS 693
Qy 691 TPRAT-----CLDQ-----CSGHGTFL-----PDTGLCSDPDSMTGHDSCIEIC 729
Db 694 SSTSTSTGTGSHLVKCAEKEKTEFCVNGGECFVMKDLNSPRLCKCPNEFTGDRCCQNYVM 753
Qy 730 AA 731
Db 754 AS 755

RESULT 4

US-08-891-845-4
; Sequence 4, Application US/08891845
; Patent No. 6096873
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Sliwowski, Mark
; TITLE OF INVENTION: Gamma-Heregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE:
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-891-845-4

Query Match          20.0%; Score 2982; DB 2; Length 560;
Best Local Similarity 99.8%; Pred. No. 1.9e-214;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDVKERKPYSLTRRRDAERRYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
Db 1 MDVKERKPYSLTRRRDAERRYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
Qy 61 KDIVPOEAEEFCRTGANFTLRELGLBEVTPPHGTLYRTDIGLPQCYSMGAGSDADMEAD 120
Db 61 KDIVPOEAEEFCRTGANFTLRELGLBEVTPPHGTLYRTDIGLPQCYSMGAGSDADMEAD 120
Qy 121 TVLSPEHPVRLWGRSTRSGRSCCLSSRANSNLTLDTEHENTETDHPGGLQNHARLRTPP 180
Db 121 TVLSPEHPVRLWGRSTRSGRSCCLSSRANSNLTLDTEHENTETDHPGGLQNHARLRTPP 180
Qy 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPAGGAQEPAAHQENWL 240
Db 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPAGGAQEPAAHQENWL 240
Qy 241 LNSNIPLETNKGQPFGLTQDNLIEMDILGASRDGAYS DGHFLFKPGGTSPLFCTTS 300
Db 241 LNSNIPLETNKGQPFGLTQDNLIEMDILGASRDGAYS DGHFLFKPGGTSPLFCTTS 300
Qy 301 PGYPLTSSVYSPPPRPLPRSTFARPAFLNKKPSKYNKWKCAALSIVISATLVILLAYF 360
Db 301 PGYPLTSSVYSPPPRPLPRSTFARPAFLNKKPSKYNKWKCAALSIVISATLVILLAYF 360
Qy 361 VAMHLFGLNWHLQPMEGQMYEITETASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGK 420
Db 361 VAMHLFGLNWHLQPMEGQMYEITETASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGK 420
Qy 421 PSSFFPEDSFIDSGEIDVGRASQKIPPGTFFWRSQVFIIDHPVHLKFNVS LGKAALVG IY 480
Db 421 PSSFFPEDSFIDSGEIDVGRASQKIPPGTFFWRSQVFIIDHPVHLKFNVS LGKAALVG IY 480
Qy 481 RKGLPPSHQTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPSPSHETGFTQYLDSGIWH 540
Db 481 RKGLPPSHQTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPSPSHETGFTQYLDSGIWH 540
Qy 541 LAFYNDGKESEVVSFLTTAI 560
Db 541 LAFYNDGKESEVVSFLTTAI 560

RESULT 5
US-09-514-573-4
; Sequence 4, Application US/09514573
; Patent No. 6500941
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Sliwowski, Mark
; TITLE OF INVENTION: Gamma-Herregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/514,573
; FILING DATE: 28 FEB 2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/891845
; FILING DATE: 10 JULY 1997
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-514-573-4

Query Match          20.0%; Score 2982; DB 2; Length 560;
Best Local Similarity 99.8%; Pred. No. 1.9e-214;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDVKERKPYSLTRRRDAERRYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
Db 1 MDVKERKPYSLTRRRDAERRYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
Qy 61 KDIVPOEAEEFCRTGANFTLRELGLBEVTPPHGTLYRTDIGLPQCYSMGAGSDADMEAD 120
Db 61 KDIVPOEAEEFCRTGANFTLRELGLBEVTPPHGTLYRTDIGLPQCYSMGAGSDADMEAD 120
Qy 121 TVLSPEHPVRLWGRSTRSGRSCCLSSRANSNLTLDTEHENTETDHPGGLQNHARLRTPP 180
Db 121 TVLSPEHPVRLWGRSTRSGRSCCLSSRANSNLTLDTEHENTETDHPGGLQNHARLRTPP 180
Qy 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPAGGAQEPAAHQENWL 240
Db 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPAGGAQEPAAHQENWL 240
Qy 241 LNSNIPLETNKGQPFGLTQDNLIEMDILGASRDGAYS DGHFLFKPGGTSPLFCTTS 300
Db 241 LNSNIPLETNKGQPFGLTQDNLIEMDILGASRDGAYS DGHFLFKPGGTSPLFCTTS 300
Qy 301 PGYPLTSSVYSPPPRPLPRSTFARPAFLNKKPSKYNKWKCAALSIVISATLVILLAYF 360
Db 301 PGYPLTSSVYSPPPRPLPRSTFARPAFLNKKPSKYNKWKCAALSIVISATLVILLAYF 360
Qy 361 VAMHLFGLNWHLQPMEGQMYEITETASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGK 420
Db 361 VAMHLFGLNWHLQPMEGQMYEITETASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGK 420
Qy 421 PSSFFPEDSFIDSGEIDVGRASQKIPPGTFFWRSQVFIIDHPVHLKFNVS LGKAALVG IY 480
Db 421 PSSFFPEDSFIDSGEIDVGRASQKIPPGTFFWRSQVFIIDHPVHLKFNVS LGKAALVG IY 480
Qy 481 RKGLPPSHQTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPSPSHETGFTQYLDSGIWH 540
Db 481 RKGLPPSHQTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPSPSHETGFTQYLDSGIWH 540
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Db 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPPSSSHETGFIQYLDGSIWH 540

Qy 541 LAFYNDGKESEVVSFLTAT 560

Db 541 LAFYNDGKESEVVSFLTAT 560

RESULT 6

US-10-290-578-4

; Sequence 4, Application US/10290578

; Patent No. 6916624

; GENERAL INFORMATION:

; APPLICANT: Schaefer, Gabriele M.

; Sliwkowski, Mark

; TITLE OF INVENTION: Gamma-Heregulin

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/290,578

; FILING DATE: 08-No. 6916624-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/891,845

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 60/021640

; FILING DATE: 12-Jul-96

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P1043

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 560 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-290-578-4

Query Match 20.0%; Score 2982; DB 2; Length 560;

Best Local Similarity 99.8%; Pred. No. 1.9e-214;

Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDVKERPYRLTRRRDAERYTSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60

Db 1 MDVKERPYRLTRRRDAERYTSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60

Qy 61 KDIVPQAEFCRTGANFTLRELGLEEVTTPHGLTYRTDGLPCGYSMGAGSDADMEAD 120

Db 61 KDIVPQAEFCRTGANFTLRELGLEEVTTPHGLTYRTDGLPCGYSMGAGSDADMEAD 120

Qy 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHEHENTETDHPGGLQNHARLRTPP 180

Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHEHENTETDHPGGLQNHARLRTPP 180

Qy 181 PPLSHAHTPNQHHASINSLNKGNFTPRSNPSPAPTDHLSGCEPPAGGAQBPAAQENWL 240

Db 181 PPLSHAHTPNQHHASINSLNKGNFTPRSNPSPAPTDHLSGCEPPAGGAQBPAAQENWL 240

Qy 241 LNSNIPLETRNLGKQBPFLGTLDNLIEMDILGASRHGDGAYSDGHFLPKPGGTSPLFCTTS 300

Db 241 LNSNIPLETRNLGKQBPFLGTLDNLIEMDILGASRHGDGAYSDGHFLPKPGGTSPLFCTTS 300

Qy 301 PGVPLTSSTVYSPPPRPLPRSTFARPAFNLKPKSKYCNWKAALSAIVISATLVILLAYF 360

Db 301 PGVPLTSSTVYSPPPRPLPRSTFARPAFNLKPKSKYCNWKAALSAIVISATLVILLAYF 360

Qy 361 VAMHLFGLNHLQPMGOMYEITETDASSWPVPTDVSYPSSGCTGLTETPDRKKGTEGK 420

Db 361 VAMHLFGLNHLQPMGOMYEITETDASSWPVPTDVSYPSSGCTGLTETPDRKKGTEGK 420

Qy 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIIDHPVHLKFNVSGLKAALVGIY 480

Db 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIIDHPVHLKFNVSGLKAALVGIY 480

Qy 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPPSSSHETGFIQYLDGSIWH 540

Db 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPPSSSHETGFIQYLDGSIWH 540

Qy 541 LAFYNDGKESEVVSFLTAT 560

Db 541 LAFYNDGKESEVVSFLTAT 560

RESULT 7

US-08-891-845-10

; Sequence 10, Application US/08891845

; Patent No. 6096873

; GENERAL INFORMATION:

; APPLICANT: Schaefer, Gabriele M.

; APPLICANT: Sliwkowski, Mark

; TITLE OF INVENTION: Gamma-Heregulin

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/891,845

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/021640

; FILING DATE: 07/12/96

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P1043

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 501 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-891-845-10

Query Match 10.6%; Score 1575; DB 2; Length 501;

Best Local Similarity 64.5%; Pred. No. 4.9e-109;

Matches 332; Conservative 22; Mismatches 83; Indels 78; Gaps 10;

Qy 268 MDILGASRHGDGAYSDGHFLPKPGGTSPLFCTTSFGVPLTSSTVYSPPPRPLPRSTFARPA 327

Db 1 MDILGASHRDGAYSDGHFLFKPGGTSPLFCTTSFGYPLTSSVYSPPPRPLRSTFARPA 60
Qy 328 FNLKPKSKYCNWKAALSAIVISATVILLAYFVAMHLFGLNHLQPMQMGOMYEITETA 387
Db 61 FNLKPKSKYCNWKAALSAIVISATVILLAYFVAMHLFGLNHLQPMQMGOMYEITETA 120
Qy 388 SSWPVPDVSILYPSGGTGLTETDRKKGKTEGKPSFFPEDSFIDSGEIDVGRRASOKIP 447
Db 121 SSWPVPDVSILYPSGGTGLTETDRKKGKTEGKPSFFPEDSFIDSGEIDVGRRASOKIP 180
Qy 448 PGTFRWSQVFDHPVHLKENVSLGKAALVGIYGRKGLPPSHTOFDFVELLDGRLLTOEA 507
Db 181 PGTFRWSQVFDHPVHLKENVSLGKAALVGIYGRKGLPPSHTOFDFVELLDGRLLTOEA 240
Qy 508 RSLGTPRQSRGTVPSSSHETGFIQYLDSGIWHLAFYNDGKSEVVVSFLTTAI---ESVD 564
Db 241 RSLGTPRQSRGTVPSSSHETGFIQYLDSGIWHLAFYNDGKSEVVVSFLTTAIAPPLK 300
Qy 565 NCPNSCYNGD-----CISGTCHCFLGL-----GPDGRASCP----- 598
Db 301 EMKSQESAAGSKVLRCETSSYSSLRFKFNGNELNRKNKPNQIKQKPKGKSELIN 360
Qy 599 -VLCGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCTGTGTCICNPGYKGBSC 657
Db 361 KASLADSGEYM-----CKVISKLGNDASAN-----ITIV-----ESN 393
Qy 658 EVDMDPTCSGRGVCVRGECFCFVGWGTNCETPRAT-----CLDQ-----CSG 702
Db 394 EIITGMPASTEGAYVSSSEPIRISVSTEGANTSSSTSTTGTSHLVKCAEKEKTCVNG 453
Qy 703 HGTF-----PDTGLCSDPSWTGHDCSIICAA 731
Db 454 GECFMVXDLNPSRYLCKPCNEFTGDRCONYMAS 488

RESULT 8

US-09-514-573-10
; Sequence 10, Application US/09514573
; Patent No. 6500941
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Sliwowski, Mark
; TITLE OF INVENTION: Gamma-Herregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/514,573
; FILING DATE: 28 FEB 2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/891845
; FILING DATE: 10 JULY 1997
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881

; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-514-573-10
Query Match 10.6%; Score 1575; DB 2; Length 501;
Best Local Similarity 64.5%; Pred. No. 4.9e-109;
Matches 332; Conservative 22; Mismatches 83; Indels 78; Gaps 10;
Qy 268 MDILGASHRDGAYSDGHFLFKPGGTSPLFCTTSFGYPLTSSVYSPPPRPLRSTFARPA 327
Db 1 MDILGASHRDGAYSDGHFLFKPGGTSPLFCTTSFGYPLTSSVYSPPPRPLRSTFARPA 60
Qy 328 FNLKPKSKYCNWKAALSAIVISATVILLAYFVAMHLFGLNHLQPMQMGOMYEITETA 387
Db 61 FNLKPKSKYCNWKAALSAIVISATVILLAYFVAMHLFGLNHLQPMQMGOMYEITETA 120
Qy 388 SSWPVPDVSILYPSGGTGLTETDRKKGKTEGKPSFFPEDSFIDSGEIDVGRRASOKIP 447
Db 121 SSWPVPDVSILYPSGGTGLTETDRKKGKTEGKPSFFPEDSFIDSGEIDVGRRASOKIP 180
Qy 448 PGTFRWSQVFDHPVHLKENVSLGKAALVGIYGRKGLPPSHTOFDFVELLDGRLLTOEA 507
Db 181 PGTFRWSQVFDHPVHLKENVSLGKAALVGIYGRKGLPPSHTOFDFVELLDGRLLTOEA 240
Qy 508 RSLGTPRQSRGTVPSSSHETGFIQYLDSGIWHLAFYNDGKSEVVVSFLTTAI---ESVD 564
Db 241 RSLGTPRQSRGTVPSSSHETGFIQYLDSGIWHLAFYNDGKSEVVVSFLTTAIAPPLK 300
Qy 565 NCPNSCYNGD-----CISGTCHCFLGL-----GPDGRASCP----- 598
Db 301 EMKSQESAAGSKVLRCETSSYSSLRFKFNGNELNRKNKPNQIKQKPKGKSELIN 360
Qy 599 -VLCGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCTGTGTCICNPGYKGBSC 657
Db 361 KASLADSGEYM-----CKVISKLGNDASAN-----ITIV-----ESN 393
Qy 658 EVDMDPTCSGRGVCVRGECFCFVGWGTNCETPRAT-----CLDQ-----CSG 702
Db 394 EIITGMPASTEGAYVSSSEPIRISVSTEGANTSSSTSTTGTSHLVKCAEKEKTCVNG 453
Qy 703 HGTF-----PDTGLCSDPSWTGHDCSIICAA 731
Db 454 GECFMVXDLNPSRYLCKPCNEFTGDRCONYMAS 488

RESULT 9

US-10-290-578-10
; Sequence 10, Application US/10290578
; Patent No. 6916624
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Sliwowski, Mark
; TITLE OF INVENTION: Gamma-Herregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/290,578
; FILING DATE: 08-No. 6916624-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/08/891,845
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/021640
FILING DATE: 12-Jul-96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-290-578-10

Query Match 10.6%; Score 1575; DB 2; Length 501;
Best Local Similarity 64.5%; Pred. No. 4.9e-109;
Matches 332; Conservative 22; Mismatches 83; Indels 78; Gaps 10;

Qy 268 MDILGASHDHGAYSDGHFLKPGCTSLFCTTSPGYPLTSTVYSPRPPLPRSTFARPA 327
Db 1 MDILGASHDHGAYSDGHFLKPGCTSLFCTTSPGYPLTSTVYSPRPPLPRSTFARPA 60

Qy 328 FNLKPKSKYCNWKAALSAIVISATLVILLAYFVAMHLFGLNWLHPMEQMYEITDITA 387
Db 61 FNLKPKSKYCNWKAALSAIVISATLVILLAYFVAMHLFGLNWLHPMEQMYEITDITA 120

Qy 388 SSWPVPTDVSYPGGTGLETPDRKGKGTTEGKPSFPEDSFIDSGEIDVGRASQKIP 447
Db 121 SSWPVPTDVSYPGGTGLETPDRKGKGTTEGKPSFPEDSFIDSGEIDVGRASQKIP 180

Qy 448 PGTWRSQVFDHPSVHLKFNYSGLKAAALVGIYGRKGLPPSHOTQDFVELLDGRELLOEA 507
Db 181 PGTWRSQVFDHPSVHLKFNYSGLKAAALVGIYGRKGLPPSHOTQDFVELLDGRELLOEA 240

Qy 508 RSLBGTTPRQSGRTGPPSSHETGFTQYLDSDGHWLAFYNDGKESVWSFLTTAI ---BSVD 564
Db 241 RSLBGTTPRQSGRTGPPSSHETGFTQYLDSDGHWLAFYNDGKESVWSFLTTAIAPRLK 300

Qy 565 NCPNVCYNGD-----CISGTCFCFLGFL-----GPDGRASCP----- 598
Db 301 EMKQESAAAGSKLVLCRTSSEYSLAPFKWPKNGNLRNKNKPNQIKQKPKGKSELIN 360

Qy 599 -VLCSGNGQYMKRCLCHSGWKGAECVPTNQCIDVACSNHGTCTITGTCICNPGYKGESC 657
Db 361 KASLADSGEY-----CRVSKLGNDSASAN-----ITIV-----ESN 393

Qy 658 BEVDCMPTCGRGVCVRGECHCFVWGTTNCETPRAT-----CLDQ-----CSG 702
Db 394 EIIITGMPASTGAYVSSSPRISVSTEGANTSSSTSTSTGTSHLVKCAKEKTEFCVNG 453

Qy 703 HGTFI-----PDTGLCSDPSWTHGDCSIBICAA 731
Db 454 GECFMVKDLSNPSRYLCKPNEFTGDRCONVMAS 488

RESULT 10
US-09-796-575-2
Sequence 2, Application US/09796575
Patent No. 6632671
GENERAL INFORMATION:
APPLICANT: Genesegues, Inc.
TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD
FILE REFERENCE: G332.12-0001
CURRENT APPLICATION NUMBER: US/09/796,575
CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US 60/185,282
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 2200
TYPE: PRT
ORGANISM: Homo sapiens
US-09-796-575-2

Query Match 4.4%; Score 649.5; DB 2; Length 2200;
Best Local Similarity 22.3%; Pred. No. 1.5e-38;
Matches 310; Conservative 166; Mismatches 492; Indels 423; Gaps 64;

Qy 545 NDGKESEVWSFLTAATESVDNCPNSCVNGDCCISGTCFCFLGFLGPDGRASCPVLCS-G 603
Db 208 DDGFTGEDCSOLA-----CFSDCNDQKCVNGVICFEGYAGADCSREICVPSCSE 259

Qy 604 NGQYMKRCLCHSGWKGAECVPTNQCIDVACSNHGTCTITGTCICNPGYKGESCEVDCM 663
Db 260 HGTCDVGLCVCHDGFAGDDCNKPL--CLN-NCYNRGRCVENECVCDGFTGEDCSELICP 316

Qy 664 DPTCSGRGVCVRGECHCFVWGTTNCETPRATCLDQCSGHGTFLPDTGLCSDPSWTHGD 723
Db 317 N-DCFDRGRCTCYCEGFTGEDCGKP--TCPHACTQGRC--BEGQCVCDGFGAGLD 371

Qy 724 CSTETCAADCGHGVCGVGTGTCRCEDGMMGAACDQACHPRCAEHGTCDGKCECSPWNG 783
Db 372 CSERKCPADCHNRGRCDVGRCECDGFTGADCGELKCPNGCSGHRGVNGQCVCEGYTG 431

Qy 784 EHCT-----IAHYLDREVKEG-----CPGLCNGNRCRTLDLNGHVCV 820
Db 432 EDCSOLRCPNDCSHRGCV-EGKVCBQGFYDSCDMSCPNDCHQGRG---VNGM-CV 486

Qy 821 CQLGWRGAGC-----DTSMETACGSKDNDGGGLV--DCMBPDC-----CL-Q 860
Db 487 CDGTYTGEDCRDRCQPRDCSNRGLCVDGQCVCEGFTGPDCAELSCPNDCGQGRVNGQ 546

Qy 861 PLCH---INPLCLGSPNPLDIIIOBTQVPVQQNLHSPYDRIKFLVGRDSTHIIIPGENPFD 917
Db 547 CVCHGFMGKDCKEQRCPSCHGQGRCDVQDCICHEGF-----TGLDG----- 589

Qy 918 GHAC-----VIRGQVMTSDGTPLVGVNLSFVNPLFGYTISSQDSFDLVNNGI 968
Db 590 GQHSFSDCNLGGQVSGRCICNEG--YSGEDCEVSPPK-----DLV----- 630

Qy 969 SIILRPERAFITQ--EHTLWLPND-RFFVMEIIMRHEENIIPSCDLSNFARENPPVSP 1025
Db 631 -----VTEVTEETVNLANDNEMRVTEYLV-----VTPP 658

Qy 1026 SPLTSPASSCAEKGPIVPEIQALQEEIISGCKMRLSYLSRTPGYKSVLRISL---THP 1082
Db 659 T-----HEGLEMQFRVPGDQTS-----TIIQLEFGVEYFIRVFAILENKK 700

Qy 1083 TIFPNLMKVLMAVEGRFLFRKFAAAPDLSSYFVINDKTDV-----YNQKVPF- 1130
Db 701 SIPVSARVATYLPAPGLKFK---SIKETSEVEWDPDLAFETWELIIFRNMKDEBGE 756

Qy 1131 -----LSEAFVSUGVEYBSCPDLI-----LMEKRTTVLQG-----YEI-----D 1164
Db 757 ITKSLRRPETSRYQTGLAPGOEYELSHIVKNNTRGFLKRVTTTRLDAPSQIEVKDVTD 816

Qy 1165 ASKLGW--SLDKHHALNIQSGI-----LHKNGENQFVSQPPVIGSIMGNGRRR 1213
Db 817 TTALITWFKPLAEIDGIELTYGIDVPGDRTTDLTDEENQY-----SIGNLKP-TEY 869

Qy 1214 SISPCSCNGLADGNKLLAPVALTCGSDGLYVGDPNYIRRFPSGNVTNILELNKDFRH 1273
Db 870 EVSLISRRGDMSSNP--AKETFTTGLDAP-----RNLRRVSQTDNSITL-----EWRN 915

Qy 1274 SHSFAHKYIATDPMGSAVFLSDNSRRVFKIKSTVVVKDLVRNSEVAVAGTGDCLPDD 1333
Db 916 GKAAIDSYRIKAPISGG-----DHAEDVDPKSOQA----- 946

QY 1334 TRCGDGKATEATLTNPRGIVTDKFGILYFVDGTMIIRRIDONGIISTILGSDNLTARPL 1393
Db 947 -----TTKTLTGLRPGT--EYGI-----GVSARKEDKESNPATINAAETLDPKDL 991
QY 1394 SCDVNDISQVRLEWPTDLA-----IN-----PMDNSLYLDNNVVLQISE 1434
Db 992 QVSETAETS-LTLWKTPLAKEFDYRLNLSLPTGQWVGQLPRNTTSYVLRG--LEPQ 1047
QY 1435 NHOVRIVAGRPHMC-----QVGDIDHFLSKVAIHATLESATL--AVSHNGVL 1481
Db 1048 EYNVLLTAEGRHKSKPARVKASTEQAPELENLTVEVGWDGLRLNWTAAOQAYEH---- 1103
QY 1482 YIAETDE-KKINRIROVTTSGEISLVAGAPSGCDCKNDANCDCFSGDGAYAKDLNTPS 1540
Db 1104 FILOVEANKVEARNLTVPG--SLRAVDIPGLKAATPYTVIYGIQY-----RTPV 1155
QY 1541 SLAVCAGDGLYVADLGNIRIRFIRKNKPFNTQNMVELSSPIDQELYLFDTTGKHLTYQS 1600
Db 1156 LSAAEASTGE--TNPGLVEVVVAEVGWDALKLN-----WT 1186
QY 1601 LPTGDIYNYFTYTGDDIITLTDNNGMNVRDSTGMPLWLVPDQGVYVWTMGTSAL 1660
Db 1187 APEGAYEYFFIQVEADTVAAQN-----LTPVGLRSTDLPLKKAAT 1229
QY 1661 K-SVTTQGHELAMMTYHNGSGLLTKSNGENWTTFVEYDSFGLRTNVTPTGOVSSFRSD 1719
Db 1230 HYITIRIGVTDFTSTPLSVELTEVPDMGNLTVEVSWDALRLNWTTPDGTYOQFT-- 1287
QY 1720 TDSVHVQVETSKODVTTITNLSAGAFYTLLOQVRNYSYIGADGSLRLLLANGMEVA 1779
Db 1288 -----IQVEA-----DQVEAHLNLTVPGLSLR-----SMEI- 1313
QY 1780 LQTEPHLAGT 1790
Db 1314 ----PGLRAGT 1320

RESULT 11

US-08-793-273C-2
; Sequence 2, Application US/08793273C
; Patent No. 6482410
; GENERAL INFORMATION:
; APPLICANT: Crossin, Kathryn L.
; APPLICANT: Phillips, Greg
; APPLICANT: Prieto, Anne L.
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE ATTACHMENT AND
; TITLE OF INVENTION: NEURITE OUTGROWTH, AND METHODS OF MAKING SAME
; FILE REFERENCE: BEC00228
; CURRENT APPLICATION NUMBER: US/08/793,273C
; CURRENT FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: PCT/US95/11684
; PRIOR FILING DATE: 1995-09-14
; PRIOR APPLICATION NUMBER: 08/308,359
; PRIOR FILING DATE: 1994-09-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2199
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-08-793-273C-2

Query Match 4.4%; Score 648.5; DB 2; Length 2199;
Best Local Similarity 21.4%; Pred. No. 1.8e-38;
Matches 280; Conservative 169; Mismatches 474; Indels 385; Gaps 55;

QY 566 CPSCYNGNDCTSGTCHCFGLGPDGCRASCPVLCSNGQYMKGRCLCHSGWKGAEC- 624
Db 314 CPNDCFRGRCINGTCYCEEGTGDGCKPTCPHACHTQGRCEGQCVCEGAGVDCSE 373
QY 625 --VPTN-----QCID-----VACSNHGTCITGTCINPGYKGESC 657

Db 374 KRCPADCHNRGRVDCRCEDDGTGADGELKCPNGSCGHGRCVNGQCVCDEGYTGEDC 433
QY 658 BEVDCMDPTCSGRGVCVRGECCHCFVGMGTNCETPRATCLDQCSGHHGFLPDTGLCSDP 717
Db 434 SQLRCPN--DCHSRGRCEVEGKVCBQGFQGYDCSD--MSPNDQCHGRCV--NGMVCVDD 488
QY 718 SWTGDCSIEICAADCGHGVCGTCCRCEDGMMGAACDORACHPRCAEHGTCRDKGCEC 777
Db 489 GYTGEDCDROCPDRCNRLCVGQCVCEBGTGTPDCAELSCPNDCGQGRCVNGQVCV 548
QY 778 SPGNWGECHTIAHYLDVRVKEGCPGLCNGNGRCTLDLNGMHCVCQLGWRGACGCDTSMETA 837
Db 549 HEGFMGKOCK-----EQRCPDCHGQRC--VDG-QCI CHEGFTGLDCG--QHS 592
QY 838 CGDSKNDGDGLVDCMDPDCLQLPCHINPLCLG-----SPNPLDIIQETOVPVSQNL 891
Db 593 CPS-----DCNNLGQCVSGRCICNEGYSGEDCSEVSP-EKDLV--VTEVTETV 638
QY 892 HSFYDR---IKFLVGRDSTHIIPGENPFDGHCACVIRGQVMTSDGTPLV-----GVN- 940
Db 639 NLANDNEMRVTEYLVVVTPTH-----EGGLEMQFR---VPGDQISTIRELEPGVEY 687
QY 941 ----ISFVNPLFGYTISRQDGSFSLVNGSGISILRPERAPFITQBHTLWLPDRFPVM 996
Db 688 FIRVFAILENKK-SIPVSARVATYLPAPG-----LKFKSIK-ETSVEVWDPLDIAPET 740
QY 997 ETIIMRHEENIIPSCDLSNPARPNPVVSPSLTSPASSCAEKGPVIEIQALQSEISISG 1056
Db 741 WEIIFRNKNKDEGEITKSLRPE-----TSYRQTGLAPG-----QEYEIS- 781
QY 1057 CKMPLSYLSRTPGKYKSVLRISLTHPTIPFNLKMHLMVAVEGRLFRKWFAAAADPLSYF 1116
Db 782 --LHIVKNTRGPGKRVTTTRLDAPS-----QIEVKDVTDTALLTWFKPLAID--- 830
QY 1117 IWKTDVYNQKVFGLSEAFVSGVEYECSPDLILWEKRTTVLQCYEIDASKLGWSLDKH 1176
Db 831 -----GIELTYGDKVPG-----DRTTIDLTEDENQYSIGNLKPOTE 867
QY 1177 HALNIQSGILHKGNGENQFVSQQPPVIGSIMGNRRSISCPSCNGLADGNKLLAPALT 1236
Db 868 YEVSLE--ISRRGD-----MSSNP-----AKETFT 889
QY 1237 CGSDGLYVGDVFNIRIFPFGNVNILELRNKDFRHSHPAHKYIYLATDPMGAVFLSD 1296
Db 890 TGLDAP-----RNLREVSTQDNSITL-----EMRNGKAAIDSYRIKYAPISG--- 932
QY 1297 SNRRVFKIKSVVVKDLVKNSEVVAAGTGQCLPFDDTRCGDGGKATEALTNPRGIVTD 1356
Db 933 -----DHAEDVDVPSQQA-----TTKTLTGLRPGT-- 958
QY 1357 KFGLIYFVDGTMIIRRIDONGIISTILGSDNLTARPLSCDSVMDISQVRLEWPTDLA--- 1413
Db 959 EYGI-----GVSARKEDKESNPATINAAETLDPKLOVSETAETS-LTLWKTPLAKEFD 1012
QY 1414 ---IN-----PMDNSLYLDNNVVLQISENHQVRIVAGRPHMC----- 1448
Db 1013 RYRLNLSLPTGQWVGQLPRNTTSYVLRG--LEPQEVNVLTAEGRHKSKPARVKAS 1069
QY 1449 --QVPGIDHFLSKVAIHATLESATL--AVSHNGVLYIAETDE-KKINRIROVTTSGEI 1503
Db 1070 TEQAPELENLTVEVGWDGLRLNWTAAOQAYEH-----FILOVEANKVEARNLTVPG-- 1123
QY 1504 SLVAGAPSGCDCKNDANCDCFSGDGAYAKDLNTPSSLAVCAGDGLYVADLGNIRIRFI 1563
Db 1124 SLRAVDIPGLKAATPYTVIYGIQY-----RTPVLSAAEASTGE--TNPGLVEVVVAE 1175
QY 1564 RKNKPFNTQNMVELSSPIDQELYLFDTTGKHLTYQSPLPTGDIYNYFTYTGDDITLTD 1623
Db 1176 GWDALKLN-----WTAPEGAYEYFFIQVEADTVAAQ 1208
QY 1624 NNGMNVRDSTGMPLWLVPDQGVYVWTMGTSNLSALK-SVTTQGHELAMMTYHNGSGLL 1682
Db 1209 N-----LTPVGLRSTDLPLKKAATHYITIRIGVTDQDFTPLSVEVL 1251

QY 1683 ATKSNENGWTFYEDYDFGLTNVPTGOVSSFRSDTSSVHVQVETSSKDDVTITNL 1742
DB 1252 TEEVPDMGNLTVEVSWDALRLNWTTPDGTYYDQFT-----IQVEA----- 1292

QY 1743 SASGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGT 1790
DB 1293 -----DQVEEAHNLTVPGSLR-----SMEI-----PGLRAGT 1319

RESULT 12
PCT-US95-11684-2
Sequence 2, Application PC/TUS9511684
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE
ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11684
FILING DATE: 14-SEP-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,359
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: BEC0019P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
FAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2199 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-11684-2

Query Match 4.4%; Score 648.5; DB 4; Length 2199;
Best Local Similarity 21.4%; Pred. No. 1.8e-38;
Matches 280; Conservative 169; Mismatches 474; Indels 385; Gaps 55;

QY 566 CPSNCGNGDCISCTCHCFGLGPDGGRASCPVLCGSGNGQYMKGRCLCHSGWKGAEC- 624
DB 314 CPNDCFDRGCLNGTCYCEBGTGDCGKPTCPHACTQGRCEBGCVCDEBGFAGVDCSE 373

QY 625 --VPTN-----QCID-----VACSNHGTCTGTCTCNPGYKGESE 657
DB 374 KRCPADCHNRGRCVDRGCECDGFTGADCGELKCPNGCSGHRGVNGVCQVCEGYTGDC 433

QY 658 BEVDCMPTCSGRGVYGECHCFVWGNTNCTPRATCLDQCSGHGTFLEPDTGLCSGCDP 717
DB 434 SQLRCPN--DCHSRGRGCEGKVCVQSGFGYDCSD--MSCPNDCQHGRGV--NGMVCVDD 488

QY 718 SWTHGDCSIECAADCGHGVGVGTGTCRCDEGMGAACDORACHPRCAEHGTCRDGKCEC 777
DB 489 GYTGEDCRDQCPRDCNRGLCVUDGQCVCEDGFTGPDCAELSCPNDCGQGRGVNGQVC 548

QY 778 SPGMNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGHVCVQLGWRGAGCDTSMETA 837
DB 549 HEGFMGKCK-----EQRCPDCHGQRC-----VDG-QCICHEGFTGLDCG-----QHS 592

QY 838 CGDSKNDGDGLVDCMDPCCQLQPLCHINPLCLG-----SPNPLDIIQETQVPVSOQNL 891
DB 593 CPS-----DCNNLQCCVSGRCICNEGYSGBDCSEVSP-PKDLV---VTEVTEEV 638

QY 892 HSFYDR-----IKFLVGRDSTHIIIPGENPFDGCHACVIRGQVMTSDCTPLV-----GVN- 940
DB 639 NLANDNEMRVTEYLVVYTPH-----EGLEMQFR---VPGDOTSIIIELEPGVEY 687

QY 941 ----ISFVNPLFGYTIQRDQGSFDLVNNGGISIIILRFERAFPIQEHHTLWLPWDRFFVM 996
DB 688 FIRVFAILENKK-SIPVSARVATYLPAPEG-----LKPKSIK-ETSVEWMDPLDIAPET 740

QY 997 ETIIWRHENEIPSCDLSNFARPNVPSPLTSPASSCAEKGPIVPEIQALQEEISISG 1056
DB 741 WEIIFRNMNKDEGEITKSLRPE-----TSYRQTGLAFG-----QYEIS- 781

QY 1057 CKMRLSYLSSRTPGVKSVLRISLTHPTIPFNLKMKVHLMVAVGRLPRKFAAAPDLSYVF 1116
DB 782 --LHVKNTRGPKLRVTTTRLDAPS-----QIEVKDVTDTALITWFKPLAED--- 830

QY 1117 IWDKTDVYNQKVFGLSEAFVSGYYESCPDLILMEKRTTVLQGYEIDASKLGGWSLDKH 1176
DB 831 -----GIELTYGIKDPG-----DRTTIDLTEDENQVSIKGLKPDTE 867

QY 1177 HALNTQSGILHKGNGENQVSOQPPVIGSIMGNGRRRSISCPSCNGLADGNKLLAPVALT 1236
DB 868 YEVSL---ISRRGD-----MSSNP-----AKETFT 889

QY 1237 CGSDGSLYVGDFNYIRIPPSGNVTNLELRNKPDRHSHPAHYKYLATDPMGSAVFLSD 1296
DB 890 TGLDAP-----RNLRRVSQTONSITL-----EWRNGKAADSIRIKVAPISGG----- 932

QY 1297 SNRRRVFKIKSTVVKDLVKNSEVAVAGTGDQCLPFDTRCGDGGKATEATLTNPRGITVD 1356
DB 933 -----DHAEDVVPKSOQA-----TTKTLTLGLRPT- 958

QY 1357 KFLGIYVDGTMIIRIDQNGIISTLGSNDLTSARPLSCDSVMDISQVRLWETDLA--- 1413
DB 959 EYGI-----GVSARKEDKESNPATINAATELTDPKDQVSETAETS-LTLLMKTPLAKPD 1012

QY 1414 ---IN-----PMDNSLYLDNNVVLQISENHQVRIVAGRPHC----- 1448
DB 1013 RYRLNYSLPTGOWGVOLPRNTTSYVLRG---LEPGQEVNVLITAEKRHSKPARVKAS 1069

QY 1449 --QVPGIDHFLLSKVAIHATLESATAL--AVSHNGVLYIAETDE-KKINRIRQVTTSGEI 1503
DB 1070 TEQAPLENLTVEVGDWGLRLNWTAAQAYEH---FIIQVEANKVEAARNLTVPG-- 1123

QY 1504 SLVAGAPSGCDCKNDANCDGFCGDDGYAKDAKANTPSSIAVCADGELYVADLGNIRIFI 1563
DB 1124 SLRAVDIPGLKAATPTVTSYIGYIQGY-----RTPVLSAEASTGE--TNLGEVWVAEV 1175

QY 1564 RKNKPFINTQNMVELSSPIDQELYLFDTTGKHLYTQSLPTGDLVLYNFTYTGDDITLITD 1623
DB 1176 GMDALKLN-----WTAPEGAYEYFIIQVEADTVEAAQ 1208

QY 1624 NNGNMVNVRRDSTGMPLWLVLVDPGVVWVTMGNTSNALK-SVTTQGHELAMMTYHNSGLL 1682
DB 1209 N-----LTVPGRLSRDLPGLKAATHYITIRIGVTDPSFTTSLSEVL 1251

QY 1683 ATKSNENGWTFYEDYDFGLTNVPTGOVSSFRSDTSSVHVQVETSSKDDVTITNL 1742
DB 1252 TEEVPDMGNLTVEVSWDALRLNWTTPDGTYYDQFT-----IQVEA----- 1292

QY 1743 SASGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGT 1790
DB 1293 -----DQVEEAHNLTVPGSLR-----SMEI-----PGLRAGT 1319

GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE
TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11684
FILING DATE: 14-SEP-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,359
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: BEC0019P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1810 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-11684-4

Query Match 4.3%; Score 641; DB 4; Length 1810;
Best Local Similarity 20.4%; Pred. No. 4.8e-38;
Matches 333; Conservative 219; Mismatches 563; Indels 520; Gaps 72;
QY 543 FYNDGKSEVVSFLTTAIESVDNCPNCGNGDCISGTCFGLGFLGPDGCRASCPVLCS 602
DB 332 FCBEGYTGDCGELT-----CPNNGNGRCENGCLVCHEGFGVDDCSQKRCPKTCN 383
QY 603 GNGQYMKGRCLCHSGWKASCD---VPTNQCIDVACSNHGTCTGTCTCINPGYKGSCEE 659
DB 384 NRGRCDVGRVCHEGLGDCGELRCND-----CHNRGRGNCQVCDEGFIDCGE 437
QY 660 VDCMDPTCSGRGVCVRGECHFCVWGNGTNCETPRATCLDCQSGHGTPLPDTGLCSDPSW 719
DB 438 LRCPN-DCQGRGRCINGQCEHGFICEDGELR--CPNDNSHGRCV--NGQCVCDEGY 492
QY 720 TGHDCSTIEICAAOCGGHGVCGGTCTCEDGMMGAACDQACHPRCABHGTCTCRGKCECSP 779
DB 493 TGEDGELRCFNDCHNRGRVCVEGRVCDNGFMGDCGELSCPNDCGHQGRVCDGRCVCHE 552
QY 780 GWNGEHTCIAHYLDVVVKEGCPGLCNGRCCTLDLNGWHVCVCLGWGAGACDTSMETACG 839
DB 553 GFTGEDCR-----ERSCPDNCCNVGR-----VEG-RCVCEGYNG----- 587
QY 840 DSKONDGDLVDCMDPCCQLPLCHINPLCLGSPNPLDIIQETQVPVSOQLNHSFYDRI- 898
DB 588 -----IDCSD-----VSP-----PTGLTVTNVTKTV--NLEWKHENLV 619
QY 899 -KFLV-----GRDSTHIIPEG-----NPFDDGHACVYRGQVMTSDGTPLVGNISF 943
DB 620 NEVLTVTVTSSTSGGLDQFTVPGNQTSAITHELEPGVEYFIRVAILKNKSI----- 672

QY 944 VNNPLFGYITISRODGSFVLVTNGGISIIILFERAPFITEHTLMLWPDRP---FVMEITII 1000
DB 673 -----PVSARVATYLPAGE-----LKPKS-----VRETSVQVMEPLSISFDGMWELV 715
QY 1001 MRHEENEIPSCDL-SNFAPNPVWSPSLTSPASSCAEKGPVPELQALOEESISGCKM 1059
DB 716 FRNMOKKDDNGDITSSLRKE-----TSYMQPGLAGP-----QQNVNS--L 754
QY 1060 RLSYLSRTPPGYKSLRISLTHPTIPFLMKVHLMAVEGRLPKRWFAAAPDLSYFIMD 1119
DB 755 HIVKNTRGPLSRVITTKLDAPS-----QIEAK-----D 784
QY 1120 KTDVYNQKVGLEAFVSVGYEYESCPDLILMEKRTTVLQGYE-----IDA 1165
DB 785 VTDT-----TALITMSKPLAEIEGIELTYGPKDVPDGRDRTIDL 822
QY 1166 SKLGWSLQKHALNIQSGILHKGNGENQVSPQPPVIGSIMNGRRS-----ISCPSC 1220
DB 823 SE-----DENQY-----SIGNLRPHTEYEYEVTLISR 849
QY 1221 NGLADGNKLLAPVALTCGSDGSLYVGDFNYIRIFPSGNVTNILELRNKPFRHSHSPA 1280
DB 850 RGMESDPA-----KEVFTDLDAPRNLKRVSTQDNTSITL---EWKSHANIDN 895
QY 1281 YVLATDPMGSAVFLSDSNRRRVFKISTVVVVKDLVKNSEVAGTGDQCLPDDTRCGDGG 1340
DB 896 YRIKPAPISGG-----DHTELTVPKGNQA----- 919
QY 1341 KATEATLTNPRGITVDKFLIYVODGTMRIRIDONGIISTLLGSNDLTSARPILSCDSVMD 1400
DB 920 -TTRATLTGLRP-----GTEYGIGTVAVRQ-DRESAPATINAGTOLDNPKDLEVSPTE 971
QY 1401 ISOVRLEWPTDLA-----INPMDSLYVLDDNNVVLQISENHQVRIV 1441
DB 972 -ITLSLRWRPVAKFRYRLTYVSPGKKNEMEIPVDSTSFILRG---LDAGTEYITSLV 1027
QY 1442 AGRPMHCQVP-----GIDHFLLSKVAIHAATLESATALAVSHNGV 1480
DB 1028 AEKGRHKSPTTIKSGTEBEPGLNLSVSETGWDGFLQTLTAADGAVE-----NFV 1078
QY 1481 LYIAETDEKKINRIQVTTSGEISLVAGAPS-----GCCKNDANCDCFSGDDGYAKDAKL 1536
DB 1079 IQVQSDNPE-----ETWNITVPGQSHVNVTLGLKANTPNYNTLYGVIRGYRTKPLY 1130
QY 1537 NTPSSLAVCADGSLYVADL-----GNIRIRIRKKNL---PF-----L 1570
DB 1131 VETTTGAHPEVGLTVSDITPESFNLSWTTTNGDFAFTIEIDSNRLLPEMFENISGNS 1190
QY 1571 NTQNMVELSPIDQELYLFDTTGKHLV-----TQSLPTGDLYLNFYTTGDDITL 1620
DB 1191 RTAHSGLSPSTDFIVLYGIS--HGFRTOAISAAATTEAPEVDNLLVSDATPDGFRLT 1248
QY 1621 ITDNG-----NMVNVRRDSTGMPLWLVP-----DQVYVVTWGT 1656
DB 1249 WTADDGVFDSFVLKIRDKTKKSD--PLELIVPGHERTHDITGLKEGTEYIELYGVSSGR 1306
QY 1657 NS-ALKSVTTQCHELAMMTYHGN-SGLLATKSNEN---CWTTFYEYDSFGRLTNVTFPT 1710
DB 1307 RSQPIINSVAT-----TVVSPKGISFSDITENSARVSWTP-----PR 1343
QY 1711 GOVSSFRSDTSSVHVQVETSSKDDVTITTNLSASGAFYTLQDQVRNSYIIGADGSLRL 1770
DB 1344 SRVDSRVVS-----YVPIITGTPNVTVDGSKTR-----TKLVKLVP-----GVDYNNVI 1388
QY 1771 LLANGMEVALQTEPHLLAGTVNPTVGRKN--VTLPIDNGLNLVEWR-----QRK 1817
DB 1389 ISVKGFE---ESEF--ISGILKTALDSPGLVVMNITDSEALATWQPAIAADVNIYVSYS 1443
QY 1818 EQARGQVT--VFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHDKFETRLILYDQA--GRPSL 1873
DB 1444 SEDEPEVTQVMSGNTVE-YDLNGLRPATEYTLRVHAVKDAOKSETJSTQTTGLDAPKDL 1502
QY 1874 WSPSSRLNGVNVTVSPGGYIAGIQIGIMSERMEYDQAGRITSIRIFADGKTWSVYLEKSM 1933

Db 1503 SATEVQSTAVITWRPP-----RAPVTDYLLTYESIDGRVKEVILDPETTSYLTTE--- 1553
Qy 1934 VLLHLSQRQYIFEDKNDRLSSVTMPNVARQLETIRSVGYRNIIYQPPEGNASVIOQDFT 1993
Db 1554 ---LSPSTQYTVKQLQALSR-----SMRSKMIQTVFTTGLLY-----PYPKDCSQALLNGEV 1602
Qy 1994 EDGHLHLLHTFYLTGR 2008
Db 1603 TSG--LYTIYLNDR 1615

RESULT 15
US-09-949-016-9270
; Sequence 9270, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9270
; LENGTH: 2254
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9270

Query Match 3.9%; Score 585; DB 2; Length 2254;
Best Local Similarity 33.1%; Pred. No. 1.1e-33;
Matches 121; Conservative 33; Mismatches 136; Indels 76; Gaps 10;
Qy 562 SVDNCPSCNYGNGDCISGTCHCFGLGFLGDCGRASCPVLCGNGQYMKGRCLCHSGWKGA 621
Db 320 STRTCPRDCRGRGRCDEGECIDTGYSGDDCGVRSQPGDCNQGRGRCDEGRCVCWFYGTGT 379
Qy 622 ECDVPTNQCIDVACSNHGTCTGTCTCINPGYKGESCEEVDNMDPTCSGRGVCVRGECHCF 681
Db 380 DCG---SRACPRDCRGRGRCENGVCVGNAGYSGEDCGVRSC-PGDCRGRGRCESGRCMCW 435
Qy 682 VCMGGTNCET-----PRATCLD-----QCSGHGTFLPDITGL 712
Db 436 PGYTGRCDCGTRACPGDCRGRGRCVDRGVCNPFGTGDCGSRRCPGDCRHHG--LCEDGV 493
Qy 713 CSCDPSWTGHGCSIETCAADCGHGVCGGTGRCEDGMMGAACDQACHPRCAEHGTGRD 772
Db 494 CVCDAGYSGEDCSTRSCPGGCRGRCQCLDGRVCEDGYSGEDCGVRQCPNDCSQHGVQCD 553
Qy 773 GKCECSPGNHGHCTIAHYLDVRVKEGCGPLCNGNGRCTLDLNGWHVCVQLGWRAGCDT 832
Db 554 GVCICWEGYVSEDCSI-----RTCPNSNCHGRGRC-----EEGRCLCDPGYGTGTCAT 600
Qy 833 SMETACGDSKNDGDGLVDMDPDCLQP--LCHIN-----PLCLGSPNPLD 877
Db 601 RMCPPA-----DCRGRGRCVQGVCLCHVGYGGEDCGQBEPPASACPGCGPRE 647
Qy 878 IIQETQ 883
Db 648 LCRAGQ 653

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2005, 15:51:23 ; Search time 178 Seconds
(without alignments)
6835.055 Million cell updates/sec

Title: US-10-029-020-14

Perfect score: 14887

Sequence: 1 MDVKRKPYRSLRRRDAER.....ELSDSANNIFMRQSEMGR 2769

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21:*

- 1: geneseqp1980s:*
- 2: geneseqp1980s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|---------|-------------|--------|-------|--------------------|
| 1 | 14887 | 100.0 | 2769 | 5 | ABG70388 Human TEN |
| 2 | 14887 | 100.0 | 2769 | 7 | ADf74830 Murine NO |
| 3 | 14748.5 | 99.1 | 2758 | 5 | ADg97359 Human CGD |
| 4 | 14610 | 98.1 | 2775 | 7 | ADf74842 Murine NO |
| 5 | 14406.5 | 96.8 | 2794 | 5 | ABb98401 Human NOV |
| 6 | 10221 | 68.7 | 2721 | 5 | ABp53587 Human NOV |
| 7 | 10221 | 68.7 | 2721 | 8 | ADh41969 Novel hum |
| 8 | 10201 | 68.5 | 2725 | 5 | ADp53586 Human NOV |
| 9 | 10201 | 68.5 | 2725 | 8 | ADh41995 Novel hum |
| 10 | 10201 | 68.5 | 2725 | 8 | ADh41991 Novel hum |
| 11 | 10201 | 68.5 | 2725 | 8 | ADh41993 Novel hum |
| 12 | 10201 | 68.5 | 2725 | 8 | ADh41997 Novel hum |
| 13 | 10201 | 68.5 | 2725 | 8 | ADh41999 Novel hum |
| 14 | 10201 | 68.5 | 2725 | 8 | ADh41973 Novel hum |
| 15 | 10196 | 68.5 | 2725 | 8 | ADh41993 Novel hum |
| 16 | 9888.5 | 66.4 | 2628 | 8 | ADp53588 Human NOV |
| 17 | 9888.5 | 66.4 | 2628 | 8 | ADh41949 Novel hum |
| 18 | 9856 | 66.2 | 2613 | 5 | ADp53589 Human NOV |
| 19 | 9856 | 66.2 | 2613 | 8 | ADh41977 Novel hum |
| 20 | 9635 | 64.7 | 2765 | 8 | ADh71220 Human pro |
| 21 | 9616.5 | 64.6 | 2802 | 5 | ADi16953 Chicken N |
| 22 | 9610.5 | 64.6 | 2764 | 5 | ADi16951 Murine NO |
| 23 | 9610.5 | 64.6 | 2764 | 8 | ADj76262 Marker ge |
| 24 | 9601 | 64.5 | 2765 | 5 | ADi16952 Rat NOVX |

| | | | | | | |
|----|--------|------|------|---|----------|--------------------|
| 25 | 9584 | 64.4 | 2725 | 7 | ADJ69881 | Adj69881 Human hea |
| 26 | 9536 | 64.1 | 2733 | 4 | AAU08680 | AAU08680 Human FCT |
| 27 | 9536 | 64.1 | 2733 | 8 | ADH71250 | Adh71250 Human pro |
| 28 | 9536 | 64.1 | 2733 | 8 | ADH71254 | Adh71254 Human pro |
| 29 | 9536 | 64.1 | 2733 | 8 | ADH71240 | Adh71240 Human pro |
| 30 | 9536 | 64.1 | 2733 | 8 | ADH71246 | Adh71246 Human pro |
| 31 | 9536 | 64.1 | 2733 | 8 | ADH71258 | Adh71258 Human pro |
| 32 | 9531 | 64.0 | 2733 | 7 | ADB32024 | Adb32024 Human FCT |
| 33 | 9530.5 | 64.0 | 2724 | 4 | AAU08681 | AAU08681 Human FCT |
| 34 | 9530.5 | 64.0 | 2724 | 7 | ADB32029 | Adb32029 Human FCT |
| 35 | 9530.5 | 64.0 | 2724 | 8 | ADH71252 | Adh71252 Human pro |
| 36 | 9501 | 63.8 | 2725 | 5 | ABG61913 | Abg61913 Prostate |
| 37 | 9501 | 63.8 | 2725 | 7 | ADN39610 | Adn39610 Cancer/an |
| 38 | 9501 | 63.8 | 2725 | 8 | ADQ21282 | Adq21282 Human sof |
| 39 | 9501 | 63.8 | 2725 | 8 | ADU06625 | Adu06625 Novel bro |
| 40 | 9418 | 63.3 | 2759 | 5 | ADi16608 | Adi16608 Human NOV |
| 41 | 9418 | 63.3 | 2759 | 8 | ADH71272 | Adh71272 Human pro |
| 42 | 9314 | 62.6 | 2833 | 6 | ABR58318 | AbR58318 BCU0205B |
| 43 | 9303 | 62.5 | 2590 | 5 | ADi16954 | Adi16954 Zebrafish |
| 44 | 9165.5 | 61.6 | 2662 | 8 | ADH71218 | Adh71218 Human pro |
| 45 | 9145 | 61.4 | 2346 | 5 | ADi16955 | Adi16955 Murine NO |

ALIGNMENTS

RESULT 1

ABG70388

ID ABG70388 standard; protein; 2769 AA.

XX

XX ABG70388;

AC

DT 05-NOV-2002 (first entry)

XX

DE Human TEN-M4-like protein.

XX

Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cell signal processing; metabolic pathway modulation; metabolic disorder; obesity; diabetes; infectious disease; neurodegenerative disorder; acne; Alzheimer's disease; Parkinson's disease; immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health; gastro-intestinal disease; reproductive; neurological disease; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBE1; TEN-M4; adipocyte complement-related C1q tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; type Ia membrane sushi-containing domain; butyrophilin; single nucleotide polymorphism.

OS Homo sapiens.

XX

Key Location/Qualifiers

FT Misc-difference 28 /note= "Asp substituted by Gly as a result of a single

FT

FT /note= "nucleotide polymorphism (SNP)"

FT

FT Misc-difference 64

FT

FT /note= "Val substituted by Ala as a result of a single

FT

FT /note= "nucleotide polymorphism (SNP)"

FT

FT Misc-difference 76

FT

FT /note= "Ala substituted by Thr as a result of a single

FT

FT /note= "nucleotide polymorphism (SNP)"

XX

XX WO200257453-A2.

XX

PD 25-JUL-2002.

XX

PF 19-DEC-2001; 2001WO-US050331.

XX

XX 19-DEC-2000; 2000US-0256704P.

PR 20-DEC-2000; 2000US-0257314P.
PR 02-MAY-2001; 2001US-0288153P.
PR 29-MAY-2001; 2001US-0294075P.
PR 24-JUL-2001; 2001US-0307506P.
PR 10-AUG-2001; 2001US-0311590P.
PR 10-AUG-2001; 2001US-0311613P.
PR 29-AUG-2001; 2001US-0315617P.
PR 14-SEP-2001; 2001US-0322358P.
XX (CURA-) CURAGEN CORP.
XX
PI Gangolli EA, Patturajan M, Vernet CAM, Malyankar UM, Kekuda R;
PI Stone DJ, Anderson D, Shinkets RA, Burgess CE, Zerhusen BD, Liu X;
PI Spytek KA, Caeman SJ, Boldog FL, Smithson G, Li L, Ji W;
XX
DR WPI; 2002-590744/63.
DR N-PSDB; ABS52100.
XX
XX Novel isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease or
PT cancer.
XX
PS Claim 1; Page 53; 318pp; English.
XX
CC The present invention relates to new NOVX polypeptides. The invention is
CC useful for treating or preventing a NOVX-associated disorder such as
CC cardiomyopathy or atherosclerosis, where the disorder is related to cell
CC signal processing and metabolic pathway modulation in a subject,
CC preferably human. The invention is also useful for treating metabolic
CC disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative
CC disorders (e.g. Alzheimer's disease, Parkinson's disease), immune
CC disorders, haematopoietic disorders and various cancers. The molecules of
CC the invention are also useful for treating or preventing cirrhosis,
CC pancreatitis, learning and memory defects, infertility, congenital heart
CC defects, acne, hair growth, pigmentation disorders, endocrine disorders,
CC respiratory disease, gastro-intestinal diseases, reproductive health,
CC neurological diseases, bone marrow transplantation, endocrine diseases,
CC allergy and inflammation, nephrological disorders, urinary system
CC disorders, neuropsychiatric disorders and age-related disorders. The
CC present amino acid sequence represents a NOVX protein of the invention
XX
SQ Sequence 2769 AA;
Query Match 100.0%; Score 14887; DB 5; Length 2769;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDVKERKPYRSLTRRRDAERRYTTSSADSEEGKAPQKYSYSETLKAYDQDARLAYGSRV 60
DB 1 MDVKERKPYRSLTRRRDAERRYTTSSADSEEGKAPQKYSYSETLKAYDQDARLAYGSRV 60
QY 61 KDIVPQAEFEFCRTGANFTLRGLBEVTPPHGTLTYRTDIGLPQCGYSGAGSDADMEAD 120
DB 61 KDIVPQAEFEFCRTGANFTLRGLBEVTPPHGTLTYRTDIGLPQCGYSGAGSDADMEAD 120
QY 121 TVLSPEHPVRLWGRSTRSGRSCLSRANSNLTLDTEHENTETDHPGCLQNHARLRTPP 180
DB 121 TVLSPEHPVRLWGRSTRSGRSCLSRANSNLTLDTEHENTETDHPGCLQNHARLRTPP 180
QY 181 PPLSHAHTPNQHAASINSNLNKGNTPRSNPSPAPTDHSLSGEPAGGAQPAHAQENWL 240
DB 181 PPLSHAHTPNQHAASINSNLNKGNTPRSNPSPAPTDHSLSGEPAGGAQPAHAQENWL 240
QY 241 LNSNIPLETRNLGKOPFLGTLODNLIEMDIILGASHDCAYSDDGHLFKPGGTSPFLCTTS 300
DB 241 LNSNIPLETRNLGKOPFLGTLODNLIEMDIILGASHDCAYSDDGHLFKPGGTSPFLCTTS 300
QY 301 PGYPLTSSVTSPPPRPLPRSTFARPAFLNKKPSKYNWKAALSAIVISATLVILLAYF 360
DB 301 PGYPLTSSVTSPPPRPLPRSTFARPAFLNKKPSKYNWKAALSAIVISATLVILLAYF 360
QY 361 VAMHLFGLNHLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKGGTTEGK 420

DB 361 VAMHLFGLNHLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKGGTTEGK 420
QY 421 PSSFFPEDSFIDSGEIDVGRRASOKIPPGTFWRQVFDHPVHLKFNVLGKAALVGIIY 480
DB 421 PSSFFPEDSFIDSGEIDVGRRASOKIPPGTFWRQVFDHPVHLKFNVLGKAALVGIIY 480
QY 481 RKGLPPSHQTPDFVELLDGRRLLTQEARSLSEGTTPRQSRGTVPSPSHETGFTQYLDSGIWH 540
DB 481 RKGLPPSHQTPDFVELLDGRRLLTQEARSLSEGTTPRQSRGTVPSPSHETGFTQYLDSGIWH 540
QY 541 LAFYNDGKESRVVSLTATIESVDCNSVCNGGDCISGTCHCFLGFLGDCGRASCPVL 600
DB 541 LAFYNDGKESRVVSLTATIESVDCNSVCNGGDCISGTCHCFLGFLGDCGRASCPVL 600
QY 601 CSGNGQYMKGRCLCHSGWKGAECDDVPTNQCIDVACSNHGTCTITGTCICNPGYKGESCEEV 660
DB 601 CSGNGQYMKGRCLCHSGWKGAECDDVPTNQCIDVACSNHGTCTITGTCICNPGYKGESCEEV 660
QY 661 DCMPTCSGRGVCVRGECHCFVGMGGTNCETPRATCLDQCSHGHTFLPDTGLCSDPSWT 720
DB 661 DCMPTCSGRGVCVRGECHCFVGMGGTNCETPRATCLDQCSHGHTFLPDTGLCSDPSWT 720
QY 721 GHDCSIEICAADCGHGVCGVGTCTCRCEBGMGAACDQACHPRCAEHGTCRDGKCECPG 780
DB 721 GHDCSIEICAADCGHGVCGVGTCTCRCEBGMGAACDQACHPRCAEHGTCRDGKCECPG 780
QY 781 WNGEHCITIAHYLDRVVKEGCPCGLCNGNGRCTLDLNGWHVCVQLGWRGAGCDTSMETACGD 840
DB 781 WNGEHCITIAHYLDRVVKEGCPCGLCNGNGRCTLDLNGWHVCVQLGWRGAGCDTSMETACGD 840
QY 841 SKONDGGLVDCMDPCCLOPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSEFYDRIKF 900
DB 841 SKONDGGLVDCMDPCCLOPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSEFYDRIKF 900
QY 901 LVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLVGVNISFVNPLFGYTTISRODGSF 960
DB 901 LVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLVGVNISFVNPLFGYTTISRODGSF 960
QY 961 DLVTNGGISIILRPERAPFITQSHTLWLPMWDRFVFMETIIMRHEENIEIPSCDLSNFARP 1020
DB 961 DLVTNGGISIILRPERAPFITQSHTLWLPMWDRFVFMETIIMRHEENIEIPSCDLSNFARP 1020
QY 1021 PVVSPSLTSPASSCAEKGPVPEIQALQEEISISGCKMRLSVLSRTPGYKSVLISLT 1080
DB 1021 PVVSPSLTSPASSCAEKGPVPEIQALQEEISISGCKMRLSVLSRTPGYKSVLISLT 1080
QY 1081 HPTIPFNLMKVHLMVAVEGRLEFRKWFAPADLSYFYFWDKTDVYNQKVFGLSEAFVSVG 1140
DB 1081 HPTIPFNLMKVHLMVAVEGRLEFRKWFAPADLSYFYFWDKTDVYNQKVFGLSEAFVSVG 1140
QY 1141 EYESCPDLILWEKRTTVLQGYEIDASKLGWSLDKHALNIQSGILHKGNGENQFVSQQP 1200
DB 1141 EYESCPDLILWEKRTTVLQGYEIDASKLGWSLDKHALNIQSGILHKGNGENQFVSQQP 1200
QY 1201 PVTGSTMGNRRRSISCPSCNGIADCKLLAPVALTCGSDGSLYVDNVIIRIFPSGNV 1260
DB 1201 PVTGSTMGNRRRSISCPSCNGIADCKLLAPVALTCGSDGSLYVDNVIIRIFPSGNV 1260
QY 1261 TNILELRNKDFRSHSPAHKYILATDPMGSAVFLSDSNRRVPFKISTVVVKDLVKNSEV 1320
DB 1261 TNILELRNKDFRSHSPAHKYILATDPMGSAVFLSDSNRRVPFKISTVVVKDLVKNSEV 1320
QY 1321 VAGTGOQCLPFDTRCGDGKATEATLTNPRGITVDKFGLLIYFVDGTMIRRIDQNGIIST 1380
DB 1321 VAGTGOQCLPFDTRCGDGKATEATLTNPRGITVDKFGLLIYFVDGTMIRRIDQNGIIST 1380
QY 1381 LIGSNDLTISARPLSCDUSVMDISQVRLWPTDLAINPMDNSLVYLDNNVLIQISENHQVRI 1440
DB 1381 LIGSNDLTISARPLSCDUSVMDISQVRLWPTDLAINPMDNSLVYLDNNVLIQISENHQVRI 1440
QY 1441 VAGRPMHCQVPGIDHFLSKVAIHATLESATALAVSHNGVLXYAETDEKKINRIQVTTTS 1500

Db 1441 VAGRPMHCQVPGIDHFLSKVAIAHATLESATALAVSHNGVLYIAETDEKKINRIQVTTTS 1500
Qy 1501 GEISLVAGAPSGCDCKNDANCDCFGDGDGAKDKLNTPTSSSLAVACADGELYVADLGNIRI 1560
Db 1501 GEISLVAGAPSGCDCKNDANCDCFGDGDGAKDKLNTPTSSSLAVACADGELYVADLGNIRI 1560
Qy 1561 RFIRKKNKPFINTQNMVELSSPIDQELYLFDTTGKHLYTQSLPTGDLNFTYTGDDITL 1620
Db 1561 RFIRKKNKPFINTQNMVELSSPIDQELYLFDTTGKHLYTQSLPTGDLNFTYTGDDITL 1620
Qy 1621 ITDNNGMVNRDSTGMBLWLVPDQGVVWTMGNTNSALKSVTTQGHELAMTYHGNSS 1680
Db 1621 ITDNNGMVNRDSTGMBLWLVPDQGVVWTMGNTNSALKSVTTQGHELAMTYHGNSS 1680
Qy 1681 LLATKSNENGWTTFFYDSFGRLTNTVFTPTGVSSFRSDTSSVHVQVETSSKDDVTIIT 1740
Db 1681 LLATKSNENGWTTFFYDSFGRLTNTVFTPTGVSSFRSDTSSVHVQVETSSKDDVTIIT 1740
Qy 1741 NLSASGAFYTLQDQVRNSYIIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVGKRV 1800
Db 1741 NLSASGAFYTLQDQVRNSYIIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVGKRV 1800
Qy 1801 TLPIDNGLNLVWRQKEQARGQVTVFGRRLRVHNRNLLSLDPDRVTRTEKIYDDHRKET 1860
Db 1801 TLPIDNGLNLVWRQKEQARGQVTVFGRRLRVHNRNLLSLDPDRVTRTEKIYDDHRKET 1860
Qy 1861 LRLYDOAGRPSSLWSPSSRLNGVNTYSPGGYTAGIQRGIMSERMEVDQAGRTTSRIFAD 1920
Db 1861 LRLYDOAGRPSSLWSPSSRLNGVNTYSPGGYTAGIQRGIMSERMEVDQAGRTTSRIFAD 1920
Qy 1921 GKTWSYTYLEKSMVLLHLSORQYIFFDKNDRLSSVTMPNVAQTLETIRSVGYRNIYQ 1980
Db 1921 GKTWSYTYLEKSMVLLHLSORQYIFFDKNDRLSSVTMPNVAQTLETIRSVGYRNIYQ 1980
Qy 1981 PPEGNASVIOQFTEDEGHLHHTFYLGTRRVVIYKYGKLSKLAETLYDTTKVSYFYDETAGM 2040
Db 1981 PPEGNASVIOQFTEDEGHLHHTFYLGTRRVVIYKYGKLSKLAETLYDTTKVSYFYDETAGM 2040
Qy 2041 LKTNINQNEGFTCTIYRQIGPLIDRQIFRFTBEGMVNARFDYNDNSPRVTSQMAVINE 2100
Db 2041 LKTNINQNEGFTCTIYRQIGPLIDRQIFRFTBEGMVNARFDYNDNSPRVTSQMAVINE 2100
Qy 2101 TPLPIDLYRVDVSGTEQKFGVYIYDINOIITAVMHTTKHFDAYGRMKVEQVEIYR 2160
Db 2101 TPLPIDLYRVDVSGTEQKFGVYIYDINOIITAVMHTTKHFDAYGRMKVEQVEIYR 2160
Qy 2161 SLMYMWTQVYDNNMGRVVKELKVGYPYANTTRYSEYDADQQLQTVSINDKPLWRYSYDLN 2220
Db 2161 SLMYMWTQVYDNNMGRVVKELKVGYPYANTTRYSEYDADQQLQTVSINDKPLWRYSYDLN 2220
Qy 2221 GNLHLLSPGNSABLTPLRYDIRITLGDVQVKMDDEGFLRORGGDI FEYNSAGLLIKA 2280
Db 2221 GNLHLLSPGNSABLTPLRYDIRITLGDVQVKMDDEGFLRORGGDI FEYNSAGLLIKA 2280
Qy 2281 YNRAGWSVRYRVDGLGRRYSKSSSHHLQFFYADLTNPKVTHLYNHSSTISLYYD 2340
Db 2281 YNRAGWSVRYRVDGLGRRYSKSSSHHLQFFYADLTNPKVTHLYNHSSTISLYYD 2340
Qy 2341 LOGHLPAMELSSGDEFYIACDNI GTPLAVFSGTGLMIKQILYATYGEIYMDTNPFI 2400
Db 2341 LOGHLPAMELSSGDEFYIACDNI GTPLAVFSGTGLMIKQILYATYGEIYMDTNPFI 2400
Qy 2401 GYHGGLYDPLTKLVHMGRRDYDLVLAGRWTSFDPHELWKHLSSSNVMPNLYMFKNNPISN 2460
Db 2401 GYHGGLYDPLTKLVHMGRRDYDLVLAGRWTSFDPHELWKHLSSSNVMPNLYMFKNNPISN 2460
Qy 2461 SQDIKCFMTDVNSMLLTFGQLHNVIPGYPKPDMADAMEPSYELIHTQMKTOEWDNSKIL 2520
Db 2461 SQDIKCFMTDVNSMLLTFGQLHNVIPGYPKPDMADAMEPSYELIHTQMKTOEWDNSKIL 2520
Qy 2521 GVQCEVQKQLKAFVTLERFPQLYGSTITSCQAPKTKKFASSGSVFGKVPALKDGRVT 2580
Db 2521 GVQCEVQKQLKAFVTLERFPQLYGSTITSCQAPKTKKFASSGSVFGKVPALKDGRVT 2580

Qy 2581 TDIISVANEDGRVAAAILNHAHYLENLHFTIDGVTHYFVKPSPSEGDIAILGSGRRT 2640
Db 2581 TDIISVANEDGRVAAAILNHAHYLENLHFTIDGVTHYFVKPSPSEGDIAILGSGRRT 2640
Qy 2641 LENGYNVTVSQINTVLNGTRTRYTDIOLOYGALCLNTRYGTTLDDEKARVLELARAVR 2700
Db 2641 LENGYNVTVSQINTVLNGTRTRYTDIOLOYGALCLNTRYGTTLDDEKARVLELARAVR 2700
Qy 2701 QAWAREQORLRGEGLRAWTEGEKQOVLSTGRVQCYDGFVVISVEQYPELSDSANNIHF 2760
Db 2701 QAWAREQORLRGEGLRAWTEGEKQOVLSTGRVQCYDGFVVISVEQYPELSDSANNIHF 2760
Qy 2761 MRQSEMGR 2769
Db 2761 MRQSEMGR 2769

RESULT 2
ADF74830
ID ADF74830 standard; protein; 2769 AA.
XX
AC ADF74830;
XX
DT 26-FEB-2004 (first entry)
XX
DE Murine NOVX protein to treat human pathological conditions (SeqID 44).
XX
KW mouse; murine; NOVX; metabolic disorder; diabetes; anorexia; cancer;
KW cardiovascular; infectious; neurodegenerative; immune;
KW haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic;
KW antiinflammatory; neuroprotective; antilipaeamic; anabolic; cardiant;
KW neurogenesis; wound healing; angiogenesis; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic;
KW single nucleotide polymorphism; SNP.
XX
OS Mus musculus.
XX
EH Key Location/Qualifiers
FT Misc-difference 168 /note= "Gly can be substituted for Ser by SNP"
FT Misc-difference 506 /note= "Glu can be substituted for Gln by SNP"
FT Misc-difference 2292 /note= "Arg can be substituted for Pro by SNP"
XX
PN WO2003076578-A2.
XX
PD 18-SEP-2003.
XX
PF 06-MAR-2003; 2003WO-US006794.
XX
PR 06-MAR-2002; 2002US-0361974P.
PR 08-MAR-2002; 2002US-00093463.
PR 08-MAR-2002; 2002WO-US007288.
PR 15-MAR-2002; 2002US-0365034P.
PR 19-MAR-2002; 2002US-0365477P.
PR 20-MAR-2002; 2002US-0365884P.
PR 20-MAR-2002; 2002US-0365984P.
PR 20-MAR-2002; 2002US-0365985P.
PR 22-MAR-2002; 2002US-0366928P.
PR 12-APR-2002; 2002US-0372018P.
PR 12-APR-2002; 2002US-0372022P.
PR 23-APR-2002; 2002US-0374882P.
PR 12-JUN-2002; 2002US-0388096P.
PR 14-JUN-2002; 2002US-0389143P.
PR 26-JUN-2002; 2002US-0391779P.
PR 15-AUG-2002; 2002US-0403743P.
PR 13-SEP-2002; 2002US-0410755P.
PR 23-SEP-2002; 2002US-0412957P.
PR 22-OCT-2002; 2002US-0420382P.
PR 05-MAR-2003; 2003US-00420382.
XX

(CURA-) CURAGEN CORP.

PA Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chaudhuri A;
PI Colman SD, Eisinger SR, Ettenberg S, Gangolli EA, Gerlach VL;
PI Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malyankar UM;
PI Mezes PS, Miller CE, Millet I, Padigaru M, Patturajan M, Peyman J;
PI Qian X, Rastelli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;
PI Sukumaran S, Vernet CAM, Voss EZ, Zhong M;
XX WPI: 2003-697890/66.
DR N-PSDB; ADF74829.
XX
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX

Claim 1; SEQ ID NO 44; 282pp; English.

CC This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The polypeptides, nucleic acid molecules and antibodies are useful in the
CC manufacture of a medicament for treating metabolic disorders, diabetes,
CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune
CC and haematopoietic diseases as well as various dyslipidaemias.
CC Accordingly, these molecules have many activities including anorectic,
CC virucide, nootropic, antiinflammatory, neuroprotective, antilipaeamic,
CC anabolic and cardiac. Furthermore, they are useful in screening assays
CC to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a murine NOVX protein of the
CC invention.

Sequence 2769 AA;

Query Match 100.0%; Score 14887; DB 7; Length 2769;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDVKERKPYRSLTRRRDARRYTSSADSEEGKAPQKYSSETLKAYDQARLAYGSRV 60
DB 1 MDVKERKPYRSLTRRRDARRYTSSADSEEGKAPQKYSSETLKAYDQARLAYGSRV 60
QY 61 KDIVPQEAEEFCRTGANTFLRELGLVEYTPPHGTLRYTDIGLPQCGYSMGAGSDADMEAD 120
DB 61 KDIVPQEAEEFCRTGANTFLRELGLVEYTPPHGTLRYTDIGLPQCGYSMGAGSDADMEAD 120
QY 121 TVLSPEHPVRLWGRSTRSGRSCSSLRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180
DB 121 TVLSPEHPVRLWGRSTRSGRSCSSLRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180
QY 181 PPLSHAHTPNQHHAAINSNLNRGNTPRNSPSPAPTDHSLGEPGAGQAPHAQENWL 240
DB 181 PPLSHAHTPNQHHAAINSNLNRGNTPRNSPSPAPTDHSLGEPGAGQAPHAQENWL 240
QY 241 LNSNIPLETRNLGKQPFLLGTQDNLIEMDIIIGASHDGCAYSDGHFLPKPGGTSPLFCTTS 300
DB 241 LNSNIPLETRNLGKQPFLLGTQDNLIEMDIIIGASHDGCAYSDGHFLPKPGGTSPLFCTTS 300
QY 301 PGYPLTSTVYSPPPRPLPRSTFARPAFNLLKPKSKYCNWKAALSIAIVISATLVILLAYF 360
DB 301 PGYPLTSTVYSPPPRPLPRSTFARPAFNLLKPKSKYCNWKAALSIAIVISATLVILLAYF 360
QY 361 VAMHLFGLNHLQPMQEGQMEYITEDTASSWVPVTDVSLYPSGGTGLETPDRKGGTTEGK 420
DB 361 VAMHLFGLNHLQPMQEGQMEYITEDTASSWVPVTDVSLYPSGGTGLETPDRKGGTTEGK 420

QY 421 PSSFFPDSFIDSGEIDVGRRASOKIPPGTFRWSQVFIIDHPVHLKFNVSIGKAALVGIY 480
DB 421 PSSFFPDSFIDSGEIDVGRRASOKIPPGTFRWSQVFIIDHPVHLKFNVSIGKAALVGIY 480
QY 481 RKGLPPSHTQDFVELLDGRRLLLTQEARSLGTPRQSRGTVPSPSHETGTFIYLDSGIWH 540
DB 481 RKGLPPSHTQDFVELLDGRRLLLTQEARSLGTPRQSRGTVPSPSHETGTFIYLDSGIWH 540
QY 541 LAFYNDGKSEVVSFLTTAIESVDNCPNSCYNGGDCISGTCHCFGLGPDGCRASCPVL 600
DB 541 LAFYNDGKSEVVSFLTTAIESVDNCPNSCYNGGDCISGTCHCFGLGPDGCRASCPVL 600
QY 601 CSGNQYMKGRCLCHSGWKAECDDVPTNQICIDVACSNHGTCTCTCICNPGYKESCEEV 660
DB 601 CSGNQYMKGRCLCHSGWKAECDDVPTNQICIDVACSNHGTCTCTCICNPGYKESCEEV 660
QY 661 DCMDDPTCSGRGVCVRGECHECFVGMGGTNCBTPTATCLDQCSGHGTFPLDPTGLCSDPSWT 720
DB 661 DCMDDPTCSGRGVCVRGECHECFVGMGGTNCBTPTATCLDQCSGHGTFPLDPTGLCSDPSWT 720
QY 721 GHDCSIBICAADCGGHGVCVGGTCRCEDGHWGAACDQACHPRCAEHGTCRDGKCECPG 780
DB 721 GHDCSIBICAADCGGHGVCVGGTCRCEDGHWGAACDQACHPRCAEHGTCRDGKCECPG 780
QY 781 WNGEHCCTIAHYLDVRVKEGCPGLCNGNGRCTLDLNGWHVCVQLGWRGAGCOTSMETACGD 840
DB 781 WNGEHCCTIAHYLDVRVKEGCPGLCNGNGRCTLDLNGWHVCVQLGWRGAGCOTSMETACGD 840
QY 841 SKNDGDGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVVSQQNLHSPYDRIKF 900
DB 841 SKNDGDGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVVSQQNLHSPYDRIKF 900
QY 901 LVGRDSTHIIPGENPFGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTTISRODQSP 960
DB 901 LVGRDSTHIIPGENPFGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTTISRODQSP 960
QY 961 DLVTNGGISIIILAFERAPFITQEHHTLWLPDRFFVMBETIIMRHEENIIPSCDLSNFAFPN 1020
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QY 1021 PVVSPSPLTSPASSCAKFGPIVPEIQALQOEIISIGCKMRLSYLSRSTPGYKSVLRISLT 1080
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QY 1081 HPTIPFNLKVLHMAVEGRLFRKWFAPAAADLSYFFIWDKTDVYVQKVGLESEAFVSVG 1140
DB 1081 HPTIPFNLKVLHMAVEGRLFRKWFAPAAADLSYFFIWDKTDVYVQKVGLESEAFVSVG 1140
QY 1141 EYESCPDLIIWEKRTTVLQGYEIDASKLGWSLDKHALNIQSGILHKGNGENQFVSQQP 1200
DB 1141 EYESCPDLIIWEKRTTVLQGYEIDASKLGWSLDKHALNIQSGILHKGNGENQFVSQQP 1200
QY 1201 PVGISMGNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGFNFIIRIFPSSNV 1260
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DB 1261 TNILELRNKDPRHSHSPAHKYIATDPMSCAVFLSDSNSRRVFKIKSTVVVKDLVKNSEV 1320
QY 1321 VAGTGDQCLPDDTRCDGGGKATEATLTNPRGTLVDKFGLIYFVDGTMIRRIIDQNGIIST 1380
DB 1321 VAGTGDQCLPDDTRCDGGGKATEATLTNPRGTLVDKFGLIYFVDGTMIRRIIDQNGIIST 1380
QY 1381 LLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDNNVLIQISENHQVRI 1440
DB 1381 LLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDNNVLIQISENHQVRI 1440
QY 1441 VAGRPHMCQVPGIDHFLLSKVAIHTLESATALAVSHNGVLYIAETDEKKINRIQVTTTS 1500
DB 1441 VAGRPHMCQVPGIDHFLLSKVAIHTLESATALAVSHNGVLYIAETDEKKINRIQVTTTS 1500

QY 1501 GEISLVAGSPGCDCKNDANCDGSGDDGYAKDAKLNTPSSSLAVACDAGELYVADLGNIRI 1560
DB 1501 GEISLVAGSPGCDCKNDANCDGSGDDGYAKDAKLNTPSSSLAVACDAGELYVADLGNIRI 1560
QY 1561 RFIRKKNKPFINTQNMVELSSPIDQELYLFTTQKHLIYQSLPTGSDVLYNFTYTGDDITL 1620
DB 1561 RFIRKKNKPFINTQNMVELSSPIDQELYLFTTQKHLIYQSLPTGSDVLYNFTYTGDDITL 1620
QY 1621 ITDNNGMNVNRDSTGMPPLMLVVPDQVYVWMTGNSALKSVTTQGHELAMWTVHGNSG 1680
DB 1621 ITDNNGMNVNRDSTGMPPLMLVVPDQVYVWMTGNSALKSVTTQGHELAMWTVHGNSG 1680
QY 1681 LLATKSNENGWITTFEYDSFGRLTNTVFTPTGVSSFRSDTSSVHVQVETSSKDDVTIIT 1740
DB 1681 LLATKSNENGWITTFEYDSFGRLTNTVFTPTGVSSFRSDTSSVHVQVETSSKDDVTIIT 1740
QY 1741 NLSASGAFVTLLOQVNRNSYIIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVGRNV 1800
DB 1741 NLSASGAFVTLLOQVNRNSYIIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVGRNV 1800
QY 1801 TLPIDNGLNLVWRQKEQARGOVTVGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKET 1860
DB 1801 TLPIDNGLNLVWRQKEQARGOVTVGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKET 1860
QY 1861 LRILYDQAGRPLSWSSRLNGVNVTVSPGYYIAGIQRGIMSRMEYDQAGRITSRIFAD 1920
DB 1861 LRILYDQAGRPLSWSSRLNGVNVTVSPGYYIAGIQRGIMSRMEYDQAGRITSRIFAD 1920
QY 1921 GKTWSYTYLEKSMVLLHLSQRYIFEFDKNDRLSSTVMPNVARQTLTETRSVYRNIVQ 1980
DB 1921 GKTWSYTYLEKSMVLLHLSQRYIFEFDKNDRLSSTVMPNVARQTLTETRSVYRNIVQ 1980
QY 1981 PPEGNASVIOQFTEDEGHLLHFTYLGTRRVIYKYGKLSKLAETLYDTTKVSVFYDETAG 2040
DB 1981 PPEGNASVIOQFTEDEGHLLHFTYLGTRRVIYKYGKLSKLAETLYDTTKVSVFYDETAG 2040
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DB 2041 LKTIINLQNEGFTCTIRYQIQLPLIDRQIFRFTBEGMVNARFDYNDNSFRVTSQVAVINE 2100
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DB 2101 TPLPIDLYRYDDVSGKTEQKFGVYYIDINQIITTAVMTHTKHFDAYGRMKVEQVEIFR 2160
QY 2161 SLMYWMTVQYDNNMGRVVKELKVGYPANTTRYSEYVDADGLOQTVSINDKPLWRYSDLN 2220
DB 2161 SLMYWMTVQYDNNMGRVVKELKVGYPANTTRYSEYVDADGLOQTVSINDKPLWRYSDLN 2220
QY 2221 GNHLHLSPGNSARLTPLRYDIRITRLGVDQYKMBDEGFLRQGGDIFEYNSAGLLIKA 2280
DB 2221 GNHLHLSPGNSARLTPLRYDIRITRLGVDQYKMBDEGFLRQGGDIFEYNSAGLLIKA 2280
QY 2281 YNRAGSWSRYRYDGLGRRYSKSSSHSHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340
DB 2281 YNRAGSWSRYRYDGLGRRYSKSSSHSHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340
QY 2341 LQGHLPAMELSSGDEFYIACDNIGTGPLAVFSGTGLMVKQILYAYGEIYMDTNPQIIII 2400
DB 2341 LQGHLPAMELSSGDEFYIACDNIGTGPLAVFSGTGLMVKQILYAYGEIYMDTNPQIIII 2400
QY 2401 GYHGGLYDPLTKLVHMGRRDYDLVAGRWTSPPDHELWKHLSSNMPNPLMYFNKNNPISN 2460
DB 2401 GYHGGLYDPLTKLVHMGRRDYDLVAGRWTSPPDHELWKHLSSNMPNPLMYFNKNNPISN 2460
QY 2461 SQDIKCFMTDVNSWLLTFGQLHNVI PGYPKPDMDAMEPSYELIHTQMTQEDWNSKSL 2520
DB 2461 SQDIKCFMTDVNSWLLTFGQLHNVI PGYPKPDMDAMEPSYELIHTQMTQEDWNSKSL 2520
QY 2521 GVOCEVQKQJKAFTLBRFPOLYGSTTSCQAPKTKKFPASSGVSFGKGVKPKALDGRVT 2580
DB 2521 GVOCEVQKQJKAFTLBRFPOLYGSTTSCQAPKTKKFPASSGVSFGKGVKPKALDGRVT 2580
QY 2581 TDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHTYFVKPGPSEGDALILGSGGRT 2640

DB 2581 TDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHTYFVKPGPSEGDALILGSGGRT 2640
QY 2641 LENGNVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDDEKARVLELARQAVR 2700
DB 2641 LENGNVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDDEKARVLELARQAVR 2700
QY 2701 QAWAREQORLREGBEGLRAWTEGEKQQLVSLSTGRVQGYDGFVFSVEQYPELSDSANNIHF 2760
DB 2701 QAWAREQORLREGBEGLRAWTEGEKQQLVSLSTGRVQGYDGFVFSVEQYPELSDSANNIHF 2760
QY 2761 MRQSEMGR 2769
DB 2761 MRQSEMGR 2769
RESULT 3
ABG97359
ID ABG97359 standard; protein; 2758 AA.
XX ABG97359;
AC ABG97359;
XX 16-DEC-2002 (first entry)
DT 16-DEC-2002 (first entry)
XX Human CGDD10, INCYTE 7488573CD1.
XX Human; cell growth; differentiation; death; CGDD; cancer;
XX cell proliferative disorder; arterioleclerosis; atherosclerosis;
XX cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; peoriiasis;
XX polycythaemia vera; primary thrombocytopaenia; developmental disorder;
XX renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS;
XX neurological disorder; Alzheimer disease; Parkinson's disease; asthma;
XX reproductive disorder; infertility; autoimmune disorder; gout; allergy;
XX inflammatory disorder; acquired immunodeficiency syndrome; uveitis;
XX autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection;
XX diabetes mellitus; glomerulonephritis; irritable bowel syndrome;
XX multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
XX rheumatoid arthritis.
XX Homo sapiens.
OS Homo sapiens.
XX WO200272830-A2.
PN WO200272830-A2.
XX 19-SEP-2002.
XX 08-FEB-2002; 2002WO-US003715.
PF 08-FEB-2002; 2001US-0268111P.
XX 23-FEB-2001; 2001US-0271175P.
PR 08-MAR-2001; 2001US-0274503P.
PR 09-MAR-2001; 2001US-0274552P.
XX (INCY-) INCYTE GENOMICS INC.
PA Yue H, Yao MG, Ison CH, Lu Y, Warren BA, Elliott VS, Baughn MR;
XX Ding L, Xu Y, Gletzen KJ, Tang TY, Lal PG, Duggan BM, Burford N;
PI Lu DAM, Richardson TW, Tran UK, Khare R, Walia NK;
XX WPI; 2002-723356/78.
DR N-PSDB; ABS78652.
XX New human proteins associated with cell growth, differentiation and
XX death, useful for diagnosing, treating or preventing autoimmune or
PT inflammatory disorders (e.g. AIDS, allergy or anemia), cancer,
PT atherosclerosis or hepatitis.
XX Claim 1; Page 155-161; 181pp; English.
XX The invention relates to an isolated polypeptide comprising CGDD1-12
CC (cell growth, differentiation and death) a naturally occurring amino
CC acid sequence at least 90% identical to CGDD, a biologically active
CC fragment or an immunogenic fragment. Also included are the
CC polynucleotides encoding CGDD1-12, a recombinant polynucleotide

comprising a promoter sequence operably linked to the CGDD comprising a cell transformed with the recombinant polynucleotide, a transgenic organism comprising the recombinant polynucleotide, an anti-CGDD antibody, screening for compounds which bind to/modulate or are ant/agonists of CGDD or alter the expression of CGDD polynucleotide and a CGDD polynucleotide microarray. The polypeptides, polynucleotides, agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of CGDD, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopaenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer disease, Parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS, (acquired immunodeficiency syndrome) allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, gout, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, rheumatoid arthritis, uveitis, or viral, bacterial, fungal, parasitic, protozoal or helminthic infections. They are also useful in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of proteins associated with CGDD. The present sequence represents a CGDD protein

XX Sequence 2758 AA;

| | | | | |
|-----------------------|--------------------------|-------------------------|-----------------------|--------------|
| Query Match | 99.1%; | Score 14748.5; | DB 5; | Length 2758; |
| Best Local Similarity | 99.3%; | Pred. No. 0; | | |
| Matches 2751; | Conservative 0; | Mismatches 7; | Indels 11; | Gaps 3; |
| QY 1 | MDVKERKPYRSLTRRRDAERRYTS | SSADSEEGKAPQKYS | SSSETLKAYDQDARLAYGSRV | 60 |
| DB 1 | MDVKERKPYRSLTRRRDAERRYTS | SSADSEEGKAPQKYS | SSSETLKAYDQDARLAYGSRV | 60 |
| QY 61 | KDIIVPOAESEFCRTGANFTLR | ELGLEEVTPPHGTLRYTDIGL | POCGYNGAGSDADMEAD | 120 |
| DB 61 | KDIIVPOAESEFCRTGANFTLR | ELGLEEVTPPHGTLRYTDIGL | POCGYNGAGSDADMEAD | 120 |
| QY 121 | TVLSPEHPVRLWGRSTRSGRSSCL | SRANSNLTLTDTEHENTETDHP | GGQLQNHARLRTPP | 180 |
| DB 121 | TVLSPEHPVRLWGRSTRSGRSSCL | SRANSNLTLTDTEHENTET - | PGQLQNHARLRTPP | 178 |
| QY 181 | PPLSHAHTPNQHAASINSLNRGN | FTPRSNPSAPTDHLSGEPAGGAQ | PAHAQENWL | 240 |
| DB 179 | PPLSHAHTPNQHAASINSLNRGN | FTPRSNPSAPTDHLSGEPAGGAQ | PAHAQENWL | 238 |
| QY 241 | LNSNIPLETRNLGKQPF | LGTLDQNLIEWDILGASRHDGAY | SDGHPFLKPGGTSPLFC | 300 |
| DB 239 | LNSNIPLETRNLGKQPF | LGTLDQNLIEWDILGASRHDGAY | SDGHPFLKPGGTSPLFC | 298 |
| QY 301 | PGYPLTSSVTYSPPPRPLPRST | FARPAFNLKPKSKYCNWKCAAL | SAIVISATLVILLAYF | 360 |
| DB 299 | PGYPLTSSVTYSPPPRPLPRST | FARPAFNLKPKSKYCNWKCAAL | SAIVISATLVILLAYF | 358 |
| QY 361 | VAMHLFGLNHLQPMQMEQYETED | TASSWPVPTDVSLYPSGGTGLE | TPDRKGGTTEGK | 420 |
| DB 359 | VGKHLF--NWLQPMQMEQYETED | TASSWPVPTDVSLYPSGGTGLE | TPDRKGGTTEGK | 416 |
| QY 421 | PSSFFPEDSFIDSGEIDVGRASQ | KIPPGTFWRSQVFDHPVHLKFN | VLGKAALVGIYG | 480 |
| DB 417 | PSSFFPEDSFIDSGEIDVGRASQ | KIPPGTFWRSQVFDHPVHLKFN | VLGKAALVGIYG | 476 |
| QY 481 | RKGLPPSHTQDFVELLDGRLLTQ | EARSLGTEGTPRQSRGTVP | PPSSHETGFIQYLDSDGIWH | 540 |
| DB 477 | RKGLPPSHTQDFVELLDGRLLTQ | EARSLGTEGTPRQSRGTVP | PPSSHETGFIQYLDSDGIWH | 536 |
| QY 541 | LAFYNDGKESEVSPFLTTAIES | VDNCPNCGNGDCISGTC | CHCFLGFLGPDGCRASCPVL | 600 |
| DB 537 | LAFYNDGKESEVSPFLTTAIES | VDNCPNCGNGDCISGTC | CHCFLGFLGPDGCRASCPVL | 596 |
| QY 601 | CSNGQYMKGRCLCHSGWKGAECD | PVTNQCIDVACSNHGTCTITG | TCICINPGYKGCSEBEV | 660 |

| | | | | | |
|---------|-----------------|------------------|-------------------|-----------------------|------|
| DB 597 | CSNGQYMKGRCLCH | SGWKGAECDPVTNQCI | DVACSNHGTCT | IMGTICINPGYKGCSEEV | 656 |
| QY 661 | DCMDPTCSGRGVCVR | GBCHECFVGMGGNCT | ETPRATCLDQCSGHGTF | FLPDTGLCSCDPSWT | 720 |
| DB 657 | DCMDPTCSGRGVCVR | GBCHECFVGMGGNCT | ETPRATCLDQCSGHGTF | FLPDTGLCSCDPSWT | 716 |
| QY 721 | GHDCSIEICAAACG | GGHVCVGGTCRC | EDGWMGAACDORACH | PRCAEHGTCBDGCECSPG | 780 |
| DB 717 | GHDCSIEICAAACG | GGHVCVGGTCRC | EDGWMGAACDORACH | PRCAEHGTCBDGCECSPG | 776 |
| QY 781 | WNGEHCITAHYLD | RVVWKEGCPGLC | NGNCRCTDLNLNGHVC | COLGMRGAGCDTSMETACGD | 840 |
| DB 777 | WNGEHCITAHYLD | RVVWKEGCPGLC | NGNCRCTDLNLNGHVC | COLGMRGAGCDTSMETACGD | 836 |
| QY 841 | SKONDGDLVDCMD | PDCCLOPLCHIN | PLCLGSPNPLDII | IOETQVPVQSNLHSPYDRIKF | 900 |
| DB 837 | SKONDGDLVDCMD | PDCCLOPLCHIN | PLCLGSPNPLDII | IOETQVPVQSNLHSPYDRIKF | 896 |
| QY 901 | LVGRDSTHIIPG | ENPPDGGHACVIR | GOVMTSDGTPLVGVNI | SFVNNPLFGVTTISRODGSF | 960 |
| DB 897 | LVGRDSTHIIPG | ENPPDGGHACVIR | GOVMTSDGTPLVGVNI | SFVNNPLFGVTTISRODGSF | 956 |
| QY 961 | DLVTNGGISIL | PERAPFITQBHTL | WLPWDRFFVME | TIIMRHEENIPSCDLSNFARP | 1020 |
| DB 957 | DLVTNGGISIL | PERAPFITQBHTL | WLPWDRFFVME | TIIMRHEENIPSCDLSNFARP | 1016 |
| QY 1021 | PVVSPLTSPAS | CAEKGPVPEIQAL | QBEISISGCKMRLS | YLSSTPGYKSVLRISLT | 1080 |
| DB 1017 | PVVSPLTSPAS | CAEKGPVPEIQAL | QBEISISGCKMRLS | YLSSTPGYKSVLRISLT | 1076 |
| QY 1081 | HPTIPFNLKMLV | MVAVEGRFLFRK | FAAAPDLVSFYI | FDVYVNVQVGLSBAFVS | 1140 |
| DB 1077 | HPTIPFNLKMLV | MVAVEGRFLFRK | FAAAPDLVSFYI | FDVYVNVQVGLSBAFVS | 1136 |
| QY 1141 | EYESCPDLILWE | KRTTVLQYEIDA | SKLGWSLDKHALNI | QSGILHKGNGENQFVSQ | 1200 |
| DB 1137 | EYESCPDLILWE | KRTTVLQYEIDA | SKLGWSLDKHALNI | QSGILHKGNGENQFVSQ | 1196 |
| QY 1201 | PVTSINGNRRRS | ISCPSCNGIADGN | KLLAPALVATCG | SGLSIYVGDVFNIRIP | 1260 |
| DB 1197 | PVTSINGNRRRS | ISCPSCNGIADGN | KLLAPALVATCG | SGLSIYVGDVFNIRIP | 1256 |
| QY 1261 | TNILELRNKD | FRSHSPAHKYI | LATDPMGAVFL | SDNSRRVFKISTVVV | 1320 |
| DB 1257 | TNILELRNKD | FRSHSPAHKYI | LATDPMGAVFL | SDNSRRVFKISTVVV | 1309 |
| QY 1321 | VAGTGOCLP | PFDDTRCGDGK | ATEATLTNPRGIT | VDKFGLIYFVDTG | 1380 |
| DB 1310 | VAGTGOCLP | PFDDTRCGDGK | ATEATLTNPRGIT | VDKFGLIYFVDTG | 1369 |
| QY 1381 | LLGSNDLTSAR | PLSCDSVMDISO | VRLEWPTDLAIN | PMDSNLVYLDNNVLI | 1440 |
| DB 1370 | LLGSNDLTSAR | PLSCDSVMDISO | VRLEWPTDLAIN | PMDSNLVYLDNNVLI | 1429 |
| QY 1441 | VAGRPMHCQV | PGIDHFLSKVAI | HALESATALAVSH | NGVLYIAETDEKKINR | 1500 |
| DB 1430 | VAGRPMHCQV | PGIDHFLSKVAI | HALESATALAVSH | NGVLYIAETDEKKINR | 1489 |
| QY 1501 | GEISLVAGAP | SGCDCKNDAN | CDCFCGDDGYA | KADAKLNTSSLA | 1560 |
| DB 1490 | GEISLVAGAP | SGCDCKNDAN | CDCFCGDDGYA | KADAKLNTSSLA | 1549 |
| QY 1561 | RFIRKKNKPF | LNTQNMVELSSP | IDQELYLFD | TTGKHLYTQSLPTG | 1620 |
| DB 1550 | RFIRKKNKPF | LNTQNMVELSSP | IDQELYLFD | TTGKHLYTQSLPTG | 1609 |
| QY 1621 | ITDNNGMVNV | RRDSTGMPLWL | VVPDQYVYV | WTMTGNSALKSV | 1680 |
| DB 1610 | ITDNNGMVNV | RRDSTGMPLWL | VVPDQYVYV | WTMTGNSALKSV | 1669 |
| QY 1681 | LIATKSNENG | WTTFEYDSFG | RLTNVPTQV | SSFRSDTSSVHV | 1740 |
| DB 1670 | LIATKSNENG | WTTFEYDSFG | RLTNVPTQV | SSFRSDTSSVHV | 1729 |

QY 1741 NLSASGAFYTLQDOVRNSYIYGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRV 1800
Db 1730 NLSASGAFYTLQDOVRNSYIYGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRV 1789
QY 1801 TLPIDNGLNLEVRQKEQARGQVTVFGRRLRVHNRNLLSLDFRVRTTEKIYDDHRKFT 1860
Db 1790 TLPIDNGLNLEVRQKEQARGQVTVFGRRLRVHNRNLLSLDFRVRTTEKIYDDHRKFT 1849
QY 1861 LRILYDQAGPSLWSPSSBLNGVNTYSPGGYTAGIQRGIMSERMEYDQAGRITSRIFAD 1920
Db 1850 LRILYDQAGPSLWSPSSBLNGVNTYSPGGYTAGIQRGIMSERMEYDQAGRITSRIFAD 1909
QY 1921 GKTWSYTYLEKSMVLLHLSORQVIFFDKNDRLSSVTMPNVARQTLTETRSVGYRNIYQ 1980
Db 1910 GKTWSYTYLEKSMVLLHLSORQVIFFDKNDRLSSVTMPNVARQTLTETRSVGYRNIYQ 1969
QY 1981 PPEGNASVIQDFTEDGHLHFTYLGTRRVIYKYGKLSKLAETLYDTTKVSFTYDSTAGM 2040
Db 1970 PPEGNASVIQDFTEDGHLHFTYLGTRRVIYKYGKLSKLAETLYDTTKVSFTYDSTAGM 2029
QY 2041 LKTINLQNGFTCTIRYQIGPLIDRQIFRFTTEEGMVNARFDYNDNSFRVTSMQAVINE 2100
Db 2030 LKTINLQNGFTCTIRYQIGPLIDRQIFRFTTEEGMVNARFDYNDNSFRVTSMQAVINE 2089
QY 2101 TPLPIDLYRVDVSGKTEQFGKFGVYIYDINQIITTAVMTHTKHPDAYGRMKEVOYEIIFR 2160
Db 2090 TPLPIDLYRVDVSGKTEQFGKFGVYIYDINQIITTAVMTHTKHPDAYGRMKEVOYEIIFR 2149
QY 2161 SLMYMTVQYDNNMGRVVKXELKVGYPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLN 2220
Db 2150 SLMYMTVQYDNNMGRVVKXELKVGYPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLN 2209
QY 2221 GNLHLLSPGNSARLTPLRYDIRITRLGDVQYKMDDEDGFLRQGGDIIFEYNSAGLLIIXA 2280
Db 2210 GNLHLLSPGNSARLTPLRYDIRITRLGDVQYKMDDEDGFLRQGGDIIFEYNSAGLLIIXA 2269
QY 2281 YNRAGSWSYRYRVDGLGRRVSSKSHHLLQRFYADLTNPTKTVTHLYNHSSEITSLYYD 2340
Db 2270 YNRAGSWSYRYRVDGLGRRVSSKSHHLLQRFYADLTNPTKTVTHLYNHSSEITSLYYD 2329
QY 2341 LQGHLPAMELSSGDEFYIACDNIGTFLAVFSGTGLMIKQILYATAYGEIYMDTNPNFQI11 2400
Db 2330 LQGHLPAMELSSGDEFYIACDNIGTFLAVFSGTGLMIKQILYATAYGEIYMDTNPNFQI11 2389
QY 2401 GYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKLHSSSNVMPFNLYMFKNNPISN 2460
Db 2390 GYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKLHSSSNVMPFNLYMFKNNPISN 2449
QY 2461 SODIKCFMTDVNSMLTFFGQLHNVI PGYKPKDMDAMEPSYELIHTQMKTOEWDNSKSL 2520
Db 2450 SODIKCFMTDVNSMLTFFGQLHNVI PGYKPKDMDAMEPSYELIHTQMKTOEWDNSKSL 2509
QY 2521 GVQCEVQKQLKAFVTLERFDQLYGSITTSQQAPKTKKFASSGSVFGKGVKFKALDGRVT 2580
Db 2510 GVQCEVQKQLKAFVTLERFDQLYGSITTSQQAPKTKKFASSGSVFGKGVKFKALDGRVT 2569
QY 2581 TDIISVANEDGRVAAILNHAHYLENLHFTIDGVDTHYFVKPSPSGDLAILGLSGRRT 2640
Db 2570 TDIISVANEDGRVAAILNHAHYLENLHFTIDGVDTHYFVKPSPSGDLAILGLSGRRT 2629
QY 2641 LENGVNVTYSQINTVLNGRRVTDIQLQYCALCLNTRVGTTLDESKARVLELARQAVR 2700
Db 2630 LENGVNVTYSQINTVLNGRRVTDIQLQYCALCLNTRVGTTLDESKARVLELARQAVR 2689
QY 2701 QAWAREOQRLREGEGLRAWTEGEKQOVLSTGRVQYDGFVIVSVEQYPLSDSANNIHF 2760
Db 2690 QAWAREOQRLREGEGLRAWTEGEKQOVLSTGRVQYDGFVIVSVEQYPLSDSANNIHF 2749
QY 2761 MRQSEMGR 2769
Db 2750 MRQSEMGR 2758

RESULT 4
ADF74842
ID ADF74842 standard; protein; 2775 AA.
XX AC ADF74842;
XX DT 26-FEB-2004 (first entry)
XX DE Murine NOVX protein to treat human pathological conditions (SeqID 56).
XX KW mouse; murine; NOVX; metabolic disorder; diabetes; anorexia; cancer;
KW cardiovascular; infectious; neurodegenerative; immune;
KW haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic;
KW antiinflammatory; neuroprotective; antilipaeamic; anabolic; cardiant;
KW neurogenesis; wound healing; angiogenesis; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic.
XX OS Mus musculus.
XX PN WO2003076578-A2.
XX PD 18-SEP-2003.
XX PF 06-MAR-2003; 2003WO-US006794.
XX PR 06-MAR-2002; 2002US-0361974P.
PR 08-MAR-2002; 2002US-00093463.
PR 08-MAR-2002; 2002WO-US007288.
PR 15-MAR-2002; 2002US-0365034P.
PR 19-MAR-2002; 2002US-0365477P.
PR 20-MAR-2002; 2002US-0365884P.
PR 20-MAR-2002; 2002US-0365984P.
PR 20-MAR-2002; 2002US-0365985P.
PR 22-MAR-2002; 2002US-0365928P.
PR 12-APR-2002; 2002US-0372018P.
PR 12-APR-2002; 2002US-0372022P.
PR 12-JUN-2002; 2002US-0374682P.
PR 12-JUN-2002; 2002US-0388096P.
PR 14-JUN-2002; 2002US-0389143P.
PR 26-JUN-2002; 2002US-0391779P.
PR 15-AUG-2002; 2002US-0403743P.
PR 13-SEP-2002; 2002US-0410755P.
PR 23-SEP-2002; 2002US-0412957P.
PR 22-OCT-2002; 2002US-0420382P.
PR 05-MAR-2003; 2003US-00420382.
XX
XX (CURA-) CURAGEN CORP.
XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chaudhuri A;
PI Colman SD, Edinger SR, Ettenberg S, Gangolli EA, Gerlach VL;
PI Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malyankar UM;
PI Mezes PS, Miller CE, Millet I, Padigaru M, Patturajan M, Peyman J;
PI Qian X, Rastelli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;
PI Sukumaran S, Vernet CAM, Voss EZ, Zhong M;
XX WPI: 2003-697890/66.
DR N-PSDB; ADF74841.
XX
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
PS Claim 1; SEQ ID NO 56; 282pp; English.
XX
CC This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their

CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The polypeptides, nucleic acid molecules and antibodies are useful in the
 CC manufacture of a medicament for treating metabolic disorders, diabetes,
 CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune
 CC and haematopoietic diseases as well as various dyslipidaemias.

CC Accordingly, these molecules have many activities including anorectic,
 CC virucide, nootropic, antiinflammatory, neuroprotective, antilipemic,
 CC anabolic and cardiatic. Furthermore, they are useful in screening assays
 CC to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a murine NOVX protein of the
 CC invention.

XX Sequence 2775 AA;

Query Match 98.1%; Score 14610; DB 7; Length 2775;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 2743; Conservative 2; Mismatches 6; Indels 42; Gaps 12;

QY 1 MDVKERKPYRSLTRRRDAERRYTSASDSEEGKAPQKYSVSSETLKAYDQDARLAYGSRV 60
 DB 1 MDVKERKPYRSLTRRRDAERRYTSASDSEEGKAPQKYSVSSETLKAYDQDARLAYGSRV 60
 QY 61 KDIVPQEAEEFCRTGANFTLRELGLLEEVTPPHGTLTYRTDIDGLPQCGYSGAGSDADMEAD 120
 DB 61 KDIVPQEAEEFCRTGANFTLRELGLLEEVTPPHGTLTYRTDIDGLPHCGYSGAGSDADMEAD 120
 QY 121 TVLSPEHPVRLNGRSTRGRSSCLSRANSNLTLDTEHENTETDHPGLQNHARLRTPP 180
 DB 121 TVLSPEHPVRLNGRSTRGRSSCLSRANSNLTLDTEHENTETDHPGLQNHARLRTPP 180
 QY 181 PPLSHAHTPNQHAASINSLNKGNFTPRSNPSAPTDHSLGSEPPAGCAQAPAAQENWL 240
 DB 181 PPLSHAHTPNQHAASINSLNKGNFTPRSNPSAPTDHSLGSEPPAGCAQAPAAQENWL 240
 QY 241 LNSNIPLLETRNLKQPFGLTLQDNLIEMDILGASRHDGAYSDDHFLFKPGGTSPLFCTTS 300
 DB 241 LNSNIPLLETRNLKQPFGLTLQDNLIEMDILGASRHDGAYSDDHFLFKPGGTSPLFCTTS 300
 QY 301 PGYPLTSSVTYSPRPRLPRSTFAPPAFLKPKSKYCNWKAALSAIVISATLVILLAYF 360
 DB 301 PGYPLTSSVTYSPRPRLPRSTFAPPAFLKPKSKYCNWKAALSAIVISATLVILLAYF 360
 QY 361 VAMHLFGLNWLHPQMEGQMYEITETASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGK 420
 DB 361 VAMHLFGLNWLHPQMEGQMYEITETASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGK 420
 QY 421 PSSFTPEASFDISGIDVGRASQKIPPGTFRSQVFDIDHPVHLKFNVSGLKAALVGIG 480
 DB 421 PSSFTPEASFDISGIDVGRASQKIPPGTFRSQVFDIDHPVHLKFNVSGLKAALVGIG 480
 QY 481 RKGLPPSHQTFDFVELLDGRLLTQEAASLSEGTQRSGTVPBSSHETGFTQYLDSGIWH 540
 DB 481 RKGLPPSHQTFDFVELLDGRLLTQEAASLSEGTQRSGTVPBSSHETGFTQYLDSGIWH 540
 QY 541 LAFYNDGKSEVVSFLP--ESVDNCPNCGYNGDCISGTCFLGLFGLPGDCCGRASCPVL 600
 DB 541 LAFYNDGKSEVVSFLP--ESVDNCPNCGYNGDCISGTCFLGLFGLPGDCCGRASCPVL 598
 QY 601 CSGNQYKMGKRLCHSGWKGAECDPVNTQCTIDVACSNHGTICITGTCINPGYKGESCEEV 660
 DB 599 CSGNQYKMGKRLCHSGWKGAECDPVNTQCTIDVACSNHGTICITGTCINPGYKGESCEEV 657
 QY 661 DCMDFTCISGRGVCVRGECHCFVWGNTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWT 720
 DB 658 DCMDFTCISGRGVCVRGECHCFVWGNTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWT 717
 QY 721 GHDCSIEICADCGHGVCGGTCTCEDGMMGAACDQACRACHPRCAEHGTCRDGKCECSPG 780
 DB 718 GHDCSIEICADCGHGVCGGTCTCEDGMMGAACDQACRACHPRCAEHGTCRDGKCECSPG 777
 QY 781 WNGEHCTI--AHYLDVRVVK--EGCPGLCNGNGRCTLDLNGHWCVCQLGWRGAGCDTSMET 836

DB 778 WNGEHCTISLAHYLDVRVVKLSEGCPLCNGNGRCTLDLNGHWCVCQLGWRGAGCDTSMET 837
 QY 837 ACSDKONDGDGLVDCMDPCCQLPCLCHINPLCLGSPNPLDIIQETQVPVSSQQLHSHFYD 896
 DB 838 ACSDKONDGDGLVDCMDPCCQLPCLCHINPLCLGSPNPLDIIQETQVPVSSQQLHSHFYD 897
 QY 897 RIKFLVGRDSTHIIPGENPFDGGHACVIRQVMTSDGTPLVGVNISFVNNPLFOYTTISRQ 956
 DB 898 RIKFLVGRDSTHIIPGENPFDGGHACVIRQVMTSDGTPLVGVNISFVNNPLFOYTTISRQ 957
 QY 957 DGSFDLVNCGISILILFERAPFTTQBHTLWLPDRFFVMTETIMRHEENEIPSCDLSNF 1016
 DB 958 DGSFDLVNCGISILILFERAPFTTQBHTLWLPDRFFVMTETIMRHEENEIPSCDLSNF 1017
 QY 1017 ARPNVVSPLTSFASSCAEKGPVPEIOALQBEISISCKMRLSYLSRTPGYKSVLR 1076
 DB 1018 ARPNVVSPLTSFASSCAEKGPVPEIOALQBEISISCKMRLSYLSRTPGYKSVLR 1077
 QY 1077 ISLTHPTIPNLKMHLMVAVEGRLFRKWFAPPAADLSYYEYFIWDKTDVYNQVFGLSAFV 1136
 DB 1078 ISLTHPTIPNLKMHLMVAVEGRLFRKWFAPPAADLSYYEYFIWDKTDVYNQVFGLSAFV 1137
 QY 1137 SVGYEYESCDLILWEKRTTVLQGYEIDASKLGSWLDKXHALNIQS-GILHKGNGENQF 1195
 DB 1138 SVGYEYESCDLILWEKRTTVLQGYEIDASKLGSWLDKXHALNIQSGGILHKGNGENQF 1197
 QY 1196 VSQPPVIGIMNGRRRSISCPSCNGLADGNKLLAPVALTCSDGSLYVDFNYIRRI 1255
 DB 1198 VSQPPVIGIMNGRRRSISCPSCNGLADGNKLLAPVALTCSDGSLYVDFNYIRRI 1257
 QY 1256 PSGNVTNILEL--RNKDFRHSHPAHKYLATDPMSCAVFLSDSNRRRPFKISTVVVKD 1313
 DB 1258 PSGNVTNILELRNKKDFRHSHPAHKYLATDPMSCAVFLSDSNRRRPFKISTVVVKD 1317
 QY 1314 LVKNSEVAGTGQCLPFDDTRCGDGGKATEALTNP--GTTVDKFGLIYFVDGTMR 1370
 DB 1318 LVKNSEVAGTGQCLPFDDTRCGDGGKATEALTNPGRPPGTVKDFGLIYFVDGTMR 1377
 QY 1371 RIDQNGIISTLLGSNDLTNSARPLSCDSVMDISQV--LEWPTDLAINPMDNSLYVLDNN 1427
 DB 1378 RIDQNGIISTLLGSNDLTNSARPLSCDSVMDISQVQVHLEWPTDLAINPMDNSLYVLDNN 1437
 QY 1428 VLIQISENHQVRIVAGRPMHCVPGIDHFLLSKVAIHTLESATALAVSHNGVLYIAETD 1487
 DB 1438 VLIQISENHQVRIVAGRPMHCVPGIDHFLLSKVAIHTLESATALAVSHNGVLYIAETD 1497
 QY 1488 EKKINRIQVTTSGEISLVAGAPSGCDCKNDANCDCFSGDDGYAKDAKLTNPSSLAVCAD 1547
 DB 1498 EKKINRIQVTTSGEISLVAGAPSGCDCKNDANCDCFSGDDGYAKDAKLTNPSSLAVCAD 1557
 QY 1548 GELYVADLGNIRIRFIRKNKPLNTONMYELSSPIDOEYLDPTTGKHYTQSLPTGDYL 1607
 DB 1558 GELYVADLGNIRIRFIRKNKPLNTONMYELSSPIDOEYLDPTTGKHYTQSLPTGDYL 1617
 QY 1608 YNFTYTGDDGITLITDNGNMVNRDSTGMPMLWLVDPGVYVWVTMGTSNALKSVTTQG 1667
 DB 1618 YNFTYTGDDGITLITDNGNMVNRDSTGMPMLWLVDPGVYVWVTMGTSNALKSVTTQG 1677
 QY 1668 HELAMTYHNGSGLLTKSNENGTTFYBYDSFGRLTNVTFTPTQVSSFRSDTSSVHVQ 1727
 DB 1678 HELAMTYHNGSGLLTKSNENGTTFYBYDSFGRLTNVTFTPTQVSSFRSDTSSVHVQ 1737
 QY 1728 VETSSKDDVTITNLSASGAFY----DQVRNSYIAGDGLSRLLLANGMEVALQTEPHLL 1787
 DB 1738 VETSSKDDVTITNLSASGAFY----DQVRNSYIAGDGLSRLLLANGMEVALQTEPHLL 1793
 QY 1788 AGTVNPTVGRKNVTLPIDNGLNLVEWRQKEARGQVTVFGRRLR---VHNRNLLSLDFD 1844
 DB 1794 AGTVNPTVGRKNVTLPIDNGLNLVEWRQKEARGQVTVFGRRLRVLQVHNRNLLSLDFD 1853
 QY 1845 RVTRTEKIYDDHRKFTLRILYDQAGPSLWSRSSRLNGVNTVYSPGCIYTAGTQRGIMSR 1904

Db 1854 RVRTTEKIYDDHRKFTLRLILYDQAGRPSLWSPSSRLNGVNVTVSPGYIAGIQRIMSER 1913
Qy 1905 MEYDQAGRTSRIFADGKTWSYTYLEKSMVLLLSHQRYIFERDKNDRLSSVTPMPNVARQ 1964
Db 1914 MEYDQAGRTSRIFADGKTWSYTYLEKAGV-----EFDKNDRLSSVTPMPNVARQ 1962
Qy 1965 TLETIRSVGYRNIYQPEGNASVIOQFTBDGHLHHTFYLGTGRRVYIKYKLSKLAETL 2024
Db 1963 TLETIRSVGYRNIYQPEGNASVIOQFTBDGHLHHTFYLGTGRRVYIKYKLSKLAETL 2022
Qy 2025 YDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTBEGMVNARPDYN 2084
Db 2023 YDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTBEGMVNARPDYN 2082
Qy 2085 YDNSFRVTSQAVINETPLIDLYRYDDVSGKTEQFGKGVYIYDNIQIITTTAVMTHTKH 2144
Db 2083 YDNSFRVTSQAVINETPLIDLYRYDDVSGKTEQFGKGVYIYDNIQIITTTAVMTHTKH 2142
Qy 2145 FDAYGRMKEVOYEIIFRSLMTWMTVQYDNMGRVVKELKVGYPYANTTRYSEYEDADGQLOQT 2204
Db 2143 FDAYGRMKEVOYEIIFRSLMTWMTVQYDNMGRVVKELKVGYPYANTTRYSEYEDADGQLOQT 2202
Qy 2205 VSINDKPLMRYSDYDLNGLHLLSPGNSARLTPLRYDIRDITRLGDVQYKQDSDGFLRQR 2264
Db 2203 VSINDKPLMRYSDYDLNGLHLLSPGNSARLTPLRYDIRDITRLGDVQYKQDSDGFLRQR 2262
Qy 2265 GGDIFEYNSAGLLIKAYNRAGSVRYRYDGLGRYSSKSSHHLQFFYADLTNPTKVT 2324
Db 2263 GGDIFEYNSAGLLIKAYNRAGSVRYRYDGLGRYSSKSSHHLQFFYADLTNPTKVT 2322
Qy 2325 HLYNHSSEITSLYDYLQGHFLFAMELSSGDEFIACDNIGTPLAVFSGTGLMIKILLYTA 2384
Db 2323 HLYNHSSEITSLYDYLQGHFLFAMELSSGDEFIACDNIGTPLAVFSGTGLMIKILLYTA 2382
Qy 2385 YGEIYMDTNPFOIIGYHGLYDPLTKLVHMGRDDYDLVLAGRWTPSDHELWKHLSSNV 2444
Db 2383 YGEIYMDTNPFOIIGYHGLYDPLTKLVHMGRDDYDLVLAGRWTPSDHELWKHLSSNV 2442
Qy 2445 MPFNLYMFKNNPISNSQDIKCFMTDVNSWLLTFGQLHNVIIPYKPKDMDAMEPSVELI 2504
Db 2443 MPFNLYMFKNNPISNSQDIKCFMTDVNSWLLTFGQLHNVIIPYKPKDMDAMEPSVELI 2502
Qy 2505 HTQMKTEWNSK-----SILGVQCEVQKOLKAFVTLERFDQLYGSTITSQQAPKT 2556
Db 2503 HTQMKTEWNSKVIIPAGQCQSILGVQCEVQKOLKAFVTLERFDQLYGSTITSQQAPKT 2562
Qy 2557 KKFASSGSVFGKGVKFKALDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVD 2616
Db 2563 KKFASSGSVFGKGVKFKALDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVD 2622
Qy 2617 HYFVKPSPSGDLAILGLSGRRTLNGVNVTVSQINTVLNGRTRRYTDILOYGALCLN 2676
Db 2623 HYFVKPSPSGDLAILGLSGRRTLNGVNVTVSQINTVLNGRTRRYTDILOYGALCLN 2682
Qy 2677 TRVGTTLDEKARVLELARGARVQAWARQORLEGEGLRAWTEGEKQOVLSTGRVQG 2736
Db 2683 TRVGTTLDEKARVLELARGARVQAWARQORLEGEGLRAWTEGEKQOVLSTGRVQG 2742
Qy 2737 YDGFVVISVQYPELSDSANNIHFMRQSEMGRR 2769
Db 2743 YDGFVVISVQYPELSDSANNIHFMRQSEMGRR 2775

RESULT 5
ID ABB98401
ABB98401 standard; protein; 2794 AA.

XX ABB98401;

XX 21-OCT-2002 (first entry)

XX Human NOV1, a TEN-M4 like protein.

Human; NOV1; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive;
Antiatherogenic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic;
Antibacterial; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic;
Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant;
Gene Therapy; NOV; cancer; heart disease; inflammation;
autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity;
asthma; Iga nephropathy; cirrhosis; arthritis; Alzheimer's disease;
infection; stroke; muscular dystrophy; epilepsy; wasting disorder;
TEN-M4 like protein.
XX Homo sapiens.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 379
ET /note= "Encoded by ATGACGGATT"
XX WO200255704-A2.
XX 18-JUL-2002.
XX 09-JAN-2002; 2002WO-US000554.
XX PF
XX 09-JAN-2001; 2001US-0260417P.
XX PR 10-JAN-2001; 2001US-0260831P.
XX PR 28-FEB-2001; 2001US-0272338P.
XX PR 09-MAR-2001; 2001US-0274876P.
XX PR 18-APR-2001; 2001US-0284704P.
XX (CURA-) CURAGEN CORP.
XX Padigar M, Li L, Zerhusen BD, Casman SJ, Shenoy S, Spytek KA;
PI Zhong M, Gangoli EA, Burgess CE, Patturajan M, Vernet CM;
PI Taylor S, Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse WM;
PI Alsebrook JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman K;
PI Macdougall J, Malyankar U, Millet I, Peyman J, Smithson G;
PI Gunther E, Stone DJ;
XX WPI; 2002-590674/63.
XX N-PSDB; ABN85378.
XX NOVX polypeptides and encoding polynucleotides, useful for preventing or
PT treating NOVX-associated disorders e.g. cancer, inflammation, or
PT Alzheimer's disease, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX Claim 1; Page 10-11; 358pp; English.
XX The present sequence is the protein sequence for a NOV protein. The NOV
CC proteins and coding sequences are useful for treating or preventing NOV-
CC associated disorders or in the manufacture of a medicament for treating
CC the disorders, such as cancer, heart disease, inflammation, autoimmune
CC disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma,
CC Iga nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections
CC (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy,
CC and other wasting disorders associated with chronic diseases. NOV1 is a
CC TEN-M4 like protein and the NOV1 gene is localised to chromosome 11
XX Sequence 2794 AA;
SQ
Query Match 96.8%; Score 14406.5; DB 5; Length 2794;
Best Local Similarity 96.7%; Pred. NO. 0;
Matches 2704; Conservative 21; Mismatches 41; Indels 31; Gaps 11;
Qy 1 MDVKERKPYRSLTRRDAERRYTSSADSEEGKAPQKSYSSSETLKAYDODARLAYGSRV 60
Db 1 MDVKERKPYRSLTRRDAERRYTSSADSEEGKAPQKSYSSSETLKAYDODARLAYGSRV 60
Qy 61 KDIVPQAEFEFCRTGANFTLRELGLSEVTPPHGTLVYRTDGLPQCYSMGAGSDADMEAD 120
Db 61 KDIVPQAEFEFCRTGANFTLRELGLSEVTPPHGTLVYRTDGLPQCYSMGAGSDADMEAD 120
Qy 121 TVLSPEHPVRLMGRSTRSGRSCCLSRANSNLFLTDEHENTTDPHGLQNHARLTTPP 180
Db 121 TVLSPEHPVRLMGRSTRSGRSCCLSRANSNLFLTDEHENTTDPHGLQNHARLTTPP 180

Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHENTETDHPGGLQNHARLRTPP 180

Qy 181 PPLSHAHTPNQHAAASINSLNRGNFTPRSNPSPAPTDHLSLSEGPAPGAGQOEPAHAQENWL 240

Db 181 PPLSHAHTPNQHAAASINSLNRGNFTPRSNPSPAPTDHLSLSEGPAPGAGQOEPAHAQENWL 240

Qy 241 LNSNIPLETENLKGQPLGTLQDNLIJEMDILGASRHDGAYSOGHFLFKPGGTSPLFCFCTS 300

Db 241 LNSNIPLETENLKGQPLGTLQDNLIJEMDILGASRHDGAYSOGHFLFKPGGTSPLFCFCTS 300

Qy 301 PGYPLTSSSTVYSPPPRPLPRSTFARPAFNLKPKPSKYCNWKCAALSAIVISATLVILLAYF 360

Db 301 PGYPLTSSSTVYSPPPRPLPRSTFARPAFNLKPKPSKYCNWKCAALSAIVISATLVILLAYF 360

Qy 361 VAMHLGELNHLQPMEGQMYETEDTASSWPVPTDVSLYPSGGTGLTPDRKGKGTTEGK 420

Db 361 VAMHLGELNHLQPMEGQMYETEDTASSWPVPTDVSLYPSGGTGLTPDRKGKGTTEGK 420

Qy 421 PSSFFPEDSFIDSGEIDVGRRASOKIPPGTFRWSOVFIIDHPVHLKFNYSLGKAAALVGIVG 480

Db 421 PSSFFPEASFIDSGEIDVGRRASOKIPPGTFRWSOVFIIDHPVHLKFNYSLGKAAALVGIVG 480

Qy 481 RKGLPPSHQTQFQVVELLDGRRLLTOEARSLEGTQRSRGTVPPSSHETGFIQYLDSGIWH 540

Db 481 RKGLPPSHQTQFQVVELLDGRRLLTOEARSLEGTQRSRGTVPPSSHETGFIQYLDSGIWH 540

Qy 541 LAFYNDGKSEVVSFLTTLTAIESVDNCPSCNYGNGDCISGTCFGLGFLGPDGCRASCPVL 600

Db 541 LAFYNDGKSEVVSFLTTLTAIESVDNCPSCNYGNGDCISGTCFGLGFLGPDGCRASCPVL 600

Qy 601 CSNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCTGTGTCINPGYKGBSCEB 660

Db 598 CSNGQYSGKRCLCFSGWKGTCDVPTTQCIDPQCGRGICIMGSCACNSGYKGBSCEBA 657

Qy 661 DCMPTCSRGVCRGECHCFVWGNTNCTETPRATCLDQCSGHGTFLPDPTGLCSDPSMT 720

Db 658 DCIDPGCSNHGCIHGECHCSFGWGSNCEILKTMCPDQCSGHGTYLQESGSCTCDPNWT 717

Qy 721 GHDCSIEICAADGGHGVCGVGTCECDGWMGAACDORACHPRCAEHGTCRDGKECSPG 780

Db 718 GFDSCNEICSVDSGSHGVCMGTCCEEGWTGPACNQACHPRCAEHGTCRDGKECSPG 777

Qy 781 WNGEHCTI--AHYLDRVVK--BEGPCLCNNGRCITLDLNGHVCVQLGWRGAGCDTSMET 836

Db 778 WNGEHCTISLAHYLDRVVKLSGCPGLCNNGRCITLDLNGHVCVQLGWRGAGCDTSMET 837

Qy 837 ACGDSKONDGDGLVDCMPDCCLOQLCHINPLCLGSPNPLDIIQBTQVPVVSQOQLHSFYD 896

Db 838 ACGDSKONDGDGLVDCMPDCCLOQLCHINPLCLGSPNPLDIIQBTQVPVVSQOQLHSFYD 897

Qy 897 RIKFLVGRDSTHIIPEGNPFDGGHACVIRGOVMTSDGTPLVGVNISFVNNPLFGVTISRQ 956

Db 898 RIKFLVGRDSTHIIPEGNPFDGGHACVIRGOVMTSDGTPLVGVNISFVNNPLFGVTISRQ 957

Qy 957 DGSFOLVNGGSIILTERAPFIIQEHNTLMLPMDRFPVMTIIMRHEENBIPSCDLSNF 1016

Db 958 DGSFOLVNGGSIILTERAPFIIQEHNTLMLPMDRFPVMTIIMRHEENBIPSCDLSNF 1017

Qy 1017 ARPNPVSPSPUTSFASSCAEKGPVPEIQALQEBEISISGCKMRLSYLSSTPGYKSVLR 1076

Db 1018 ARPNPVSPSPUTSFASSCAEKGPVPEIQALQEBEISISGCKMRLSYLSSTPGYKSVLR 1077

Qy 1077 ISLTHPTIPFNLKMLVHLVAVVEGRLFKRWFAAAPDLSYFFIWDKTDVYNQVFLGSEAFV 1136

Db 1078 ISLTHPTIPFNLKMLVHLVAVVEGRLFKRWFAAAPDLSYFFIWDKTDVYNQVFLGSEAFV 1137

Qy 1137 SVGYEYESCPDLIILWEKTTVLQGYEIDASKLGGWSLDKHALNIQS--GILHKGNGENQF 1195

Db 1138 SVGYEYESCPDLIILWEKTTVLQGYEIDASKLGGWSLDKHALNIQS--GILHKGNGENQF 1197

Qy 1196 VSQQPPVLGSIWNGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFFNYIRRIIP 1255

Db 1198 VSQQPPVLGSIWNGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFFNYIRRIIP 1257

Qy 1256 PSGNVNTILEL--RNKOFRSHSHSPAHHYYLATDPMGAVFLSDSNSRRVFKIKSTVVVKD 1313

Db 1258 PSGNVNTILELRVNRKDFRSHSHSPAHHYYLATDPMGAVFLSDSNSRRVFKIKSTVVVKD 1317

Qy 1314 LVKNSVAVAGTGDQCLPDDTRCGDGGKATEATLTNPR--GITVDKEGLIYFVDGTMR 1370

Db 1318 LVKNSVAVAGTGDQCLPDDTRCGDGGKATEATLTNPRPGGITVDKFGLIYFVDGTMR 1377

Qy 1371 RIDQNGIISTLLSGNDLTARSPLSCDSVMDISQVR---LEWPTDLAINPMDNSLYVLDNN 1427

Db 1378 RIDQNGIISTLLSGNDLTARSPLSCDSVMDISQVRQVHLEWPTDLAINPMDNSLYVLDNN 1437

Qy 1428 VVLOISENHQVRIIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETD 1487

Db 1438 VVLOISENHQVRIIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETD 1497

Qy 1488 EKKINRIQVTTSGEISILVAGAPSGCDKNDANCDFSGDDGYAKADAKLANTPSSLAVCAD 1547

Db 1498 EKKINRIQVTTSGEISILVAGAPSGCDKNDANCDFSGDDGYAKADAKLANTPSSLAVCAD 1557

Qy 1548 GELYVADLGNIRIRFIRKNKPFPLNTQNMYSLSPIQELYLFDTTGKHLTYQSLPTGDYL 1607

Db 1558 GELYVADLGNIRIRFIRKNKPFPLNTQNMYSLSPIQELYLFDTTGKHLTYQSLPTGDYL 1617

Qy 1608 YNFTYTGDDITLITDNNGMNVNRRDSTGMPLWLVPDQGVVWVTMTNSALKSVTTQG 1667

Db 1618 YNFTYTGDDITLITDNNGMNVNRRDSTGMPLWLVPDQGVVWVTMTNSALKSVTTQG 1677

Qy 1668 HELAMTYHNGSLGATKSNENGTTFEYDSFGRLTNVTFPTGOVSSFRSDTSSVHVQ 1727

Db 1678 HELAMTYHNGSLGATKSNENGTTFEYDSFGRLTNVTFPTGOVSSFRSDTSSVHVQ 1737

Qy 1728 VETSSKDDVTITNLSASGAFYTLLOQVNRNSYIIGADGSLRLLLANGMEVALQTEPHLL 1787

Db 1738 VETSSKDDVTITNLSASGAFYTLLOQVNRNSYIIGADGSLRLLLANGMEVALQTEPHLL 1797

Qy 1788 AGTVNPTVGKENVTLPIDNGLNLVWRQKEQARGQVTVFGRRLR---VHNRNLLSLD 1844

Db 1798 AGTVNPTVGKENVTLPIDNGLNLVWRQKEQARGQVTVFGRRLRVLQVHNRNLLSLD 1857

Qy 1845 RVTRTEKIYDHRKFTLRILYDQAGPSPSLWSPSSRLNGVNVTVSPGGYIAGIQRMISER 1904

Db 1858 RVTRTEKIYDHRKFTLRILYDQAGPSPSLWSPSSRLNGVNVTVSPGGYIAGIQRMISER 1917

Qy 1905 MEYDQAGRITSRIPADGKTWSYTYLEK---SMVLLLHSSQRYIFBFDKNDRLSSVTMPN 1960

Db 1918 MEYDQAGRITSRIPADGKTWSYTYLEKAGVQSMVLLLHSSQRYIFBFDKNDRLSSVTMPN 1977

Qy 1961 VARQTLTETIRSVGYRNIVOPPEGNASVIOQDFTEDGHLHHTFVLGTGRRVIYKYGKLSKL 2020

Db 1978 VARQTLTETIRSVGYRNIVOPPEGNASVIOQDFTEDGHLHHTFVLGTGRRVIYKYGKLSKL 2037

Qy 2021 AETLYDTTKVSFTYDETAGMLKTIINLQNEGFTCTIRYQIGPLIDRQIFRFTTEEGMVNAR 2080

Db 2038 AETLYDTTKVSFTYDETAGMLKTIINLQNEGFTCTIRYQIGPLIDRQIFRFTTEEGMVNAR 2097

Qy 2081 FDYNYDNSFRVTSQMAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINOIITTAVMT 2140

Db 2098 FDYNYDNSFRVTSQMAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINOIITTAVMT 2157

Qy 2141 HTKHFDAYGRMKVEQVEIFRSLMYMWTVOYDNMGRVVKELKVPVANTTRYSEYDADG 2200

Db 2158 HTKHFDAYGRMKVEQVEIFRSLMYMWTVOYDNMGRVVKELKVPVANTTRYSEYDADG 2217

Qy 2201 QLOTVSINDKPLWRSYDLNGLNHLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEGF 2260

Db 2218 QLOTVSINDKPLWRSYDLNGLNHLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEGF 2277

Qy 2261 LRORGGDIPEYNSAGLLIKAYNRRAGSWSVRYRYDGLGRVSSKSSSHHLOPPYADLTNP 2320

Db 2278 LRORGGDIPEYNSAGLLIKAYNRRAGSWSVRYRYDGLGRVSSKSSSHHLOPPYADLTNP 2337

QY 2321 TKVTHLYNHSSTSLTYDLOQHLFAMELSSGDEFYIACDNIQTPLAVFSGLMIKQI 2380
DB 2338 TKVTHLYNHSSTSLTYDLOQHLFAMELSSGDEFYIACDNIQTPLAVFSGLMIKQI 2397
QY 2381 LYTAYGEIYMDTNPFIIGYHGGYDPLTKLVHMGRRDYDVLGRWTSPOHMLWKHLS 2440
DB 2398 LYTAYGEIYMDTNPFIIGYHGGYDPLTKLVHMGRRDYDVLGRWTSPOHMLWKHLS 2457
QY 2441 SSVNMPFNLYMKNPNINSQDIKCFMTDVNSWLLTFGQLHNVI PGYPKPKMDAMEPS 2500
DB 2458 SSVNMPFNLYMKNPNINSQDIKCFMTDVNSWLLTFGQLHNVI PGYPKPKMDAMEPS 2517
QY 2501 YELIHTQMTQEWNSK-----SILGVQCEVQKQKAFVTLERFDQLYGSSTITSQQ 2552
DB 2518 YELIHTQMTQEWNSKVI PAQCQSILGVQCEVQKQKAFVTLERFDQLYGSSTITSQQ 2577
QY 2553 APKTKFPASSGVFGKVPALKDGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTID 2612
DB 2578 APKTKFPASSGVFGKVPALKDGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTID 2637
QY 2613 GVDTHYFVKPSPSEGDLAILGLSGRRITLNGVYNTVTSQINTVLNGRTRYTDIQLQYGA 2672
DB 2638 GVDTHYFVKPSPSEGDLAILGLSGRRITLNGVYNTVTSQINTVLNGRTRYTDIQLQYGA 2697
QY 2673 LCINTRYGTTLDEKARVLELQRAVROAWAREQORLREGEGLRAWTEGEKQOVLSTG 2732
DB 2698 LCINTRYGTTLDEKARVLELQRAVROAWAREQORLREGEGLRAWTEGEKQOVLSTG 2757
QY 2733 RVQGYDGFVVISVEQPELSDSANNIHFMRQSEMGR 2769
DB 2758 RVQGYDGFVVISVEQPELSDSANNIHFMRQSEMGR 2794
RESULT 6
ABP53587
ID ABP53587 standard; protein; 2721 AA.
AC ABP53587;
DT 17-DEC-2002 (first entry)
DE Human NOV15b protein SEQ ID NO:38.
XX Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular;
KW cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide;
KW antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide;
KW antianaemic; antibacterial; protozoacide; antihelminthic; gene therapy;
KW cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy;
KW stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy;
KW Pick's disease; vesicular transport disease; cystic fibrosis; goitre;
KW diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine;
KW ulcerative colitis; Gastric disorder; duodenal disorder; infection;
KW autoimmune disease; allergic reaction; autoimmune haemolytic anaemia;
KW rheumatoid arthritis; chromosome 4.
XX Homo sapiens.
OS
XX WO200262999-A2.
PN
XX 15-AUG-2002.
PD
XX 31-DEC-2001; 2001WO-US049976.
PF
XX 29-DEC-2000; 2000US-0258928P.
PR 02-JAN-2001; 2001US-0259415P.
PR 04-JAN-2001; 2001US-0259785P.
PR 20-FEB-2001; 2001US-0259814P.
PR 09-MAR-2001; 2001US-0279863P.
PR 29-MAR-2001; 2001US-0279832P.
PR 29-MAR-2001; 2001US-0279833P.
PR 13-APR-2001; 2001US-0283889P.
PR 18-APR-2001; 2001US-028447P.
PR 25-APR-2001; 2001US-0286683P.

PR 29-MAY-2001; 2001US-0294080P.
PR 16-AUG-2001; 2001US-0312915P.
PR 17-AUG-2001; 2001US-0313325P.
PR 17-SEP-2001; 2001US-0322699P.
PR 26-NOV-2001; 2001US-0333350P.
XX
PA (CURA-) CURAGEN CORP.
XX Spyttek KA, Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;
PI Malvankar U, Shinkens RA, Tchernev VT, Spaderna SK, Gorman L;
PI Kekuda R, Paturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
PI Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
PI Gunther E, Smithson G, Millet I, Macdougall JR;
XX WPI: 2002-732706/79.
DR N-PSDB; ABQ82344.
XX
XX New NOVX polypeptides and polynucleotides useful for treating NOVX-
PT associated disorders, such as cancers, neurological disorders, disorders
PT of vesicular transport, gastrointestinal disorders, and autoimmune
PT diseases.
XX
XX Claim 1; Page 117-118; 44pp; English.
XX
XX The present invention describes novel human proteins designated NOVX,
CC where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective,
CC cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular,
CC antidiabetic, antiinflammatory, antirheumatic, antiarthritic, virucide,
CC immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide,
CC protozoacide and antihelminthic activities, and can be used in gene
CC therapy. The NOVX proteins, nucleotides or antibodies can be used in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease selected from NOVX-associated disorder, such as cancers
CC (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle,
CC ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke,
CC ischaemic cerebrovascular disease, Alzheimer's disease or Pick's
CC disease), disorders of vesicular transport (e.g. cystic fibrosis,
CC diabetes mellitus, Grave's disease, or goitre), gastrointestinal
CC disorders (e.g. ulcerative colitis, or gastric and duodenal disorders),
CC autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic
CC anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic
CC and protozoal infections. The NOVX proteins can be used as immunogens to
CC produce antibodies and as vaccines. The NOVX nucleotide sequences may be
CC used in chromosome mapping, identifying individuals from minute
CC biological samples (tissue typing), and in forensic identification of a
CC biological sample. The present sequence represents human NOV15b, which is
CC located on chromosome 4
XX
XX Sequence 2721 AA;
Query Match 68.7%; Score 10221; DB 5; Length 2721;
Best Local Similarity 67.0%; Pred. No. 0;
Matches 1873; Conservative 362; Mismatches 461; Indels 98; Gaps 20;
QY 1 MDVKERPKYRSLTR-RRDAERRYTSSSADSEEGKAP-QKSYSSSETLKAYDQD-ARLAYG 57
DB 1 MDVKERRYCSLTYSRREKERRYTNSSADNEECRVPTQKSYSSSETLKAFDHDSSRLLYG 60
QY 58 SRVKDITVQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDGLQCQGYMAGSDADM 117
DB 61 NRVKDLVHREADEFTQQGNFTLRQLGVCEPATRRGLAFCAEMGLPHRGYSISAGSDADT 120
QY 118 EADTVLSPHPVPLWGRSTRSGSSCLSSRANSNLTTDTEHEN---TETDHPGGQLNHA 174
DB 121 ENEAVMSPEHAMRLWGRGVKSGKSSCLSSRSNSALTITDTEHENKSDSENEQASVQGS 180
QY 175 RLRTPPPLPSHAHTPNQHAASINSLNRGNFTPRSNPSPAPTDSLSGPPAGCAQ---- 230
DB 181 TLQPLPP--SHKQHSQAHH-PSITSLNRNSLTNRNQSAP-----PAALPAELQTT 229
QY 231 -EPAHAQENWLLNSNIPLETNRNLGKQPFGLTQDNLIEMDILGASHRDGAYSOGHFLFKP 289
DB 230 PESVQLQDSWVLGNSVPLESR-----HFLFKT 256

Db 2397 I-GKDPAPFNLYMFRNNPASKIHVDKDYITDVNSMLVTFGFLHNAIFGFPVPKEDLTE 2455
Qy 2499 PSVELIHTQMTQEWNSKSLGVOCEVOKLAFVTLERFDOLYGSTITSQOAPKTK 2558
Db 2456 PSYELV---KSOQDDIPPIFGVQOQVAKAFUSLQKAEVQ----VSRRRAGAQS 2507
Qy 2559 ---FASGSGVFGKGVKFPALXGRVTDTIISVANEDGRRVAAIINHAHYLENLHFTIDGVD 2615
Db 2508 WLFATVKSJLIGKVMFVSGRVTNVNANEDCIKVAVLNNAFYLENLHFTIEGKD 2567
Qy 2616 THYFVKPGEGLAILGLSGGRTLENGVNVTVSQINTVLNGTRRYRTYDIQLQYCALCL 2675
Db 2568 THYFIKTTTPESDLGTLRLTSGKALENGINVTVSQSTTVVNGTRRFADVENMQFAGAL 2627
Qy 2676 NTRYGTTLDREKARVLELARAQRVRAQWAREQQRLAREGEGRLAWTEGEKQOVLSTGRVQ 2735
Db 2628 HVRYGTMFLDEKARILEQARALARAWAREQQRRVDRGEGEARLWTEGEKQRLLSAGKVQ 2687
Qy 2736 GYDGFVVISVEQYPELSDSANNIHFMRQSBMGR 2769
Db 2688 GYDGYVLSVEQYPELSDSANNIQFLRQSBIGRR 2721

RESULT 7
ADH41969
ID ADH41969 standard; protein; 2721 AA.
XX AC ADH41969;
XX
DT 25-MAR-2004 (first entry)
XX
DE Novel human protein NOV40s.
XX
KW cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
KW antiparkinsonian; antiasthmatic; antinfertility; cardiomyopathy;
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
KW multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.
XX
OS Homo sapiens.
XX
XN WO2003102159-A2.
XX
PD 11-DEC-2003.
XX
XX 04-JUN-2003; 2003WO-US017573.
XX
PR 04-JUN-2002; 2002US-0385490P.
PR 04-JUN-2002; 2002US-0385615P.
PR 04-JUN-2002; 2002US-0385755P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386355P.
PR 06-JUN-2002; 2002US-0386357P.
PR 06-JUN-2002; 2002US-0386447P.
PR 06-JUN-2002; 2002US-0386459P.
PR 06-JUN-2002; 2002US-0386465P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0386701P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0387078P.
PR 07-JUN-2002; 2002US-0387081P.
PR 10-JUN-2002; 2002US-0387083P.
PR 10-JUN-2002; 2002US-0387429P.
PR 10-JUN-2002; 2002US-0387540P.
PR 10-JUN-2002; 2002US-0387866P.
PR 11-JUN-2002; 2002US-0387606P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387659P.
PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 12-JUN-2002; 2002US-0388432P.
PR 12-JUN-2002; 2002US-0388479P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389604P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390144P.
PR 19-JUN-2002; 2002US-0390209P.
PR 25-JUN-2002; 2002US-0391726P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402268P.
PR 12-AUG-2002; 2002US-0402822P.
PR 13-AUG-2002; 2002US-0403458P.
PR 15-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403732P.
PR 26-AUG-2002; 2002US-0406182P.
PR 12-SEP-2002; 2002US-0410085P.
PR 12-SEP-2002; 2002US-0410505P.
PR 23-SEP-2002; 2002US-0412955P.
PR 30-SEP-2002; 2002US-0415195P.
PR 23-OCT-2002; 2002US-0420627P.
PR 23-OCT-2002; 2002US-0420718P.
PR 24-OCT-2002; 2002US-0420852P.
PR 31-OCT-2002; 2002US-0422750P.
PR 01-NOV-2002; 2002US-0423095P.
PR 05-NOV-2002; 2002US-0423748P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
PI Ellerman K, Ethenberg S, Gangolli EA, Gerlach VL, Gorman L;
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;
PI Khrantsov NV, Larochele WJ, Li L, Liang H, Low K, Macdougall JR;
PI MacLachlan T, Malyankar UM, McQueeney K, Mezick AJ, Miller CE;
PI Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L;
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
PI Spytek KA, Stone DJ, Sukumaran S, Szekeeres ES, Vernet CAM, Voss EZ;
PI Wolenc AR, Zhong M, Zhong H;
XX
XX WPI; 2004-053467/05.
DR N-PSDB; ADH41968.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.
XX
PS Claim 2; SEQ ID NO 522; 1503pp; English.
XX
XX The invention relates to 566 new isolated human polypeptides and their
CC encoding genes, sequences that are at least 95% identical to these or
CC sequences comprising one or more conservative substitutions in these. The
CC polypeptide, polynucleotide and antibodies against the polypeptides are
CC useful in diagnosing, treating or preventing NOVX-associated disorders,
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
CC The nucleic acids are further used as hybridization probes, in chromosome
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
CC polypeptides are also useful as vaccines. This sequence represents an
XX example of the polypeptide of the invention.
SQ Sequence 2721 AA;

| | | | | | |
|-----------------------|-----|---|-----------------|--------|--------------|
| Query Match | | 68.7%; | Score 10221; | DB 8; | Length 2721; |
| Best Local Similarity | | 67.0%; | Pred. No. 0; | | |
| Matches 1873; | | Conservative 362; | Mismatches 461; | Indels | Gaps 20 |
| Qy | 1 | MDVKKERYSLTR--RRDAERRYSSADSEKAP-OKSYSSTLAKAYDOD-ARLAYG | 57 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 1 | MDVKERRYSLUTSRREKERYTNSSADNEECRVPTOKSYSSSTLKAFOHDSRLLYG | 60 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 58 | SRVKDIVPQEAEEFCRTGANFTRELGLVEEYTPPHGTLTYRTDIGLPQCQSGMGASDAM | 117 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 61 | NRVKDLVHREADEFTRQGNFTLRQLGVCEPATRGLAFCAEMGLPHRGYSISAGSDADT | 120 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 118 | EADVLSPEHPVRLWGRSTRGRSSCLSPRANSNLTLTDTEHEN---TETHDPGLQNHWA | 174 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 121 | ENAVMSPEHAMRWLGVRGVKGRSCSLSSRSNSALTTLTDTEHKNKSDSENQPASNQGS | 180 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 175 | RLRTPPPLSHAHTPNQHAAASINSLNRGNFTPRSNPSAPTDLHLSLSEPPAGGAQ--- | 230 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 181 | TLQPLPP--SHKHSAQHH-PSITSLNRSNLNRRNQSPAP-----PAALPAELQTT | 229 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 231 | -EPHAQENWLNNINIPIETRNILGKPPLTGLTLQNLIEMDIIGASRHGDAYSVDGHFLPKP | 289 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 230 | PESVLQLODSWLVGSNVPLESR-----HFLEKT | 256 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 290 | G-GTSPLPCTTS PGVPLTSSVTVPPLPRSTFAPAFLNKPKSKYNMKCAALSIAIV | 348 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 257 | GTGTTPLFSTATPGYTMASSGVSPTRPLRPNTLSRSAFKFKSKSKYCSWKCTALCAVG | 316 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 349 | ISATLVILLAYFVAHMLFGLNWHLPQMEGQMYE---ITEDASSWPVPTDVLSYPSGGTG | 405 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 317 | VSVLLAILLSFYIAMHLFGLNWQLQOTENDTFENGKVNSDT-----MPTNTVSLPSG--- | 368 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 406 | LETPDRKGKGTTEGKPSFFBEDSFDISEGIDVGRASOKIIPCGTFWBSOVFIIDHPVHLK | 465 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 369 | -----DNKLGLOGFTQENNITDSEGLEDIGHRAIQEIQPPGLFWBSQJFIDQPQFLK | 417 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 466 | FNVLGKAALVGIYGRKGLPSPHQTFDFVELLDGRRLLTOBARSLEGTPROSRGTVPPSS | 525 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 418 | FNISLQKDALLGVYGRKGLPSSHQTYQDFVELLDGSRLLIARQRSILLETERAGRQARSVSL | 477 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 526 | HETGFIOYLDGSIWHLAFYNDGKSESVVVFUATAIESVDNCPSNYGNGDCISGTCHCFL | 585 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 478 | HEAGFIOYLDGSIWHLAFYNDGKNAEQVSFNITIYESVVECPRNCHGNAGECVSGTCCHF | 537 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 586 | GFLLPDCCGRACPVLCGSGNGYMKGRCLCHSGWGKAECDVPTNOCIDVACSNHGHTCI | 645 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 538 | GFLLPDCSRACPVLCGSGNGYSGKRCLCFSGWKGTECDVFTTQCIDPCOCCRIGICINGS | 597 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 646 | CIGNPYKGBSCEEVDMDPTCSGRGVCVRGECHCFVWGWTNCTETPRATCLDCOSGHGT | 705 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 598 | CACSNGYKGBSCEEADCTDPCSNHNGVICIHGECHSCPWWGSGNSEILLTMCPDQCSGHGT | 657 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 706 | FLPTDGLSCDSPSWTHGDCSIICAADCGHGVCVGGTCRCEDGMWGAACDORACHPCA | 765 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 658 | YLBESGSGCTDPNWTGPDCSWEICSVDCSGHGVCMGGTCRCSEGTGPACNQRAHPCA | 717 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 766 | EHGTCDRKCKCSPGWNGEHCTIAHYLDREV-----KEGPCGLCNGNRCRTLNLNGHC | 819 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 718 | EHGTCKDGKCBSCSQWNNGEHCTIAHYLDKI VKDKIGYKEGCPGLCNSNGRCTLAQNGHC | 777 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 820 | VCQLGWGAGCDTSMETACGSKDNDDGLVDCHMDPCCLOPLCHIINPLCLGSPNPLDII | 879 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 778 | VCOFGWRGAGCDVAMETLCTDSKNEGDELDCMDPCCLOQSSCQNPYCRGLEPDPQII | 837 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 880 | QETQVPVPSQNLHLSFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGOWMTSDGTPLVGV | 939 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 838 | SQSILOSFSQAAKSFYDRIFLIGSDTHVIPGESPFNKSLASVIRGOVLTAQTGTPLIGV | 897 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 940 | NI SPVNPLPGYTTISRODGSFDLVNTNGGISIIILAFERAPFTIOBHTLWLPMDFRFVNETI | 999 | | |
| Dd | | : : : : : : : : : : | | | |
| Qy | 898 | NVSFFHYPEYGYTTITRODGFDFLVANGASLTLVFERSPFTOYHTVMIPNWNVYVMDTL | 957 | | |
| Dd | | : : : : : : : : : : | | | |

Db 2037 AREFYSYDNSFRVTSQGVNETPLPIDLYQFDDISGKVBQFGKFGVYIYDINQIISTAV 2096
Qy 2139 MTHTKHFDAYCRMEKVEQYETFRSLMYMTVOYDNMGVRVVKELKVGYPYANTTYSYEYDA 2198
Db 2097 MTTTKHFDAGRITKEIYEIFRSLMYWITTYQDNMGVRVTKREIKIGPFANNTTKYAYEYDV 2156
Qy 2199 DGLOQTVSINDKPLWRSYDOLNGLHLLSPGNSARLTPLRYDIRITRLGDDVQYKMDSD 2258
Db 2157 DGLOQTYLNEKIMRYNYDNLNGLHLLSPNSARLTPLRYDLRDRITRLGDDVQYRLDSD 2216
Qy 2259 GFLRQRGDITFYNSSAGLLIKAYNRAGSVRYRYDGLGRVRSKSHSHHLOFFVADLT 2318
Db 2217 GFLRQRGTEIFEYSKGLLTRVYSKSGWTVIYRYDGLGRVRSKTSGLQHLOFFVADLT 2276
Qy 2319 NPTKVTYHLNHSSEITSLYDYLQGHLPAMELSSGDEFFYIACDNIGTPLAVRSGTGIMIX 2378
Db 2277 YPTRITHVYHNSSSEITSLYDYLQGHLPAMEISSGDEFFYIASDNTGTPLAVRSGGLMLK 2336
Qy 2379 QILYTAGETYMDTNPNFQIIIGVHGLYDPLTKLVHMGRRDYDVLAGRWTSPDHLELWKH 2438
Db 2337 QIQYTAGETYFDSNDTDFQIVGFHGLYDPLTKLHFGERDYDILAGRWTTPDIEIWK 2396
Qy 2439 LSSSNVMPENLYMFKNNPISNSQDIKCFMTDYNMMLLTGFGQLHNVIPGYKPDMDAME 2498
Db 2397 I-GKDPAPPFLYMFRRNNPASKIHDKYITDYNMMLVTGFLHNAIPGFPVPKFDLTE 2455
Qy 2499 PSYELIHTQMTQEWDSKSIILGVOCEVQKQKAFVTLERFDQLYGSTTSCQQAQPKTK 2558
Db 2456 PSYELV-----KSQOWDDIPPIFGVQOQVARQAKAFSLGKVAEVQ-----VSRRRAGGAQS 2507
Qy 2559 ---PASSGSVFGKGVFALKDGRVTDTIISVANEDGRRVAAIILNHAHYLENLHFTIDGVD 2615
Db 2508 WLFPATVKSILGKGVMLAVSGRVQTVNVLINAECDIKVAVLNNAFYLENLHFTIEGKD 2567
Qy 2616 THYFVKPSEGDIAILGLSGRRRTLENGVNVTVSQINTVNGKTRRYTDIQLQYGALCL 2675
Db 2568 THYFIKTTTPESDGLTURLTSRKALENGINVTVSQSTTVVNGKTRRFADVEMQFGALAL 2627
Qy 2676 NTRYGTTLDEKARVLELARAQRAVQAWAREQOBLREGEGLRAWTEGEKQOVLSTGRVQ 2735
Db 2628 HVRYGTTLDEKARILEQARALARAWAREQOVRDGEGRARLWTEGEKQOLLGAKVQ 2687
Qy 2736 GYDGFYVSVYQPELSDSANNTHFMQSEMGRR 2769
Db 2688 GYDGYVLSVEQYPELADSANNIQLRQSEIGRR 2721

RESULT 8

ABP53586
ID ABP53586 standard; protein; 2725 AA.

XX AC ABP53586;

XX DT 17-DEC-2002 (first entry)

XX DE Human NOV15a protein SEQ ID NO:35.

XX KW Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular;
KW cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide;
KW antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide;
KW antianaemic; antibacterial; protozoacide; antihelminthic; gene therapy;
KW cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy;
KW stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy;
KW Pick's disease; vesicular transport disease; cystic fibrosis; goitre;
KW diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine;
KW ulcerative colitis; gastric disorder; duodenal disorder; infection;
KW autoimmune disease; allergic reaction; autoimmune haemolytic anaemia;
KW rheumatoid arthritis; chromosome 4.

XX OS Homo sapiens.

XX PN W0200262999-A2.

XX PD 15-AUG-2002.
XX PF 31-DEC-2001; 2001WO-US049976.
XX PR 29-DEC-2000; 2000US-0258928P.
PR 02-JAN-2001; 2001US-0259415P.
PR 04-JAN-2001; 2001US-0259785P.
PR 20-FEB-2001; 2001US-0269814P.
PR 09-MAR-2001; 2001US-0279863P.
PR 29-MAR-2001; 2001US-0279832P.
PR 29-MAR-2001; 2001US-0279833P.
PR 13-APR-2001; 2001US-0283889P.
PR 18-APR-2001; 2001US-0284447P.
PR 25-APR-2001; 2001US-0286683P.
PR 29-MAY-2001; 2001US-0294080P.
PR 16-AUG-2001; 2001US-0312915P.
PR 17-AUG-2001; 2001US-0313325P.
PR 17-SEP-2001; 2001US-0322699P.
PR 26-NOV-2001; 2001US-0333350P.
XX PA (CURA-) CURAGEN CORP.
XX PI Spytek KA, Li L, Wolenc AP, Vernet CAM, Eisen A, Liu X;
PI Malyanekar U, Shinkets RA, Tchernev VT, Spaderna SK, Gorman L;
PI Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
PI Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
PI Gunther E, Smithson G, Millet I, Macdougall JR;
XX PR MPI; 2002-732706/79.
XX DR N-PSDB; ABQ82343.
XX PT New NOVX polypeptides and polynucleotides useful for treating NOVX-
PT associated disorders, such as cancers, neurological disorders, disorders
PT of vesicular transport, gastrointestinal disorders, and autoimmune
PT diseases.
XX PS Claim 1; Page 113; 444pp; English.
XX CC The present invention describes novel human proteins designated NOVX,
CC where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective,
CC cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular,
CC antidiabetic, antiinflammatory, antirheumatic, antibacterial, virucide,
CC immunosuppressive, antiallergic, antianaemic, antihelminthic, fungicide,
CC protozoacide and antihelminthic activities, and can be used in gene
CC therapy. The NOVX proteins, nucleotides or antibodies can be used in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease selected from NOVX-associated disorder, such as cancers
CC (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle,
CC ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke,
CC ischaemic cerebrovascular disease, Alzheimer's disease or Pick's
CC disease), disorders of vesicular transport (e.g. cystic fibrosis,
CC diabetes mellitus, Grave's disease, or goitre), gastrointestinal
CC disorders (e.g. ulcerative colitis, or gastric and duodenal disorders),
CC autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic
CC anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic
CC and protozoal infections. The NOVX proteins can be used as immunogens to
CC produce antibodies and as vaccines. The NOVX nucleotide sequences may be
CC used in chromosome mapping, identifying individuals from minute
CC biological samples (tissue typing), and in forensic identification of a
CC biological sample. The present sequence represents human NOV15a, which is
XX CC located on chromosome 4
XX SQ Sequence 2725 AA;

Query Match 68.5%; Score 10201; DB 5; Length 2725;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 1872; Conservative 362; Mismatches 462; Indels 102; Gaps 21;

Qy 1 MDVKERKPYRSLTR-RRDAERRVYTSSSADSECKAP-OKSYSSSETLKAYDQD-ARLAYG 57
Db 1 MDVKERRPYCSLTKSRREKERRYNTSSADNEECRVPTQKSYSSSETLKAFDHOSSRLLYG 60

Db 2157 EYVDGQLOTVYLNEKIMRWRYNDLGNLHLLNPSNSARLTPLRYDLDRITRLGDVQVR 2216
Qy 2255 MDEGRLRGQGDIFEVNSAGLLIKAYNRAGSVRYRVDGLGRVYSSKSSHHLLQFFY 2314
Db 2217 LDEGFLURGTETEFYSSKGLLTRYVYSGSGMTVIYRYDGLGRVSSKTSLSQHLLQFFY 2276
Qy 2315 ADLTNPFTKTHLYNHSSEITSLYYDIQGHFLFAMELSSGDEFYIACDNIGTGPLAVFSGTG 2374
Db 2277 ADLTYPTRITHVYNHSSEITSLYYDIQGHFLFAMEISSGDEFYIADNTGTPLAVFSSNG 2336
Qy 2375 LMKQILYTAIGEIMYNTNPFQIIIGYHGLYDPLTKLVHMGRRDYDLVLAGWTSPDHE 2434
Db 2337 LMLKQIQYTAIGEYFDSNIDFQVIGFHGGLYDPLTKLVHFGERYDYDILAGRWTTPDIE 2396
Qy 2435 LMKHLSSNVPNLYMKNNPNSQDIKCFMTDYNSSLTFFGFLHNVIRGYPKPDM 2494
Db 2397 IWKRI-GKDPAPFNLYMFRNNPASKIHDVKDYITDYNSSLVTFPGFLHNAIFGFPVKF 2455
Qy 2495 DAMEPSYELIHTQMTQEWDSKSIILGVQCEVQKQKAFVTLERFDOLYGSTTITSQOAP 2554
Db 2456 DLTEPSYELV---KSQWDDIPPIFGVQQVQAKAFSLGKMAEVQ---VSRERAG 2507
Qy 2555 KTKK---FASGSGVFGKVPALKDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTI 2611
Db 2508 GAQSWLWFATVKSLLIGKVMNAVSGRVTQVNLNANEDCIKVAALVNNAFYLENLHFTI 2567
Qy 2612 DGVDTHFVRGPGSEGDLAILGLSGGRTLENGVNTVVSQINTVLANGTRRYTDIOLQYG 2671
Db 2568 EGKDTYFIKTTPESLDGLRLTSGRKALENGINVTVSQSTTVVNGTRFRFADVENQFG 2627
Qy 2672 ALCLNTRYGTTLDKARVLELQRAVRQAWAREQORLREGEGLRAWTEGKQOVLST 2731
Db 2628 ALALHVRVYGMTLDEKARIILEQARALARAWAREQQRVDRGEGARLWTEGKQOLLSA 2687
Qy 2732 GRVQYDGFVVISVEQYPELSDSANNIHFWRQSEMGRR 2769
Db 2688 GKVGQYGYVLSVEQYPELADSANNIQLRQSEIGRR 2725

RESULT 9
ADH41995
ID ADH41995 standard; protein; 2725 AA.
XX
AC ADH41995;
XX
DT 25-MAR-2004 (first entry)
XX
DE Novel human protein NOV40f #2.
XX
KW cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
KW antiparkinsonian; antispasmodic; antiinfectivity; cardiomyopathy;
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
KW multiple sclerosis; graft-veraus-host disease; Alzheimer's disease;
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.
XX
OS Homo sapiens.
XX
PN WO2003102159-A2.
XX
PD 11-DEC-2003.
XX
PF 04-JUN-2003; 2003WO-US017573.
XX
PR 04-JUN-2002; 2002US-0385490P.
PR 04-JUN-2002; 2002US-0385615P.
PR 04-JUN-2002; 2002US-0385755P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386355P.
PR 06-JUN-2002; 2002US-0386357P.
PR 06-JUN-2002; 2002US-0386447P.
PR 06-JUN-2002; 2002US-0386459P.

PR 06-JUN-2002; 2002US-0386465P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0386701P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0387078P.
PR 07-JUN-2002; 2002US-0387081P.
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PR 10-JUN-2002; 2002US-0387429P.
PR 10-JUN-2002; 2002US-0387540P.
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PR 11-JUN-2002; 2002US-0387806P.
PR 11-JUN-2002; 2002US-0387810P.
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PR 11-JUN-2002; 2002US-0387868P.
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PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
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PR 12-JUN-2002; 2002US-0388479P.
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PR 14-JUN-2002; 2002US-0389146P.
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PR 19-JUN-2002; 2002US-0390209P.
PR 25-JUN-2002; 2002US-0391726P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402688P.
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PR 13-AUG-2002; 2002US-0403458P.
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PR 12-SEP-2002; 2002US-0410855P.
PR 13-SEP-2002; 2002US-0410505P.
PR 30-SEP-2002; 2002US-0412955P.
PR 23-OCT-2002; 2002US-0415195P.
PR 23-OCT-2002; 2002US-0420627P.
PR 24-OCT-2002; 2002US-0420718P.
PR 24-OCT-2002; 2002US-0420852P.
PR 31-OCT-2002; 2002US-0422750P.
PR 01-NOV-2002; 2002US-0423095P.
05-NOV-2002; 2002US-0423748P.
(CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
PI Ellerman K, Entenberg S, Gangolli EA, Gerlach VL, Gorman L;
PI Grosse WM, Gunther E, Guo X, Gusev VV, Herrmann JL, Ji W, Kekuda R;
PI Khramtsov NV, Larochele WJ, Li L, Liang H, Low K, Macdougall JR;
PI MacIachlan T, Malyankar UM, McQueeney K, Mezick AJ, Miller CE;
PI Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L;
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;
PI Wolenc AR, Zhong M, Zhong H;
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XX WFI; 2004-053467/05.
DR N-PSDB; ADH41994.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.
XX
PS Claim 2; SEQ ID NO 548; 1503pp; English.

xx The invention relates to 566 new isolated human polypeptides and their
cc encoding genes, sequences that are at least 95% identical to these or
cc sequences comprising one or more conservative substitutions in these. The
cc polypeptide, polynucleotide and antibodies against the polypeptides are
cc useful in diagnosing, treating or preventing NOVX-associated disorders,
cc e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
cc diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
cc Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
cc The nucleic acids are further used as hybridization probes, in chromosome
cc mapping, tissue typing, preventive medicine, and pharmacogenomics. The
cc polypeptides are also useful as vaccines. This sequence represents an
cc example of the polypeptide of the invention.
xx
SQ Sequence 2725 AA;

Query Match 68.5%; Score 10201; DB 8; Length 2725;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 1872; Conservative 362; Mismatches 462; Indels 102; Gaps 21;

QY 1 MDVKERKPYRSLTR-RRDAERRYVTSSADSEBEGKAP-OKSYSSSETLKAYDOD-ARLAYG 57
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QY 58 SRVKDIPVQEADEFCTRGTANFTLRELGLBEVTPPHGTLTYRTDIGLPQCGYSMGAGSDADM 117
DB 61 NRVKDLVHREADFTROQGNFTLRQLGVCEPATRRGLAFCAEMGLPHRGYSISAGSDADT 120

QY 118 EADTVLSPHPVLRWGRSTRGRSSCLSRANSNLTLDTEHEN---TETHIPGGLQNH 174
DB 121 ENEAVNSPEHAMRLMGRGVKSRSSCLSRNSALTLDTEHENKSDSENEOPASNOQGS 180

QY 175 RLRTPEPLLSHAHTPNQHHAAINSINLRGNFTPRSNPAPDTHSLSGEPAGGAQ---- 230
DB 181 TLQPLPP--SHQKQSAQH-PSITSINLRNLTNRNRQSPAP-----PAALPAELQTT 229

QY 231 -BPAHAQENWLLNSIPIETRLNGLKQPLFTGLQDNLNLIEMDILGASRHDGAYSDGHFLKFP 289
DB 230 PESVOLQDSWVLGNSVPLESR-----HFLPKT 256

QY 290 G-GTSPFLCTTSPGYPPLTSSVYSPPPRLPRSTFARPAFNLKPSKYCNWKAALSAIV 348
DB 257 GTGTTPLFSTATPGYTMASGYSYSPPTPLPRNTLSRSAFAFKSKSKYCSWKCTALCAVG 316

QY 349 ISATILVILAYVAMHFLGNLHLOPMQOME---ITEDASSPVPVTDVSLVPSGGTG 405
DB 317 VSVLLAILLSYFIAMHLFGLNLQLOQTENDTFENGKVNST-----MPTNVSPLSG--- 368

QY 406 LETPDRKGGTTEGKPSGFFPDSFIDSGEIDVGRASQKIPPGTFWRSQVFIHPVHLK 465
DB 369 -----DNGKLGGLFTQENNTIDSGELDIGRAIOEIPPGIFWRSQVFIHPVHLK 417

QY 466 FNVSLGKAALVCIYGRKGLPPSHT---QDFVELLDGRLLTQEARSLGTPRQSRGTV 521
DB 418 FNVSLGKAALVCIYGRKGLPPSHT---QDFVELLDGRLLTQEARSLGTPRQSRGTV 477

QY 522 PPSSHETGFIQYLDGSIWHLAFYNDGKSEVSVFLLTAIESVDNCPSCYNGDCISGTC 581
DB 478 SVSLHEAGFIQYLDGSIWHLAFYNDGKNAEQVSFNTIVIESVVECPNCHNGECVSGTC 537

QY 582 HCFGLFLGPDGCRASCPVLCSNGGYMKGRCLCHSGWKGAECVPTNOCIDVACSNHGTC 641
DB 538 HCFGFLGPDGCRASCPVLCSNGGYMKGRCLCHSGWKGAECVPTNOCIDVACSNHGTC 597

QY 642 IGTGTCINPGYGKESCEEVDCMDPTCSGRGVCRGECFCFGWGNTCETPRATCLDQCS 701
DB 598 IGTGTCINPGYGKESCEEVDCMDPTCSGRGVCRGECFCFGWGNTCETPRATCLDQCS 657

QY 702 HGHTFLPDTGLGCDSPSWTGHDCSTIEICAAADCGHGVGVCGGTCTCRCEGMMGAACDQRACH 761
DB 658 HGHTFLQESGSCCTDPNWTGPDSCNEICSVDCSGHGVCMGCTCRCEBGTGPAQNQRACH 717

QY 762 PRCAEHGTCRDGKCECPGWNGEHCCTIAHYLDRVV-----KEGCPGLCNGNGRCTLDLN 815

DB 718 PRCAEHGTCRDGKCECPGWNGEHCCTIAHYLDKIVDKIGYKEGCPGLCNGRCTLDLN 777
QY 816 GWHCVQLGWRGACDTSMETACDSDKNDGDGLVDCMDPDCCLQIPLCHINPLCLGSPNP 875
DB 778 GGHCVQCPGWRGACDVAMETLCTDSKDNBEGDGLIDCWDPDCLQSSCQNPYCRGLPDP 837
QY 876 LDITQETQVPVQOQLNLSHFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGOWMTSDGTP 935
DB 838 QDIISQLSQSPQQAASFYDRISFLIGSDSTHVPGESPNKSLASVIRGQVLUADGTP 897
QY 936 LVGVNIFSVNPLFGYTIISRQDGSFDLVTNGGISIIILFRERAPPITQHTLWLWPDWPFV 995
DB 898 LIGVNVSFHYEYGYTIITRQDGMFVLVANGASLTLVFERSPLTQVHTVWIPWNVFYV 957
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DB 958 MDTLVMEKEENDIPSCDLSGFVRPNPIIVSSPLSTFFRSPEDSPIIETQVLEHETIP 1017
QY 1056 GCKMRLSVLSRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAPADLSYV 1115
DB 1018 GTDLKLSYLSRAAGYKSVLKITWTQSIIPFNLMKVHLMVAVGRLFKQKFPAPSNLAYT 1077
QY 1116 FIWDKTDVYAKVQFGLSEAFVSVGYEYESCPLILWEKRTTVLQGYEIDASKLGSWLDK 1175
DB 1078 FIWDKTDVYAKVQFGLSEAFVSVGYEYESCPLILWEKRTTVLQGYEIDASKLGSWLDK 1137
QY 1176 HHALNIOSGLHKNGENQFVSQPPVIGSIMGNGRRRSISCPSCNGLAGNKLAPVAL 1235
DB 1138 HHVLDVQNGILYKNGENQFISQPPVYSSIMGNGRRRSISCPSCNGLAGNKLAPVAL 1197
QY 1236 TCSDGSLYVGDYFNIRRIIPSGNVTNILERNKDPRHSHSPAHKYVLTADPMGSAVPLS 1295
DB 1198 ACGIDGSLYVGDYFNIRRIIPSGNVTNILERNKDPRHSHSPAHKYVLTADPMGSAVPLS 1257
QY 1296 DSNRRYFKIKSTVWVKDLVKNSEWAGTGDQCLPDDTRCGDGGKATEATLTNPRGITV 1355
DB 1258 DTNTRRIYRPSLTKGADLTNAEVAAGTGEQCLPDEARCGDGGKATEATLTNPRGITV 1317
QY 1356 DKFGLIYFVDTGTRIRRIDQNGIISLLGSDNLTISARPLSCDSVMDISQVLEWPTDLAIN 1415
DB 1318 DKNGLIYFVDTGTRIRRIDQNGIISLLGSDNLTISARPLSCDSVMDISQVLEWPTDLAIN 1377
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DB 1378 PMDNSLVLDNNVYQIENHQRVIRVAGRPMHQVPGVE-YPGVKAHATLESATALAV 1436
QY 1476 SHNGVLIATDEKKINRQVTTSGEISLVAGAPSCDCKNDANCDYCSGDDGYAKDAK 1535
DB 1437 SYSGVLIATDEKKINRQVTTSGEISLVAGAPSCDCKNDANCDYCSGDDGYAKDAK 1496
QY 1536 LNTPSSILAVCAGDELVYVADLGNIRIFIRKNKPLANTONMYELSSPIDQELYLPTDTGKH 1595
DB 1497 LSAPSSILAVCAGDELVYVADLGNIRIFIRKNKPLANTONMYELSSPIDQELYLPTDTGKH 1556
QY 1596 LYTQSLPTGDLNFTYVTGDDITLITDNNGNMNVRRDSTGMPLMLVDPDGVYVWTMG 1655
DB 1557 QYTVSLVTGDLNFTYVTGDDITLITDNNGNMNVRRDSTGMPLMLVDPDGVYVWTMG 1616
QY 1656 TNSALLKSVTTQGHLELAWTVHNGSGLLATKNSNGENWMTTFYEDYSGFRLTNVTPPTGOVSS 1715
DB 1617 TNGCLKGMTAQGLELVLFTYHNGSGLLATKNSNGENWMTTFYEDYSGFRLTNVTPPTGOVSS 1676
QY 1716 FRDSTSSVHVVOVETSSK-DDVTITNLSAGAFYTLLODQVNSYVIGADGSLRLLAN 1774
DB 1677 LHGDMKAITVDILESSREEDVSITNLSIDSFYTWVQQLRNSYQIGVDGSLRIIYAS 1736
QY 1775 GMEVQLQTEPHLLAGTVNPTVGRNVTLPIDNGLNLEVMRQRKEQARGQVTVFGRRLRVH 1834
DB 1737 GLDSSHQTEPHVLAGTANPTVAKRNMTLPGENQNLVEMRFRKEQAGQKVNVEGRKLNV 1796
QY 1835 NRLLSLDPRVTRTEKIYDDHKKFTIRILYDQAGRPSLWSPSSRLNGVNVTVSPGYIA 1894

Db 1797 GRNLLSVDFORTTKTEKIYDHRKFLIRIAYDTSGHPTLWLPSSKLMVNVVTSSTGQIA 1856
Qy 1895 GIORGIMSEMEVDQAGRIISRIFADGKTWSYTYLEKSMVLLHSHSQRYIFEDKNDRLS 1954
Db 1857 SIQORTTSEKVDYDGGRIIVSRVFADGKTWSYTYLEKSMVLLHSHSQRYIFEDKNDRLS 1916
Qy 1955 SVTPMNVARQTLTETIRASGVYRNIYOPPEGNASVIOQFTEDGHLHHTFVLGTRRVIYKY 2014
Db 1917 AITMPSVARHTMQTIRSIGYRNIYNPPESNASIITDYNEEGLLQTAFLGTSRVLFKY 1976
Qy 2015 GKLSKLAETLYDTTKVSYFTYDETAGMLKTNLQNEGFTCTIRYRQIGPLIDROIPTTEE 2074
Db 1977 RRQTRLSEILYDTRVSFTYDETAGMLKTNLQSDGFICTIRYRQIGPLIDROIPTTEE 2036
Qy 2075 GMYNARFDYNDNSFRVTSNQAVINETPLDILYRVDDVSGKTEQKFGVVIYDINQII 2134
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Qy 2135 TTAVMTHTKHFDAYGRMKVQYEIFRSLMYMTVQYDNMGRVVKELKVGYPYANTTRYSY 2194
Db 2097 STAWMYTKHFDAGRIKEIQYEIFRSLMYWIIQYDNMGRVTKREIKGFPANTTKYAY 2156
Qy 2195 EYDADGQLOTVSINDKPLMRYSDYDLNGLHLLSPGNSARLTPLRYDIRDRITRLGDVQYK 2254
Db 2157 EYDVGQLOTVLNEKIMRWYNDLGNLHLLNPSNSARLTPLRYDLDRITRLGDVQYR 2216
Qy 2255 MDEGFLRQGGDIFFENYSAGLLIKAYNRAGSVRYRYDGLGRRVSSKSSHSHLQFFY 2314
Db 2217 LDEGFLRQGTETFEYSKGLLTRVYSKSGWTVIYRYDGLGRRVSSKTSLOHLOFFY 2276
Qy 2315 ADLTNPTKVTHLVNHSSETSYLDLQGHFLAMELSSGDEFYIACDNIGTPLAVFSGTG 2374
Db 2277 ADLTYPTRIHVNVNHSSETSYLDLQGHFLAMEISSGDEFYIADNIGTPLAVFSNG 2336
Qy 2375 LMIKQILYTAIGYIMDNTNPFQIIIGYHGLYDPLTKLVHMGRRDYDVLGRTWSPDHE 2434
Db 2337 LMLKQIQYTAIGYIMDNTNPFQIIIGYHGLYDPLTKLVHMGRRDYDVLGRTWSPDIE 2396
Qy 2435 LWKHLSSNVMPNLYMFRNNPISQDIKCPMTDVNSWLLTFGOLHNVIPGYKPKDM 2494
Db 2397 IWKRI-GKDPAPFNLYMFRNNPASKIHDVKDVIITDVNSWLVTFGFLHNAIFGFPVPKF 2455
Qy 2495 DAMEPSVELHTQWKTQWDSNKSILGVQCEVOKLKAFTVTLERFDOLYGTSTITSQOAP 2554
Db 2456 DLTEPSVELV----KSQWDDIPPIFGVQOQVARQAKAFSLGKMAEVQ----VSRRAQ 2507
Qy 2555 KTKK---FASGSGVFGKVPALKDGRVTTDIIISVANEDGRRVAALNHAAHYLENLHFTI 2611
Db 2508 GAQSMLWFATVKSILGKVMVAVSQGRVQTNVLNANEDCIKVAALNNNAFYLENLHFTI 2567
Qy 2612 DGVDTHTYFVPGPSEGLAILGLSGGRRTLENGWNTVVSQINTVNGRTRRYTDIQLQY 2671
Db 2568 EGDYTHYFIKTTTPESDLGLRLTSGKALENGINVTVSQSTTVNGRTRRFRFADVENQFG 2627
Qy 2672 ALCLNTRYGTTLDEEKAARVLELQARAVQAWAREQORLEBEGEGLRAMTEGEKQOVLST 2731
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Qy 2732 GRVQGYDGFVISVEQYPELSDSANNIHFMRQSEMGR 2769
Db 2688 GKVGQYDGYVLSVEQYPELADSANNIQFLRQSEIGRR 2725

RESULT 10

ADH41991

ID ADH41991 standard; protein; 2725 AA.

XX

AC ADH41991;

XX 25-MAR-2004 (first entry)

DT

XX Novel human protein NOV40d #2.

DE

XX

KW cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
KW antiparkinsonian; antiasthmatic; antiinfertility; cardiomyopathy;
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
KW multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.
OS Homo sapiens.
XX
XX WO2003102159-A2.
XX PD 11-DEC-2003.
XX PF 04-JUN-2003; 2003WO-US017573.
XX PF 04-JUN-2002; 2002US-0385490P.
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PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0387078P.
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PR 10-JUN-2002; 2002US-0387429P.
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PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387934P.
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PR 12-JUN-2002; 2002US-0388096P.
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PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
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PR 18-JUN-2002; 2002US-0389604P.
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PR 06-AUG-2002; 2002US-0401628P.
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PR 30-SEP-2002; 2002US-0412955P.
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PR 24-OCT-2002; 2002US-0420852P.
PR 31-OCT-2002; 2002US-0422750P.
PR 01-NOV-2002; 2002US-0423095P.

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PR 05-NOV-2002; 2002US-0423748P.
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PI Alsobrook JP, Anderson DM, Baumgartner JC, Berghs C, Boldog FL;
PI Burgess CB, Caeman SJ, Catterton E, Dhanabal M, Edinger SR;
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
PI Grosse WM, Gunther E, Guo X, Gusev VV, Harrmann JL, Ji W, Kekuda R;
PI Khramteov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;
PI MacLachlan T, Malyanar DM, McQueeney K, Mezick AJ, Miller CB;
PI Millet I, Padigar M, Pattarajan M, Peyman JA, Qian X, Rastelli L;
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;
PI Wolenc AR, Zhong M, Zhong H;
XX
DR WPI: 2004-053467/05.
DR N-PSDB; ADH41990.
XX
DR New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.
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PS Claim 2; SEQ ID NO 544; 1503pp; English.
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CC The invention relates to 566 new isolated human polypeptides and their
CC encoding genes, sequences that are at least 95% identical to these or
CC sequences comprising one or more conservative substitutions in these. The
CC polypeptide, polynucleotide and antibodies against the polypeptides are
CC useful in diagnosing, treating or preventing NOVX-associated disorders,
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
CC The nucleic acids are further used as hybridization probes, in chromosome
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
CC polypeptides are also useful as vaccines. This sequence represents an
CC example of the polypeptide of the invention.
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SQ Sequence 2725 AA;
Query Match 68.5%; Score 10201; DB 8; Length 2725;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 1872; Conservative 362; Mismatches 462; Indels 102; Gaps 21;
QY 1 MDVKERRPYRSTR-RRDAERYTSSADSEBKAP-QKSYSSSETLKAYDQD-ARLAYG 57
DB 1 MDVKERRPYCSLTKSRREKERYTSSADNEBCRYPTQKSYSSSETLKAFDHDSSRLLYG 60
QY 58 SRVKDIPVQEAERECRTGANTLRELGLEEVTPPHGTLRYTDIGLPQCGYMGAGSDADM 117
DB 61 NRKQVLRHREADFTQQGNFTLRQLGCEPATRRGLAFCAEMGLPHRGYSISAGSDADT 120
QY 118 EADTVLSPEHPVRLMGRSTRSGRSCSLSSRANSNLTLTDTEHEN---TETHDPCGLQNH 174
DB 121 ENEAVMSPEHAMRLAGRVKSGRSSCLSSRSNSALTTLTDTEHKNSENEQPNASNOQS 180
QY 175 RLRTPPPLSHAHNTQNHAAASINSLNKGNTTPRNSPAPTDLHSLGEPGAGGAQ---- 230
DB 181 TLQPLPP--SHKQSAQHH-PSITSLNRNSLTNRNRNQSPAD-----PAALPAELQTT 229
QY 231 -EPAAHAQENLLNSNIPLNETNLGKQPLFLGLQDNLEMDTLGASRHDGAYSOGHFLFKP 289
DB 230 PESVOLQDSWLGNSVPLESR-----HFLFKT 256
QY 280 G-GTSPFLCTTSPGYLTSSTVYSPPPPLPRSTFARPAFLNKKPKSKYCNWKAALSAIV 348
DB 257 GTGTITPSTATPGYTMAAGSVYSPPTPLPRNTLSRSFAKFKSKSKYCSWKCTALCAVG 316
QY 349 ISATIVILLAYFVAMHLFGLNWHLOPWEGQWYE---ITEDTASSWPVPTDVSLPSGGTG 405
DB 317 VSVLAILLSYFIAMHLFGLNWLQQTENDTTFENGKNSDT-----NPTNTVSLPSG--- 368
QY 406 LETPDRKGKGTTEGKPSFPFEDSFIDSIGDEIDVGRASQKIPPGTFRWSQVFDHPVHLK 465
Db 369 -----DNGKLGFTQENNTIDSGELDIGRAIQEIPPGIFWRSOLFIDQPOFLK 417
QY 466 FNVSLGKAALVGIYGRKGLPPSHT-----QPDFVELLDGRRLLTOEARSLEGTQSRGTV 521
Db 418 FNIISLOKDALGVTRKKLPPSHTQSSFDVVELLDGSRLLIAREQRSLLETERAGQAR 477
QY 522 PPSHETGFIQYLDGSIWHLAFYNDGKESEVVSFLTITAIIESVDNCPSCYNGGDCISGTC 581
Db 478 SVSLHEAGFIQYLDGSIWHLAFYNDGKNAEQVSPNTIVIESVVECPNCHGNGGCVSGTC 537
QY 582 HCFGLGFGPCGRASCVPILCSGNGQYMKGRCLCHSGHWKGAECQVPTTQCIQDVAQSNHGTC 641
Db 538 HCFPGFLGPDCSRACVPILCSGNGQYMKGRCLCFSGHWKGTCEQVPTTQCIQDQCGGRGIC 597
QY 642 ITGTCICNPYKGBSCBEVDMPTCSGRGVGVGRGCHCFVGMGGTNCETPRATCLDQCS 701
Db 598 IMGSCACSSGVKGBSCBEADUCIDPGCSNHGVCTHGECHCSFGWGGSCNCEILKTMCPDQCS 657
QY 702 GHGTFLLPDTGLSCDPSWTHGDCSIEICAAADCGHGVYCVGGTCRCEDGMWGAACDQRAH 761
Db 658 GHGTYLQESGSGCTCDPNWTGPDCSNEICSVDCSHGVCMGGTCRCBEGMTGPACNQRAH 717
QY 762 PRCAEHGTCRDGKCECSPGNGGHCCTIAHYLDRVV-----KEGCPCLNGNGRCTLDLN 815
Db 718 PRCAEHGTCRDGKCECSPGNGGHCCTIAHYLDRVV-----KEGCPCLNGNGRCTLDLN 777
QY 816 GWHCVCOLGWRGACDTSMETACGSKDNNDGDLVDMDDCCCLQPLCHINPLCLGSPNP 875
Db 778 GGHCVCPQWRGACDVAMETLCTDSKDNEDGLIDCMPDCCCLQSSCQNPYCRGLPDP 837
QY 876 LDIIQETQVPSQNLHSFYDRKFLVGRDSTHIIIGENPFDDGHCACVIRGQWNTSDGTP 935
Db 838 QDIISQLOSQPSQAAKSFYDRISFLIGSDSTHVIPEGSPFNKSLASVIRGQVLTADGTP 897
QY 936 LVGVNISFVNPNLFGYITISRGQGSFOLVTNGGISIILRPERAFITQEHMLPWPDRFFV 995
Db 898 LIGVNVSFHYPEYGYITITQDGMFDLVANGASLTIVFERSFPLTYHTVWIPWNVFV 957
QY 996 METIIRHENEIPSCDLNFPARNPNVPSPLTSPASSCAEKGPVIVPEIQALQBEIS 1055
Db 958 MDTLVMEKEENDIPSCDLNFPARNPNIIIVSSPLSTFFRSPEDSPIPETQVLHEETTIP 1017
QY 1056 GCMRLSYLSRTPGVKSVLRISLTHPTIPNLMKVLHVMVAVGRLFRQWFAAADLSY 1115
Db 1018 GTDLKLSYLSRRAAGYKSVLKITMTQSIIPFNLKVLHVMVAVGRLFRQWFAAADLSY 1077
QY 1116 FIWKTDDVYNQKVFGLSEAFVSVEYSECPDLILWEKRTTVLQGYEIDASKLQWMSLDK 1175
Db 1078 FIWKTDAVYNQKVFGLSEAFVSVEYSECPDLILWEKRTTVLQGYEIDASKLQWMSLDK 1137
QY 1176 HHALNTQSGILHKGNGENQVSOQPPVIGSINGNRRRISCPSCNGLADGNKLAPVAL 1235
Db 1138 HHVLDVQNGLLYKNGENQFISQPPVSSINGNRRRISCPSCNGLADGNKLAPVAL 1197
QY 1236 TCGSDGLSYVGFNTRIRIPPSGNVTNILELNKDPFRSHSPAHKYVILATDPMGAVFLS 1295
Db 1198 ACGIDGSLYVGFNTRIRIPPSGNVTNILELNKDPFRSHSPAHKYVILATDPMGAVFLS 1257
QY 1296 DSNRRVFKIKSTVVVVKOLVKNSVAVAGTGQDCLPDDTTRCDGGKATEATLTNPRGITV 1355
Db 1258 DNTNRRIRVPKSLTGAOKLTQNAEVVAVAGTGEQCLPDEARCGDGGKATEATLMSPKMAV 1317
QY 1356 DKFGLIYFDGFMIRRIDONGIITLLGSDNLTARPSLSCDSVMDISQVRLEWPTDLAIN 1415
Db 1318 DKNGLIYFDGFMIRRIDONGIITLLGSDNLTARPSLSCDSVMDISQVRLEWPTDLAIN 1377
QY 1416 PMDNSLYLDNNVNLQISENHQVRIAGRPCHQVPGIDHFLLSKVAIHTATLESATLAV 1475
Db 1378 PMDNSLYLDNNVNLQISENHQVRIAGRPCHQVPGIDHFLLSKVAIHTATLESATLAV 1436
QY 1476 SHNGVLYIAETDEKINRIQVTTSGEISLVAGAPSGCDCKNDANCDGSGDDGYAKDAK 1535
```

| | | | |
|-----------|---|--|------|
| Db | 1437 | SYSGVLVITETDEKKINIRQVTTDGBISLVAGIPSECDCKNDANCDYQSGDGYAKDAK | 1496 |
| Qy | 1536 | LNTPESSLAVCADGELYVADLGNIRIRFIRKKNKPLANTQNMVELSSPDDOELYLFDITGKH | 1595 |
| Db | 1497 | LSAPSSLAASPFDGLTYADLGNIRIRAVSKNKLPLNSMNFYEVASPTDQBELYIPDINGTH | 1556 |
| Qy | 1596 | LYTQSLPTGDLVLYNFTYTGDDITLIIDNNNGMNVNRRDSTGMPLMLVDPDGOVYVWTMG | 1655 |
| Db | 1557 | QYTVSLVTGDIYLYNFSVNDNDITAVTDSNGNTLRIRDPDNRMPVRVSPDNQVIMLTIG | 1616 |
| Qy | 1656 | TNSALKSVTTQGHELAMMTYHNGSGLLATKSNENGWTFYEDSFGRLTNVTPTGQVSS | 1715 |
| Db | 1617 | TNGCLKGMTAAGLELVLFYHNGSGLLATKSDGTWTTFFDYSDEGRLTNTVPTGVVTN | 1676 |
| Qy | 1716 | FRSDTSSVHVQVETSSK-DDVITITNLSAGAFYTLLODVNSYYIGADGSLRLLAN | 1774 |
| Db | 1677 | LHGDMDKAITVDIESSREEDSVTSNLSIDSEFTYMWQDLRNSYQIGYDGSRLIUYAS | 1736 |
| Qy | 1775 | GMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEMQORKEAQGVTVFGRLRLRVH | 1834 |
| Db | 1737 | GLDSHYQTEPHVLGANTPNTVAKRNMTLPGENGQNLVEWFRKEAQAGKVNFGKRLRVN | 1796 |
| Qy | 1835 | NRNLLSDFORVTRTEKIYDHRKFTLRILYDQAGRPSSLMSPPSRLNGVNVYSPGCGYIA | 1894 |
| Db | 1797 | GRNLLSVDFDRTTKTEKIYDHRKFLRLRIAYDTSGHPTLMLPSSKLMVNVVYSSYTGQIA | 1856 |
| Qy | 1895 | GIQGISRMEXYDQAGRITSRIPADGKTWSYTYLEKSMWLLLSHQRYIFEPDKNDRLS | 1954 |
| Db | 1857 | SIQRTGTTSEKVDYDQGRIVSRVPADGKTWSYTYLEKSMWLLLSHQRYIFEYDMWDRLS | 1916 |
| Qy | 1955 | SVTMPNVAROTLETIRSVGVYRNITYOPPEGNASVIOQFTEGHLHLHTFYLGCTGRVYKY | 2014 |
| Db | 1917 | AITPMSVARHTMQTIRSIGYRNINYPNPNESNIIITYNBEGLLQTAFLGTSRVLFKY | 1976 |
| Qy | 2015 | GKLSKLAETLYDTTKVSFTYDETAGMLKTLNLQNEGFTCTIRYRQIGLPLDRQIFRTEE | 2074 |
| Db | 1977 | RQOTRLSEILLYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGLPLDRQIFRPSD | 2036 |
| Qy | 2075 | GMVNARFDYNDNFRVTSMAQVNETPLPLDLYRYDDVSGKTEQFGKFGVYIYDINOII | 2134 |
| Db | 2037 | GMVNAREFDYSYDNSFRVTSMQGVNETPLPLDLYQFDDISGKVEQFGKFGVYIYDINOII | 2096 |
| Qy | 2135 | TTAVMTTKHFDAYGRKKEVOYEYFRSLYMWMTVOYDMGRVVKELKVGYPANTTRYSY | 2194 |
| Db | 2097 | STAVMTYTKHFDAGRKEIKEYEYFRSLYMWITTIQYDNMGVRYKREIKIGFANTTKVAY | 2156 |
| Qy | 2195 | EYDADGQLOTVSINDKPLWRYSYDLNGLMLHLLSPGNSARLTPLRYDIRITRLGDVOYK | 2254 |
| Db | 2157 | EYDVGQLOTVYVLEKIMWRNYDNLGNLHLNPSNSARLTPLRYDLRDRITRLGDVOYR | 2216 |
| Qy | 2255 | MDEGFLRQRGDIFEVNSAGLLIKAVNRAGSWVRVRYDGLGRVRSKSSHSHLOFFY | 2314 |
| Db | 2217 | LDEGFLRQRGTEIFEYSSKGLLTRVYSKSGWTVIYRYDGLGRVRSKSLSGHLOFFY | 2276 |
| Qy | 2315 | ADLTNPTKVTHLYNHSSEITSLYDLOGLHLPAMELSSGDEFYIACDNIGTFLAVFSGTG | 2374 |
| Db | 2277 | ADLTPTKTRITHVYNHSSEITSLYDLOGLHLPAMEISSGDEFYIASONTGTFLAVFSSNG | 2336 |
| Qy | 2375 | LMIKQILYATAGEIYMDNPNFQIIIGYHGGYLDPLTKLVHMGRRDYLVLGRWTSDPHE | 2434 |
| Db | 2337 | LMLKQIQYATAGEIYFDSNIDFQVIGFHGGYLDPLTKLIHFGERYDYLILAGRWTTPDIE | 2396 |
| Qy | 2435 | LWKHLSSNVMPFNLMPKNNPITSNSODIKCFMTDVSNSWLLTFTGFLQHNHVPYKPKDM | 2494 |
| Db | 2397 | IKWKRI-GKDPAPFNLMPERNNPASKIHDKVDYITDVNSWLVTFEGFLHNAIPGPPVKF | 2455 |
| Qy | 2495 | DAMEPSYELIHTQMKTOEMDNSKSLGVQCEVQKQKAFVTLERFDQLYGSSTITSQOAP | 2554 |
| Db | 2456 | DLTPESELYELV---KSQWMDIIPPIFGVQQQVAKAKAFLSLGKMAEVQ-----VSRRRAG | 2507 |
| Qy | 2555 | KTKK---PASSGSVFGKGVKALDKDGRVTTDIIISVANEDGRRVAAILNHAHYLENLHPTI | 2611 |
| Db | 2508 | GAQSWLWFAVTKSLIGKGMVLAVSQGRVQTVNLNANEDCIIKVAALVNNAFYLENLHPTI | 2567 |
| Qy | 2612 | DGVDTHTYFKPGPSEGDLAIGLSGGRRTLENGVNVTVSQINTVLNNGRTRRYTDIQLQVG | 2671 |
| Db | 2568 | EKGOTHTYFKTTPTESDGLTSLRSGKALENGINTVSQSTTVNNGRTRRFPADVEMQFG | 2627 |
| Qy | 2672 | ALCLNTRYGTTLDEEKARVLELARQRAVQAWAREQOORLREBEGELRAWTEGSKQOVLST | 2731 |
| Db | 2628 | ALALHVRYGWTLDEEKARILEQARALARAWAREQOORVDRDGBEGARLWTEGSKROLLSA | 2687 |
| Qy | 2732 | GRVQGVDPGFVLSVEQYPELSDSANNIHFMRQSEMGRR | 2769 |
| Db | 2688 | GRVQGVDPGFVLSVEQYPELSDSANNIQLRQSEIGRR | 2725 |
| RESULT 11 | | | |
| ADH41933 | ADH41933 standard; protein; 2725 AA. | | |
| ID | ADH41933 | | |
| AC | ADH41933; | | |
| XX | AC | | |
| DT | 25-MAR-2004 (first entry) | | |
| XX | Novel human protein NOV40a. | | |
| DE | cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic; | | |
| XX | anti-diabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; | | |
| KW | anti-parkinsonian; anti-asthmatic; anti-infectility; cardiomyopathy; | | |
| KW | atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; | | |
| KW | multiple sclerosis; graft-versus-host disease; Alzheimer's disease; | | |
| KW | Parkinson's disease; asthma; fertility disorder; chromosome mapping; | | |
| KW | tissue typing; preventive medicine; pharmacogenomic; vaccine. | | |
| XX | Homo sapiens. | | |
| OS | Homo sapiens. | | |
| XX | WO2003102159-A2. | | |
| PN | XX | | |
| XX | XX | | |
| PD | 11-DEC-2003. | | |
| XX | XX | | |
| PF | 04-JUN-2003; 2003WO-US017573. | | |
| XX | XX | | |
| PR | 04-JUN-2002; 2002US-0385490P. | | |
| PR | 04-JUN-2002; 2002US-0385615P. | | |
| PR | 04-JUN-2002; 2002US-0385755P. | | |
| PR | 05-JUN-2002; 2002US-0386041P. | | |
| PR | 06-JUN-2002; 2002US-0386355P. | | |
| PR | 06-JUN-2002; 2002US-0386357P. | | |
| PR | 06-JUN-2002; 2002US-0386447P. | | |
| PR | 06-JUN-2002; 2002US-0386459P. | | |
| PR | 06-JUN-2002; 2002US-0386465P. | | |
| PR | 06-JUN-2002; 2002US-0386701P. | | |
| PR | 07-JUN-2002; 2002US-0386796P. | | |
| PR | 07-JUN-2002; 2002US-0386931P. | | |
| PR | 07-JUN-2002; 2002US-0387078P. | | |
| PR | 07-JUN-2002; 2002US-0387083P. | | |
| PR | 07-JUN-2002; 2002US-0387083P. | | |
| PR | 10-JUN-2002; 2002US-0387429P. | | |
| PR | 10-JUN-2002; 2002US-0387540P. | | |
| PR | 10-JUN-2002; 2002US-0387866P. | | |
| PR | 11-JUN-2002; 2002US-0387806P. | | |
| PR | 11-JUN-2002; 2002US-0387810P. | | |
| PR | 11-JUN-2002; 2002US-0387659P. | | |
| PR | 11-JUN-2002; 2002US-0387668P. | | |
| PR | 11-JUN-2002; 2002US-0387896P. | | |
| PR | 11-JUN-2002; 2002US-0387859P. | | |
| PR | 12-JUN-2002; 2002US-0387934P. | | |
| PR | 12-JUN-2002; 2002US-0387960P. | | |
| PR | 12-JUN-2002; 2002US-0388022P. | | |
| PR | 12-JUN-2002; 2002US-0388096P. | | |
| PR | 12-JUN-2002; 2002US-0388432P. | | |
| PR | 12-JUN-2002; 2002US-0388479P. | | |
| PR | 13-JUN-2002; 2002US-0389123P. | | |
| PR | 14-JUN-2002; 2002US-0389120P. | | |

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PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389604P.
PR 18-JUN-2002; 2002US-0389884P.
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PR 06-AUG-2002; 2002US-0401628P.
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PR 26-AUG-2002; 2002US-0406182P.
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PR 23-SEP-2002; 2002US-0412955P.
PR 30-SEP-2002; 2002US-0415195P.
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PR 23-OCT-2002; 2002US-0420718P.
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PR 31-OCT-2002; 2002US-0422750P.
PR 01-NOV-2002; 2002US-0423095P.
PR 05-NOV-2002; 2002US-0423748P.
XX (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;
PI Khramtsov NV, Larochele WJ, Li L, Liang H, Low K, Macdougall JR;
PI MacLachlan T, Malyankar UM, McQueeney K, Mezick AJ, Miller CE;
PI Millet I, Padigar M, Patturajan M, Peyman JA, Qian X, Rastelli L;
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss E;
PI Wolenc AR, Zhong M, Zhong H;
XX
PI WPI; 2004-053467/05.
DR N-PSDB; ADH41932.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.
XX
PS Claim 2; SEQ ID NO 486; 1503pp; English.
XX
CC The invention relates to 566 new isolated human polypeptides and their
CC encoding genes, sequences that are at least 95% identical to these or
CC sequences comprising one or more conservative substitutions in these or
CC polypeptide, polynucleotide and antibodies against the polypeptides are
CC useful in diagnosing, treating or preventing NOVX-associated disorders,
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
CC The nucleic acids are further used as hybridization probes, in chromosome
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
CC polypeptides are also useful as vaccines. This sequence represents an
CC example of the polypeptide of the invention.
XX
SQ Sequence 2725 AA;
Query Match 68.5%; Score 10201; DB 8; Length 2725;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 1872; Conservative 362; Mismatches 462; Indels 102; Gaps 21;
QY 1 MDVKERKPYRSLTR-RRDAERYTSSADSBEKAP-OKSYSSSETLKAYDQD-ARLAYG 57
DB 1 MDVKERRPYCSLTKSRREKERYTNSADNEECRVPTOKSYSSSETLKAPDHDSSRLLYG 60
QY 58 SRVKDIVQEAEEPCRTGANFTLRELGLEEVTPPHGLTYRTDIGLPQCGYSMGAGSDADM 117
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Db 1078 FWDKTDAYNQKVGSLSEAVSVVSGYEYESCLIDLTLWEKRTAILQGYELDASNMGGWTLDK 1137
Qy 1176 HHALNIQSGILHKNGENOFVUSQPPVIGSFMNGRRRSISCPSCNGLADGNKLLAPVAL 1235
Db 1138 HHVLDVQNGILYKNGENQFISQPPVSVSSIMNGRRRSISCPSCNQAQGNKLLAPVAL 1197
Qy 1236 TCGSDGSLYVGDNFYIRIRIPSGNVNITLRLNKKDFRSHSPAHKYLYLATDPMGSAVFLS 1295
Db 1198 ACGIDGSLYVGDNFYVIRIPSGNVNITLRLNKKDFRSHSNPAHRYLYLATDPTVGDLYVS 1257
Qy 1296 DSNRRVFKTSVTVVKKDLVKNSVAVAGTGQCPLPDDTRCGDGGKATEATLNPGRITV 1355
Db 1258 DNTNRIYRPKSLTGAKDLTKNAEAVAGTGQCPLPDEARGDGGKAVEATLSPKGMV 1317
Qy 1356 DKFGLYVFDGTMIRRIDONGIISTLGSNDLTSARPLSCDSVMDISQVLEWPTDLAIN 1415
Db 1318 DKNGLIYVFDGTMIRKVDQNGIISTLGSNDLTSARPLTCDTSHISQVLEWPTDLAIN 1377
Qy 1416 PMDNSLVLDNNVVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAV 1475
Db 1378 PMDNSIYLDNNVVLQITENRQVRIAGRPMHCQVPGVE-YPGVKHAYQITLESATAIV 1436
Qy 1476 SHNGVLYIAETDEKINRIQVTTSGEISLVAGAPSGCDCKNDANCDGSDGDAYKADAK 1535
Db 1437 SYSGVLYITETDEKINRIQVTTDGEISLVAGIPSECDCKNDANCDGSDGDAYKADAK 1496
Qy 1536 LNTPSSSLAVCADGELYADLGNIRIRIRKKNKPLNTQNMVELSPDQELYLPTTGKH 1595
Db 1497 LSAPSSLAASPDGLYIADLGNIRIRAVKKNKPLNSMNFYEASPTDQELYIFDINGTH 1556
Qy 1596 LYTSQSLPTGDLYNFTYTGCDGIDTLITDNNGMNVNRDSTGMPLLWLVPDQGVYVWTMG 1655
Db 1557 QYTVSLVTGDLYNFSVNSNDIITAVTDSNGWTRIRARDPNRMPRVVSPDNQVIMLTIG 1616
Qy 1656 TNSALKSVTTQGHELAMMTYHNGSGLLATKSNENGTTFEYDSFGRLTNTVFTPGOVSS 1715
Db 1617 TNGCLKGMTAQGLELVLFTYHNGSGLLATKSDGTGTTFFDYDSEGRLTNTVFTPGVVTN 1676
Qy 1716 PRSDTSSVHVQVETSSK-DDVTTITNLSASGAFYTLLOQVRSYIYGADGSLRLLLAN 1774
Db 1677 LHGDMDKAITVDIESSEEREEDSVTSNLSIDSFYTMVQDLRNSYQIYDGSURIIYAS 1736
Qy 1775 GMEVALQTEPHLLAGTNPTVGNKNTLPIONGNLNVEWRQKEQARGOVTVFGRRLRVH 1834
Db 1737 GLDSHYQTEPHVLGANTPTVAKNNTLPGENGQNLVEWRFRKEQAQGVKNNVFGKLRVN 1796
Qy 1835 NRNLLSDFDRVTRTEKIYDDHRKFTLLILYDQAGRPSLWSPSRLNGVNVVYSPGGVIA 1894
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Db 1857 SIQRTGTTEKYVDYDQGRIVSRVADGKTWSYTYLEKSMVLLLSHQRYIEFYDMDRLS 1916
Qy 1955 SVTMENVAROTLETIRSVGYRNTIYOPPEGNASVIQDFTEDGHLHPTFLGTGRVRVYKY 2014
Db 1917 AITPMVARHTWQIRTSIGYRNTIYNPPESNASIITDYNBEGLLLOTAFLGTSRVLFKY 1976
Qy 2015 GKLSKLAETLYDTTKVSFTYDQAGMLKTLNLQNEGFTCTIRYQIQIGPLIDRQIFRFTEE 2074
Db 1977 RRQTRLSILYDSTRVSTYDQAGVLKTNLQSDGFICTIRYQIQIGPLIDRQIFRFSQD 2036
Qy 2075 GWNARFPYNDSPRVTSMAQVNETPLPIDLRYDDVSGKTEQFGKFGVIYDINQII 2134
Db 2037 GWNARFSDYDSPRVTSMQGVNETPLPIDLYQFDDISGKVEQFGKFGVIYDINQII 2096
Qy 2135 TTAVMTNKHFDAYGRMEKVEQYIEIPRSLMYNWTVOYDNNGRVVKELKGVYANTTRYSY 2194
Db 2097 STAVMTYTKHFDAGRIKIEIQIEIPRSLMYNWTVOYDNNGRVVKELKIGFANTTRYKAY 2156
Qy 2195 EYDADGQLQTVSINDKPLWRYSDYDLNGLHLLSPGNSARLTPLRYDIRDTRLGDVOYK 2254
Db 2157 EYDVGQQLQTVYVYLNKIMWRYNDLNGNLHLLNPSNARLTPLRYDLRLDRITRLGDVQYR 2216

Qy 2255 MDEBDGFLRQGGDIFEYNSAGLLIKAYNRAGSMVRYRDGLGRRVSSKSSHHLQFFY 2314
Db 2217 LDEBDGFLRQGTETFEYSKGLLTRVYKSGSGWTVIYRYDGLGRRVSSKSTLQHLQFFY 2276
Qy 2315 ADLTNTKTVTHLYNHSSEISLTYLOQLHFMELSSGDEFYIACDNTGTPPLAVFSGTG 2374
Db 2277 ADLTYPTRITHVYNHSSEISLTYLOQLHFMELSSGDEFYIASDNTGTPPLAVFSSNG 2336
Qy 2375 LMTKQILYATAGBIYMDTNPFOIIGYHGLGYDPLTKLVHMGRRDDVVLAGRWTSPDHE 2434
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Qy 2435 LMKHLSNNSMPPENLYMFKNNNPISNSQDIKCFMTDVSNSMLLTFFGOLFHNVIIPGYPKDM 2494
Db 2397 IMKRI-GKOPAPENLYMFRNNNPASKIHVDKVIITDVNSMLVTFGFHLHNAIPGFVPVKF 2455
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Db 2456 DLTPESYELV----KSQWDDIPPIFGVQQQVQARQAKAFSLGKMAEVQ----VSRRRAG 2507
Qy 2555 KTKK----FASGSGVFGKGVKFAKDGRTVTDIISVANEDGRRVAAIILNHAHYLENLHFTI 2611
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Db 2568 EGKQTHYFIKTTPTPESDLGTLRLTSGRKALENGINTVTSQTTVNGRTRRFADVENQFG 2627
Qy 2672 ALCNTRYGTTLDEEKARVLELQARAVRQAWAREOQRLREGEGLRANTEGEKQVLTST 2731
Db 2628 ALALHVRYGMLTDEEKARILEQARQALARAWAREOQVRDGBEGARLWTEGEKROLLSA 2687
Qy 2732 GRVQGYDGFVISVEQYPELSDSANNHFMRSQSEMR 2769
Db 2688 GKVGQYDGYVYVLEQYPELADSANNIQFURQSEIGRR 2725

RESULT 12

ADH41997

ID ADH41997 standard; protein; 2725 AA.

XX AC ADH41997;

XX DT 25-MAR-2004 (first entry)

XX DE Novel human protein NOV40g #2.

XX KW cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
XX KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
XX KW antiparkinsonian; antiaschmatic; antifertility; cardiomyopathy;
XX KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
XX KW multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
XX KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
XX KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX OS Homo sapiens.

XX PN WO2003102159-A2.

XX XX

XX PD 11-DEC-2003.

XX XX 04-JUN-2003; 2003WO-US017573.

XX PR 04-JUN-2002; 2002US-0385490P.

XX PR 04-JUN-2002; 2002US-0385615P.

XX PR 04-JUN-2002; 2002US-0385755P.

XX PR 05-JUN-2002; 2002US-0386041P.

XX PR 06-JUN-2002; 2002US-0386355P.

XX PR 06-JUN-2002; 2002US-0386357P.

XX PR 06-JUN-2002; 2002US-0386447P.

XX PR 06-JUN-2002; 2002US-0386459P.

XX PR 06-JUN-2002; 2002US-0386465P.

Db 718 PRCAEHGCTKDGKCECSQGNGBHCTIAHYLDKIVKDKIGYKEGCPCLCNSNGRCTLDQN 777
Qy 816 GWCVCOLGWRGAGCDTSMETACDSDKNDGDGLVDCMDPDCCLOPLCHINPLCLGSPNP 875
Db 778 GGHCVCPQWRGAGCDVAMETLCTDSDKNDGBGLIICMDPDCCLOQSSCQNPVCRGLPDP 837
Qy 876 LDIIQETQVPSQONLHFSFYDRIKFLVGRDSTHIIIGENPFDPGHCACVIRQVMTSDGTP 935
Db 838 QDIISQSLQSPSQAAKSFYDRISFLIGSDSTHIVIGESPENKSLASVIRGQVLTADGTP 897
Qy 936 LVGNISFVNPLPFGYITISQDGSFDLVTNGGIIILIRFAPFIQEHTLWLWPDFFV 995
Db 898 LIGVNSFFHYPEGYITITRQDGMFGLVANGGASLTLPFRSPFLTQYHTVWIPWNVFY 957
Qy 996 METIIMRHEBNEIPSCDLSFARPNPVSPSLTSPASSCAEKGPVPEIQALQOEISIS 1055
Db 958 MDLVMKEENDIPSCDLSGFVRPNPIIVSPSLSTFFRSPSPESPIIPEIQVUHEBTIP 1017
Qy 1056 GCKMRLSYLSRTPGYKSVLRISLTHPTIPFNLMKVHLMAVEGRFLFRKFAAAPDLSY 1115
Db 1018 GTDLKLSYLSRAAGYKSVLKIWTQSIIPFNLMKVHLMAVVGRFLFQKWFASPPLAYT 1077
Qy 1116 FIWDKTDVYNQKVFGLSEAFVSVGYEYESCPDLILMEKRTVLQGYEIDASKLGGWSLDK 1175
Db 1078 FIWDKTDVYNQKVFGLSEAFVSVGYEYESCLDLTLMEKRTAILQGYELDASNMGWTLDK 1137
Qy 1176 HHALNTQSGILHKGNGENQFVSQOPPVIGSIMGNRRRSISCPSCNGQADGNKLLAPVAL 1235
Db 1138 HHVLDVQNGLYLXGNGENQFISQOPPVVSSIMGNRRRSISCPSCNGQADGNKLLAPVAL 1197
Qy 1236 TCSDGSLYVGDFFNYIRIIPSPGNVTNILELRNKKDFRSHSPAHKYKYLATDPMGAVFLS 1295
Db 1198 ACGIDGSLYVGDFFNYIRIIPSPGNVTNILELRNKKDFRSHSPAHKYKYLATDPMGAVFLS 1257
Qy 1296 DSNRRVFKTKSTVVKDLVNSEWAGTGDQCLPFDDTRCGDGGKATEATLTPNPGITV 1355
Db 1258 DTNTRIRYRPSKLTGAKDLTKNAEVAAGTGEQCLPFDEARCGDGGKAVEATLSPKGMV 1317
Qy 1356 DKGLIYFVDTWIRRRDQNGIISTLGSNDLTSARPLSDSVMDISOVLEWPTDLAIN 1415
Db 1318 DKGLIYFVDTWIRRVQNGIISTLGSNDLTSARPLSDSVMDISOVLEWPTDLAIN 1377
Qy 1416 PMDNLVLDNNVVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIAHATLSSATALAV 1475
Db 1378 PMDNLVLDNNVVLQITENQVRIAGRPMHCQVPGVE-YPYGKHAVQTLSSATAIV 1436
Qy 1476 SHNGVLYAETDEKKINRIQVTTSGEISLVAGAPSCDCNDANCDGSGDGGYAKDAK 1535
Db 1437 SYSGVLYITETDEKKINRIQVTTSGEISLVAGIPSECDCKNDANCDGSGDGGYAKDAK 1496
Qy 1536 LNTPSSLAVCADGELYVADLGNIRIRIRKNKPLNTQNMVELSSPIDQELYLFDITGKH 1595
Db 1497 LSAPSSLAAAPDGLTYLADLGNIRIRIRAVSKNPLNLSMNFYEVASPTDQELYIFDINGTH 1556
Qy 1596 LYTOSLPTGDVLYNFTYTGDDITLITDNNGNMVNRDSTGMPMLWLVPDGOVWYTMG 1655
Db 1557 QYTVSLVTGDVLYNFSVNDNDITAVTDSNGNTLIRIRDPNRPVRVVSFDNQVIMLTIG 1616
Qy 1656 TNSALKSVTTQGHELAMWYTHGNSGLLATKSNENGMWTFYEDSFGLTNTVPTQGVSS 1715
Db 1617 TNGCLKGWTAQGLVLFVTHGNSGLLATKSDETGWTTFDYDSEGRLTNTVPTGVVTN 1676
Qy 1716 FRSDTSSVHVQVETSSK-DDVTITTNLSAGAFYTLLOQVRSYIIGADGSLRLLAN 1774
Db 1677 LHGDMDKAITVDIESSREEDVSITNSLSDISFTYTWQDLRNSYQIGYDGLSLRIIYAS 1736
Qy 1775 GMEVALQTEPHLLAGTVPTVGRNVTLPTDNGNLNVLEWRQKEQARGQVTVFGRRLRVH 1834
Db 1737 GLDHYQTEPHVLTAGTNPTVAKRNTLPGENGQNLVLEWRQKEQAGCKVNVFGRKLVRN 1796
Qy 1835 NRNLSSLDPRVTRTEKIYDDHRKFTLRIILYDQAGRPSLSPSRNLGNVNTYSPGYYIA 1894
Db 1797 GRNLLSVDFDRTTKTEKIYDDHRKFTLRIAYDTSGHPTLWLPSSKLMVNVNTYSSTGOIA 1856

Qy 1895 GIQGRIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLHLSQROYIFBFDKNDRLS 1954
Db 1857 STIORGTSETKVDYDGGRIVSRVAFADGKTWSYTYLEKSMVLLHLSQROYIFBFDKNDRLS 1916
Qy 1955 SVTMENVARQUTLETIRSVCYIYENIYQPPPEGNASVTDQFTEDGHLLHTFLTGTRRVIKY 2014
Db 1917 AITMPSVARHTWQTIRSICGYIYENIYNPPESNASIITDYNEEGLLQTAFLGTSRRVLFKY 1976
Qy 2015 GKLSKLAETLYDTTKVSFTYDETAGMLKTINLQNEGTCTIRYRQIGPLIDROIPIRFTTEE 2074
Db 1977 RQOTRUSELIXOSTRVSFTYDETAGVKTIVNLOSDGFICTIRYRQIGPLIDROIPIRFTTEE 2036
Qy 2075 GVNARFIDYNDNSFRVTSQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYDINQII 2134
Db 2037 GVNARFIDYNDNSFRVTSQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYDINQII 2096
Qy 2135 TTAVMTHTKHFDAYGRMKVOYVEIIFRSLMYWMTVQYDNMGRVVKKELKVPYANTTRYSY 2194
Db 2097 STAVMTYTKHFDAGRIKEIQVEIFRSLMYWMTVQYDNMGRVVKKELKVPYANTTRYSY 2156
Qy 2195 EYDADGLOTVSINDKPLWRYSYDLNGLHLLSPGNSARLTPLRYDIRDIRITRLGDVQYK 2254
Db 2157 EYDVGLOTVLVLEKIMMYRYDNLGNLHLLSPGNSARLTPLRYDIRDIRITRLGDVQYK 2216
Qy 2255 MDDEGFLRQGGDIFEYNSAGLLIKAYNRAGSWSRYRYDGLGRRVSSKSSHSHHLOFFY 2314
Db 2217 LDEGFLRQGGDIFEYNSAGLLIKAYNRAGSWSRYRYDGLGRRVSSKSSHSHHLOFFY 2276
Qy 2315 ADLTNPYKTHLYNHSSEISITSLYDLOGLHFLAMESSGDEFFIACDNTGTPLAVPSGTG 2374
Db 2277 ADLTNPYKTHLYNHSSEISITSLYDLOGLHFLAMESSGDEFFIACDNTGTPLAVPSGTG 2336
Qy 2375 LMKQIQLYTAGYELIYMDTNPFIIGYHGLYDPLTKLVHMGRRDYDVLGRWTSPDHE 2434
Db 2337 LMKQIQLYTAGYELIYMDTNPFIIGYHGLYDPLTKLVHMGRRDYDVLGRWTSPDHE 2396
Qy 2435 LMKHSSSNMPPNLYMFKNNPISNSODIKCFMTDVSNSWLLTFGQLHNHVIPIGYPKPD 2494
Db 2397 LMKHSSSNMPPNLYMFKNNPISNSODIKCFMTDVSNSWLLTFGQLHNHVIPIGYPKPD 2455
Qy 2495 DAMEPSYELIHTOMKTQEWDSKSIILGVQCEVQKQKAFVTLERFQLYGSTITSQOAP 2554
Db 2456 DLTEPSYELV---KSQWDDIPPIFGVQOVARQAKAFSLSGKMAEVQ----VSRRRAG 2507
Qy 2555 KTKK---FASSGSVFGKGVKFKALCKGRVTTDIISVANEDGRRVAAATLNHAHYLENLHFTI 2611
Db 2508 GAQSWLWFAVTKSLIGKVMNLAVSQGRVQTVNVLNANEDCIRKVAALNNAFLENLHFTI 2567
Qy 2612 DGVDTHYFVKPSPSEGLLAILGLSGGRTLENGVNVTSQINTVLNGRTRRYTDIQLQYQ 2671
Db 2568 EGKDTHYFKITTTPESDLTGLTLTSCRKALENGINVTVSQSTTVVNGRTRRPADVEMQFG 2627
Qy 2672 ALCLNTRYGTTLDEEKARVLEIARQAVROAWAREOQRUREBEGIRAMTEGSKQVLSL 2731
Db 2628 ALALHVRVGMWTLDEEKARILEQARALAREOQRVRDGBEGARLWTEGSKROLLSA 2687
Qy 2732 GRVQYDGFVFSVEQYPELSDSANNHFMROSEMR 2769
Db 2688 GRVQYDGFVFSVEQYPELSDSANNHFMROSEMR 2725

RESULT 13

ADH41999

ID ADH41999 standard; protein; 2725 AA.

XX ADH41999;

XX AC

DT 25-MAR-2004 (first entry)

XX Novel human protein NOV40h #2.

DE cardiovacular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
XX KW

Db 369 -----DNKLGFTQENNTIDSGELDIGRRAIQIBPPIFWRSQLFIDQPQFLK 417
Qy 466 FNVSLGKAALVGYIRKGLPPSHT---OPDFVELLDGRELLOEARSLEGTQRQSGTV 521
Db 418 FNISLQKDALIGVYGRKKLPPSHQSSPQDFVELLDGSLRIAREORSLETERAGQAR 477
Qy 522 PPSHETGFTQYLDLSGIWHLAFYNDGKESVWFLTTAIBSVNCPSCNYGNGDCISGTC 581
Db 478 SVSLHEAGFTQYLDLSGIWHLAFYNDGKNAEQVSFNTIVIESVVECPNCHNGNECVSGTC 537
Qy 582 HCFGLFGLPGDGRASCPVLCSGNGQYMKGRCLCHSGWKGAECDPVNTQCIDVACSHGTC 641
Db 538 HCFPGFLPGDGRASCPVLCSGNGQYMKGRCLCHSGWKGAECDPVNTQCIDPQCGRGIC 597
Qy 642 ITGTCICNPYKESCEEVDCMPTCSGRGVYRGEGCHFCFVGNGTNCETPRATCLDQCS 701
Db 598 IMGSCASSGYKESCEADCIIPGCSNHGVCIHGECHCPGNGGNCCEILKTMCPDOCS 657
Qy 702 GHGTFPLPDTGLCSDPSWTHGDCSIEICAAADCGHGVYCGGTGCRCEBGMGAACDQACH 761
Db 658 GHGTYLOESGSCDTPNMTGPDCSNEICSVDCSGHGVCMGGTCRCBEGMTGPACNQACH 717
Qy 762 PRCAEHGTCRDKCECSPGNGBHCCTIAHYLDVV-----KEGCPGLCNGNGRCTLDLN 815
Db 718 PRCAEHGTCRDKCECSPGNGBHCCTIAHYLDKIVKDKIGYKEGCPGLCNSNGRCTLDOQ 777
Qy 816 GWHVCOLGHRGACDTSMETACGDSKNDGDGGLVDCMDPCCLOPLCHINPLCLGSPNP 875
Db 778 GHGVCVQPGRGAGCDVAMETLCTDSKXNDEGDLDCMDPCCLOQSSCQNPYCRGLPDP 837
Qy 876 LDIIQETQVPVSOQNLSHFYDRKFLVGRDSTHIIIPGENPFDGCHACVIRGOVMTSDGTP 935
Db 838 QDIISQSLQSPQQAASFFDRISFLIGSDSTHVIPGESFPNKSASVIRGOVLTADGTP 897
Qy 936 LVGNISFVNNPLFGYITISRDQGSFDLVNNGGISILRPERAPFITQETHLWLPWRFFV 995
Db 898 LIGVNVSFHYPEGYITITRDQGMFDLVANGGASLTVFERSPFLTQYHTWIPWNVFV 957
Qy 996 METIIMRHEBNEIPSCDLSNFARPNPVVSPSLTSPASSCAEKGPVIVPEIQALQEELIS 1055
Db 958 MDLVMEKEENDIPSCDLSGFVRPNPIIVSPSLTSPFRSPSPEDSPIIPETQVLIHEETIP 1017
Qy 1056 GCKMRLSYLSRTPGYKSLRISLTHPTIPFNLMKVLHMAVAGERLPRKFWFAAPDLSYY 1115
Db 1018 GTDLKLSYLSRAAGYKSVLKITWQSIIPFNLMKVLHMAVVGRLEFQKFPFASPLAYT 1077
Qy 1116 FIWDKTDVYNQKVFGLSEAFVSVGYEYESCDPLILMEKRTTVLQGYEIDASKLGGNSLDK 1175
Db 1078 FIWDKTDVYNQKVFGLSEAFVSVGYEYESCDPLILMEKRTTVLQGYEIDASKLGGNSLDK 1137
Qy 1176 HHALNIOGILHKGNGENQFVSQOPPVIGSIMNGRRRSISCPSCNGLADGNKLLAPVAL 1235
Db 1138 HHVLVDQNGILYKNGENQFISQOPPVVVSIMNGRRRSISCPSCNGQADGNKLLAPVAL 1197
Qy 1236 TCGSDGSLYVGDNFYIRIIPSGNVNWIILRNKDFRSHSPAHKYLYATDPMGSAVFLS 1295
Db 1198 ACGIDGSLYVGDNFYIRIIPSGNVISVLELRNKKDFRSHSNPAHYLYATDPTVGDLYVS 1257
Qy 1296 DSNRRRVFKIKSTVVVKDLVKNSEVAVAGTGDQCLPFDTRCGDGKATEATLTPRGITV 1355
Db 1258 DTNTRRIYRPKSLTGAKDLTKNAEVAVAGTGEQCLPFDEARGDGGKAVEATLMSPKGMV 1317
Qy 1356 DKFGLIYFVGTMTIRRDQNGIISTLLGSNDLTSARPLSCDSVMDISQVLEWPTDLAIN 1415
Db 1318 DKNGLIYFVGTMTIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVLEWPTDLAIN 1377
Qy 1416 PMDNLVLDNNVVLQISENHQVRIVAGRPMHCOVPGIDHFLSKVAIHATLESATALAV 1475
Db 1378 PMDNLVLDNNVVLQITENQVRIIAAGRPMHCOVPGVE-YPVGKHAVQTTLESATALAV 1436
Qy 1476 SHNGVLYAETDEKINRIQVTTSGBISLVAGAPSCDCKNDANCDCFSGDGDGYAKDAK 1535
Db 1437 SYSGVLYITETDEKINRIQVTTDGBISLVAGIPSCDCKNDANCDYQSGDGDGYAKDAK 1496

Qy 1536 LNTPSSLAYCADGELYVADLGNIRIRIFIRKNKPFPLNTQNMYSBELSSPIDQELYLFDTTGKH 1595
Db 1497 LSAPSSLAASPDGTLVIADLGNIRIRAVSKNPKLLNSMNFYEVASPTDQELYFIDNGTH 1556
Qy 1596 LYTQSLPTGDYLYNFYITGDDITLITDNGNVMNVRRDSTGMPMLVVPDGOVYVWTMG 1655
Db 1557 QYTVSLVTGDYLYNFYSNDNDITAVTDSNGNLTIRIRDPNRMFVRVVPDGOVILWTIG 1616
Qy 1656 TNSALKSVTTQGHLEAMTYHNGSGLLATKSNENGWMTTFEYDVSFGLRNTNVTPTQOVSS 1715
Db 1617 TNGCLKGMTAQGULVLFTYHNGSGLLATKSBETGWTTFEYDVSSEGLRNTNVTPTGVVN 1676
Qy 1716 FRSDTDSVHVQVETSSK-DDVTITTNLSASGAFYTLQDQVRNSYYIIGADGSLRLLAN 1774
Db 1677 LHGDMDKAITVDIESSREEDVSITNLSSIDSFYTMVQDLRNSYQIGDGLRIYAS 1736
Qy 1775 GMEVALQTEPHLLAGTVNVTGKBNVTLPIDNGLNLEVORKEOARGOVTVFGRRLRVH 1834
Db 1737 GLDSHYQTEPHVLAGTANPTVAKRNMTPGNGQNLVEWFRKBOAQGVNVPFGRKLVRN 1796
Qy 1835 NRNLLSLDFDRVTRTEKIYDDHRKFTLRILYDOAGRPSLWSPSSRLNGVNVYSPGQYIA 1894
Db 1797 GRNLLSVDFRRTTKTKIYDDHRKFLRLRAYDTSCHPTLWLPSKLMANVNTYSSGQIA 1856
Qy 1895 GIQRGIMSRMEYDOAGRITSRIFADGKTWSTYLEKSMVLLHLSQRYVIFEPDKNDRLS 1954
Db 1857 SIQRGTTSEKVDYDQGRIVRSRVFADGKTWSTYLEKSMVLLHLSQRYVIFEDMDMDRLS 1916
Qy 1955 SVTMPNVAROTLETIRSVGYRNIYOPPEGNASVIOQFTEDDGHLHLLTFYLGTCRRVLYKY 2014
Db 1917 AITMPSVARHTMQTIRSIGYRNIYNPPESSNASIITDYNEBEGLLQTAFLTSRRVLPKY 1976
Qy 2015 GKLSKLAETLYDTTKVSYFYDETAGMLKTINLQNEGFTCTIRYRQJGLPLDROI FRTEE 2074
Db 1977 RQTRUSEILYDSTRVSFTYDETAGLVKTVNLQSDGFCITIRYRQJGLPLDROI FRPES 2036
Qy 2075 GVMNARFDYNDONSFRVTSNQAIVNETPLPIDLYRYDDVSGKTEQFGKFGVYIYDINOII 2134
Db 2037 GVMNARFDYNDONSFRVTSNQAIVNETPLPIDLYRYDDVSGKTEQFGKFGVYIYDINOII 2096
Qy 2135 TTAVMTHTKHFDAYGRMKEVQYEIFRSLMWTMTVYDNNMGRVVKELKVGPIYANTYYSY 2194
Db 2097 STAVMTYTKHFDAHGRKEIQYEIFRSLMWTMTVYDNNMGRVVKELKVGPIYANTYYSY 2156
Qy 2195 EYDADGLOQTVSINDKPLARYSYDGLNHLHLSPGNSARLTPLRYDIRDRITRLGDVQYK 2254
Db 2157 EYDADGLOQTVYLNEXIMWRNYDNLGNLHLLNPSNSARLTPLRYDIRDRITRLGDVQYK 2216
Qy 2255 MDEDGFLRORGGDIFEYNSAGLLIKAYNRAGSWSRYRYDGLGRRVSSKSSHSHHLLQFFY 2314
Db 2217 LDEDGFLRORGGDIFEYNSAGLLIKAYNRAGSWSRYRYDGLGRRVSSKSSHSHHLLQFFY 2276
Qy 2315 ADLTNPTKVTYHLYNHSSEITSYLDLQGHLPAMELSSGDEFYIACNITGTPPLAVPSGTG 2374
Db 2277 ADLTNPTKVTYHLYNHSSEITSYLDLQGHLPAMELSSGDEFYIACNITGTPPLAVPSGTG 2336
Qy 2375 LMIKQIILYTAGYIYMDTPNFQIIGYHCGLYDPLTKLHVMMGRDYDVLAGRWTSPDHE 2434
Db 2337 LMIKQIILYTAGYIYMDTPNFQIIGYHCGLYDPLTKLHVMMGRDYDVLAGRWTSPDHE 2396
Qy 2435 LWKHLSSSNVMPNPNLWYKNNPISNQDIKCFMTDVNSMLLTFGQLHNVIPGYKPKDM 2494
Db 2397 IWKRI-GKDPAPNPNLWYKNNPISNQDIKCFMTDVNSMLLTFGQLHNVIPGYKPKDM 2455
Qy 2495 DAMEPSYELIHTQMKTEQWDNKSIILGVQCEVQKQKAFVTLERFPOLYGSTTSCQAP 2554
Db 2456 DLTEPSYELV---KSQWDDIPPIFGVQOQVARQAKAFSLGKMAEVQ----VSRRRAG 2507
Qy 2555 KTKK---FASGSGVFGKGVKFAKDGRTVTDIISVANEDGRRVAAIILNHAHYLENLHFTI 2611
Db 2508 GAQSWLWFAVTKSLIGKGVMLAVSQGRVQTNVLNIANEDCICKVAALNNAFYLENLHFTI 2567

Db 61 NRVKDLVHREADEFTROQCNFTLRQLGVCBPATRRGLAFCAEMGLPHRGYSISAGSDADT 120
Qy 118 EADTVLSPREHVPRLWGRSTSGRSSCLSSRANSLTLTDTHEHN---TETHDPGGQLNHA 174
Db 121 ENBAVMSPEHMLWGLVSGRSSCLSSRANSLTLTDTHEHNKSDSENEQSPASQOGQS 180
Qy 175 RLRTPPPLSHAHTPNQHHASINSLNRGNFTPRSNPSPAPTDSHLSGEPAGGAQ----230
Db 181 TLQPLPP--SHKQHSQAHH--PSITSLNRLNSLTNRNQSAP-----PAALPAELQTT 229
Qy 231 -EPAHQENWLLNSNIPLETRNLGKQPLGLTLQDNLIEMDILGASHDGAYSOGHFLFKP 289
Db 230 PESVQLQDSWVLGNSVPLESR-----HFLFKT 256
Qy 290 G-GTSPLEFCTTSCYPLTSTSVYSPPPRPLPRSTFEARPAFLKPKSKYCNWKAALSAIV 348
Db 257 GTGTTPPLFSTATPGYTWASGVSPPTPLPRNLTLRSAPFKKSKYCSWKCTALCAVG 316
Qy 349 ISATVLILLAYFVAMHLFGLNWLQPMEGQMYE---ITEDTASSWPVPTDVSLYPSGGTG 405
Db 317 VSVLLAALLSYFAMHLFGLNWLQQTENDTFENGKYNST-----MPTNVTSLPSG---368
Qy 406 LETPDRKGKGTTEGKPSFPPEPSFIDSGEIDVGRRASQKIPPGTFWRSQVFDHPVHLK 465
Db 369 -----DNKLGFTQENNTIDSGELDIGRRAIQBIPIPGIFWRSQLFIDQPOFLK 417
Qy 466 PNVSGLKAALVGIYGRKGLPSHT-----QDFVELLDGRLLTQEARSLGTPRQSGTV 521
Db 418 FNISLOKDALIGVYGRKGLPSHTQSSPQYDFVELDGRLLIAREQSRSLLETERRAGQAR 477
Qy 522 PPSHETGFTQYLDGSGIWHLAFYNDGKSEVWSPLTAAIESVNCPNCGNCGDCISGTC 581
Db 478 SVSLHEAGFTQYLDGSGIWHLAFYNDGKNAQVSEFNTVIESVVECPNCHNGNECVSGTC 537
Qy 582 HCFGLFGLPGCGRASCVPVLCGNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGT 641
Db 538 HCFPGFLGPCSRAACVPVLCGNGQYSGKRCCLFCFSGWKGTEDCVPTTQCIDPQCGGRGIC 597
Qy 642 ITGTCINPGYKGESCEVDCMDPTCSGRGVCVRGECHECFVGGTNCETPRATCLDOCS 701
Db 598 IMGSCACSGYKGESCEADCIDPGCSNHGVCITHGECHCPGWSGNSCEILKTMCPDQCS 657
Qy 702 GHGTFLPDTGLCSDPWSWTGHDCSIEICAADCGHGVCGVGTCECDGWMGAACDORACH 761
Db 658 GHGTYLQESSCTCDPNTWTPDCSNEICSVDCSGHGVCMGTCECEBGTGPGACNQRACH 717
Qy 762 PRCAEHGTCRDGKCECPGNGEHCITIAHYLDRVV-----KBCPGCLNGNGRCTLDLN 815
Db 718 PRCAEHGTCRDGKCECSQGWNGEHCITIAHYLDKIVDKIGYKCGCPGLCNSNGRCTLDN 777
Qy 816 GWHCVCOLGWRGACDTSMETACGDSKONDGDGLVDCMDPCCLQPLCHINPLCLGSPNP 875
Db 778 GGHCVCPQWRGAGCDVAMETLCTDSDKDNEDGLIDCMDPCCLQSSCQNPQYCRGLPDP 837
Qy 876 LDIIQETQVPSVQONLHSEFYDRIKFLYGRDSTHIIIPGENPFDGHCACVIRGVNMTSDGTP 935
Db 838 QDIISLQSQSPQAASFFDRIISFLGSDSTHVPGESFPNKSASVIRGOVLTAUTGP 897
Qy 936 LVGVNISFVNPNPLFGYITISROGSDFLVTNGGIIILRFERAPFIQIETHLWLPWDFV 995
Db 898 LIGVNVSFHYPEYGYITIQDGMFDLVANGGASLTLVFRSPPLTYHTVWPWNVFY 957
Qy 996 METIMRHEBNEIPSCDLSPARNPNPVVSPSLTSPASSCAEKGPVPEIQALQEBEISIS 1055
Db 958 MDTLVMEKEENDIPSCDLSPVRPNPIIVSSPLSTFFRSPSPEDSPIPETQVLHEETIP 1017
Qy 1056 GCKMRLSVLSRTPGYKSVLRIISLTHPIIPNLMKVHLMAVAGRLFRKWFAPAADLSY 1115
Db 1018 GTDULKLSYLSRAAGYKSVLKITMQSIIIPNLMKVHLMAVAGRLFKQFPFAPSNLAYT 1077
Qy 1116 FIWKTDTVYNQKVFGLSEAFVSGYEYESCPDLTLWEKRTTTLQGYEIDASKLGWSLDK 1175
Db 1078 FIWKTDTAYNQKVGLESAVVSGYEYESCLDLTLWEKRTAILQGYELDASNMGWTLDK 1137

Qy 1176 HHALNIQSGILKHKGNGENQFVSQQPEVIGSIMGNRRRSISCPSCNGLADGNKLLAPVAL 1235
Db 1138 HHVLDVQNGILYKNGENQFISQQPPVSSIMGNRRRSISCPSCNQADGNKLLAPVAL 1197
Qy 1236 TCGSDGLYVGFDPNYIRRIFFPSGNVTNILELRNKDPRHSHSPAKEYLATDPMGAVFLS 1295
Db 1198 ACCIDGSLYVGFDPNYIRRIFFPSGNVTSVLELRNKDPRHSSNPAHRYLATDPTVTDGLYVS 1257
Qy 1296 DNSRRVFXIKSTVVVKDLVKNSVAVAGTGDOCLPFDDTRCGDGKGKATEATLNPGRITV 1355
Db 1258 DYNTRIYIPKSLTGAKDLTKNAEVVAGTGEQCLPFDEARCGDGKGKAVATLNSPKGMV 1317
Qy 1356 DKFGLYFYVDGTMIRIDQNGIISTLLGSDNLTARSAPLSCDSVMDISQVRLEWPTDLAIN 1415
Db 1318 DKNGLIYFYVDGTMIRKVDQNGIISTLLGSDNLTARSAPLTCDSMHISQVRLEWPTDLAIN 1377
Qy 1416 PMDNSLYVDNNVVOIQRSENHQRVIRVAGPMHCQVPGIDHFLLSKVIAHTLESATALAV 1475
Db 1378 PMDNSIYVDNNVVOIQRSENHQRVIRVAGPMHCQVPGVE--YPVGKHAVQTLESATAIIV 1436
Qy 1476 SHNGVLYIAETDEKKINRIROVTTSGEISIVAGAPSGCDCKNDANDCDFSGDDGYAKDAK 1535
Db 1437 SYSGVLYIITETDEKKINRIROVTTDGEISIVAGIPSECDCKNDANDCCDYOSGDDGYAKDAK 1496
Qy 1536 LNPSSSLAVACDGEYVADLGNIRIRIFIRKNKPFPLNTONMYELSSPIDOELYLFTDTGKH 1595
Db 1497 LNPSSSLAASPDTGLYIADLGNIRIRAVSKNKLNSMNFYEVASPTDOELYFIDINGTH 1556
Qy 1596 LYTQSLPTGDYLYNFYTGDDITLITDNGNMVNRVRRSTGMPMLVLPDQGVYVWTMG 1655
Db 1557 QYTVSLVTDGDLNFYSFNSDNDITAVTDSNGNLTIRRRDPNRPVRSVSPDNQVILWTIG 1616
Qy 1656 TNSALASVTTQGHSLAMVTHGNSGLATKSNENGWTTTFVEYDSFGLTNVTPTGQVSS 1715
Db 1617 TNGCLGKMTAQAGLELVLFYTHGNSGLATKSDGTWTTTFDYDSBGLTNVTPTGVTN 1676
Qy 1716 FRSDTSSVHVQVETSSK--DDVTITNLSASGAFYTLLOQVRSNYIYGADGSLRLLLAN 1774
Db 1677 LHGDMDKAITVDIESSREEDVSITNSLSDISFYTWQDLNSYQIYDGSRLRIYAS 1736
Qy 1775 GMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWRQKEQARGQVTVFGRRLRVH 1834
Db 1737 GLDSHYQTEPHVLAGTANPTVAKRNMTLPGENQNLVEWRFRKEQAGKKNVFGKRLVN 1796
Qy 1835 NRLLSLDPRVTRTEKIIDHKKFTLRILLYDOAGRPSLWSPSSRLNGVNVTVSPGVI 1894
Db 1797 GRNLLSVDFDRTTKTEKIIDHKKFLLRITAYDTSGHPTLWLPSSKLMVNVTVSSSQIA 1856
Qy 1895 GIQRGLMSRMEYDQAGRITSIRIFADGKTSYTYLEKSMVLLHLSQRYIFEFDKNDRLS 1954
Db 1857 SIQRGTTSEKVDYDQGRIVSRVFDGKTSYTYLEKSMVLLHLSQRYIFEYDMWDL 1916
Qy 1955 SVTMPNVARQTLTIRSVGYRNIYQPEGNASVIOQFTEDGHLLHFFYTGRRVYKY 2014
Db 1917 AITMPSVARHTMQTIRSIGYRNIYNPPESNASIIITDYNBEGLLQTAFLGTSSRVLFKY 1976
Qy 2015 GKLSKLAETLYDTKVSFYDETAGLKTINLQNEGFTCTIRYRQIGPLDROIREFTEE 2074
Db 1977 RRQTRLSEILYDSTRVSFTYDETAGLKTVNLQSDGFICTIRYRQIGPLDROIREFSED 2036
Qy 2075 GMYNARFDYNDNSFRVTSMOAVINETPLIDLYRYDDVSGKTEQFGKFGVYVDINQII 2134
Db 2037 GMYNARFDYNDNSFRVTSMOAVINETPLIDLYQFDDISGKVEQFGKFGVYVDINQII 2096
Qy 2135 TTAVMTHTHKFDAYGRMKEVQYBEIFRSLYMTVYDNNMGRVVKELKVGYPANTTRYSY 2194
Db 2097 STAVMTYTHKFDAGRIKEIQYBEIFRSLYMTIITQDNNMGRVTKREIKIGFANTTKYAY 2156
Qy 2195 EYDADQOLQTVSINDPLWRYSYDLNGLNHLSPGHSARLTPLRYDIRDRITRLGDVOYK 2254
Db 2157 EYDVGQLOQTYYLNEKIMRWYNDLNGNHLNPSNSARLTPLRYDRDLRITRLGDVOYR 2216

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2005, 17:39:23 ; Search time 41 Seconds
(without alignments)
6498.152 Million cell updates/sec

Title: US-10-029-020-14
Perfect score: 14887
Sequence: 1 MDVKERKPYRSLTRRRDAER.....ELSDSANNIHFMRQSEMGR 2769

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------|--------------------|
| 1 | 14269 | 95.8 | 2825 | T14271 | Doc4 protein, stre |
| 2 | 3804.5 | 25.6 | 2515 | S47008 | tenascin-like prot |
| 3 | 3515.5 | 23.6 | 2406 | A54148 | odz protein - fru |
| 4 | 3111.5 | 20.9 | 849 | T46253 | hypothetical prote |
| 5 | 2109 | 14.2 | 2531 | T16743 | hypothetical prote |
| 6 | 1175.5 | 7.9 | 782 | A61625 | tenascin-like prot |
| 7 | 943 | 6.3 | 184 | T12457 | hypothetical prote |
| 8 | 659.5 | 4.4 | 2019 | JQ1322 | tenascin precursor |
| 9 | 652 | 4.4 | 1746 | S19694 | tenascin precursor |
| 10 | 649.5 | 4.4 | 2201 | A32160 | tenascin-C - human |
| 11 | 641 | 4.3 | 1810 | A32230 | tenascin precursor |
| 12 | 626 | 4.2 | 4006 | T09070 | probable tenascin |
| 13 | 592 | 4.0 | 3566 | A40701 | tenascin-X precurs |
| 14 | 577.5 | 3.9 | 647 | A43902 | tenascin - eastern |
| 15 | 572.5 | 3.8 | 4135 | T42629 | tenascin-X - bovin |
| 16 | 438.5 | 2.9 | 2703 | A24420 | notch protein - fr |
| 17 | 429 | 2.9 | 2524 | A35844 | Xotch protein - Af |
| 18 | 428.5 | 2.9 | 2555 | A40043 | notch protein homo |
| 19 | 427.5 | 2.9 | 2531 | A46019 | notch-1 protein - |
| 20 | 424 | 2.8 | 1203 | A49175 | Notch B protein - |
| 21 | 423.5 | 2.8 | 1064 | A40136 | fibropellin Ia - s |
| 22 | 422.5 | 2.8 | 2531 | S18188 | notch protein homo |
| 23 | 422 | 2.8 | 1620 | T27283 | hypothetical prote |
| 24 | 420 | 2.8 | 2471 | A49138 | cell-fate determin |
| 25 | 419.5 | 2.8 | 1220 | A56136 | jagged protein pre |
| 26 | 413 | 2.8 | 2437 | S42612 | transmembrane prot |
| 27 | 410 | 2.8 | 3191 | T22945 | hypothetical prote |
| 28 | 400.5 | 2.7 | 1295 | A32901 | Gip1 protein precu |
| 29 | 399 | 2.7 | 2531 | T31070 | notch homolog - se |

| | | | | | | |
|----|-------|-----|------|---|--------|--------------------|
| 30 | 392.5 | 2.6 | 1353 | 1 | JH0675 | restrictin precurs |
| 31 | 392.5 | 2.6 | 2321 | 2 | S78549 | notch3 protein - h |
| 32 | 388 | 2.6 | 1574 | 2 | T13954 | MEGF6 protein - ra |
| 33 | 387.5 | 2.6 | 1722 | 2 | E89753 | protein F11C7.4 [i |
| 34 | 387.5 | 2.6 | 1964 | 2 | T09059 | notch4 - mouse |
| 35 | 385.5 | 2.6 | 1356 | 2 | A45445 | janusin precursor, |
| 36 | 384 | 2.6 | 2318 | 2 | S45306 | notch 3 protein - |
| 37 | 383 | 2.6 | 1408 | 2 | S16148 | gene serrate prote |
| 38 | 382.5 | 2.6 | 2139 | 2 | A35672 | crumbs protein - f |
| 39 | 382 | 2.6 | 2352 | 2 | T30201 | Notch homolog prot |
| 40 | 381 | 2.6 | 861 | 2 | A48825 | Notch homolog Motc |
| 41 | 373.5 | 2.5 | 833 | 2 | S19087 | gene Delta protein |
| 42 | 372.5 | 2.5 | 832 | 2 | A31246 | neurogenic protein |
| 43 | 372.5 | 2.5 | 880 | 2 | S00670 | neurogenic repetit |
| 44 | 369.5 | 2.5 | 1111 | 2 | T26972 | hypothetical prote |
| 45 | 356.5 | 2.4 | 473 | 2 | A56175 | adhesive plaque pr |

ALIGNMENTS

RESULT 1

T14271

Doc4 protein, stress-induced - mouse
N;Alternate names: odz protein homolog
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14271

R;Wang, X.Z.; Kuroda, M.; Sok, J.; Batchvarova, N.; Kimmel, R.; Chung, P.; Zinszner, H.;
EMBO J. 17, 3619-3630, 1998
A;Title: Identification of novel stress-induced genes downstream of chop.
A;Reference number: Z17951; MUID:98315054; PMID:9649432
A;Accession: T14271
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2825 <WAN>
A;Cross-references: UNIPROT:O70465; UNIPARC:UPI00000294B0; EMBL:AF059485; NID:g3170614;
C;Genetics:
C;Gene: Doc4

Query Match 95.8%; Score 14269; DB 2; Length 2825;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 2654; Conservative 47; Mismatches 52; Indels 88; Gaps 4;

| | | | |
|----|-----|--|-----|
| Qy | 1 | MDVKERKPYRSLTRRRDAERRTSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV | 60 |
| Db | 1 | MDVKERKPYRSLTRRRDAERRTSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV | 60 |
| Qy | 61 | KDIVPQEAEEFCRTGANFTLRELGLBEVTPPHGTLVYRTDGLPQCGYSGAGSDADMEAD | 120 |
| Db | 61 | KDINVQEAEEFCRTGNTFTLRELGLGEMTPPHGTLVYRTDGLPHCGYSGAGSDADLEAD | 120 |
| Qy | 121 | TVLSPEHPVRLWGRSTRSGRSSCLSRANSNLTLTDEHENTET----- | 164 |
| Db | 121 | TVLSPEHPVRLWGRSTRSGRSSCLSRANSNLTLTDEHENTETGAPLHCSSASSTPIEQ | 180 |
| Qy | 165 | -----DHPGGL | 170 |
| Db | 181 | SPSPPPPPANESQRRLLNGVQAQPTDSDSEEFVNSFLVSGSASLGVANDHPSLL | 240 |
| Qy | 171 | QNHARLTTPPPPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDLHSLSGEPAGGAQ | 230 |
| Db | 241 | QNHPRLETTPPPPLPHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDLHSLSGEPAGGAQ | 300 |
| Qy | 231 | EPAAHGNWLLNSNIPLETNKGQPLGTQONLIEMDILGASRHDCAYSDGHFLKPG | 290 |
| Db | 301 | EPTHAQDNWVLNSKIPVETRNKGQPLGTQONLIEMDIFASARRDGYSDGHFFKPG | 360 |
| Qy | 291 | GTSPFLCTTSPGVLTSSTVYSPRPLPRSTFARPAFLNKPSKYNWKAALSAIVIS | 350 |
| Db | 361 | GTSPFLCTTSPGVLTSSTVYSPRPLPRSTFARPAFLNKPSKYNWKAALSAIVIS | 420 |
| Qy | 351 | ATLVILLAYFVAMHLFGLNWLQPMEG--QWYEITETASSWPVPTDVSLYPSGGTGLT | 408 |

| | | | | | | | | |
|----|--|------|--|------|----|------|---|------|
| Db | | 421 | ATLVILLAYFVAMHFLGLENHLOPMEGQOMYEITEEDTASSWPVPTDVSLYPSGGTGLET | 480 | Db | 1485 | VLOISENHQVRIIVAGRPMHCQVPGIDQFLLSKVAIHATLESATALAVSHNGVLYIAETDE | 1544 |
| Qy | | 409 | PRKKGKTEGKPSFFEDSIDSGEIDVGRASQKIPPGTFWRSQFIDHPVHLKFN | 468 | Qy | 1489 | KKINRIQVTTSGEISIVAGAPSGCDCKNDANCCFSGDDGYAKDAKLNTSSSLAVCADG | 1548 |
| Db | | 481 | PDRKGGAEGKPSLFPEDSIDSGEIDVGRASQKIPPGTFWRSQFIDHPVHLKFN | 540 | Db | 1545 | KKINRIQVTTSGEISIVAGAPSGCDCKNDANCCFSGDDGYAKDAKLNTSSSLAVCADG | 1604 |
| Qy | | 469 | SIGKAALVGIYGRKGLPPSHTOFDFVELLDGRLLLTQBARSLLEGTPROSRTGVPSPSSHET | 528 | Qy | 1549 | ELYVADLGNIRIRFIRKKNKPFNTQNNYELSSPIDQELYLFPDTSQKHLTYTQSLPTGDIYLY | 1608 |
| Db | | 541 | SUGKAALVGIYGRKGLPPSHTOFDFVELLDGRLLLTQBARSLLEGTPROSRTGVPSPSSHET | 600 | Db | 1605 | ELYVADLGNIRIRFIRKKNKPFNTQNNYELSSPIDQELYLFPDTSQKHLTYTQSLPTGDIYLY | 1664 |
| Qy | | 529 | GFIQYLDGSIWHLAFYNDKSEVSVFLTTAIESVDNCPSCYNGDGCISGTCCHCFLGFL | 588 | Qy | 1609 | NFTYTGDDITLITDNNGNMNVNRDSTGMPDLWLVPDQVYVWVTMGNTNSALKSVTTTQGH | 1668 |
| Db | | 601 | GFIQYLDGSIWHLAFYNDKSEVSVFLTTAIESVDNCPSCYNGDGCISGTCCHCFLGFL | 660 | Db | 1665 | NFTYTGDDITLITDNNGNMNVNRDSTGMPDLWLVPDQVYVWVTMGNTNSALKSVTTTQGH | 1724 |
| Qy | | 589 | GPDCGRASCPVLCSNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCTIGTCTIC | 648 | Qy | 1669 | ELAMWYTHGNSGLLATKSNENGWTTFFEYDSFGRLTNVPTFGOVSSFRSDTSSVHVQV | 1728 |
| Db | | 661 | GPDCGRASCPVLCSNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCTIGTCTIC | 720 | Db | 1725 | ELAMWYTHGNSGLLATKSNENGWTTFFEYDSFGRLTNVPTFGOVSSFRSDTSSVHVQV | 1784 |
| Qy | | 649 | NPGYKGESCEEVDCMDPTCSGRGVCVRGCHCFVGMGGTNCETPRATCLDQCSHGHTFLP | 708 | Qy | 1729 | ETSSKDDVTITNLSASGAFYTLLOQDVNRNSYIIGADGSLRLLLANGMEVALQTEPHLLA | 1788 |
| Db | | 721 | NPGYKGESCEEVDCMDPTCSGRGVCVRGCHCFVGMGGTNCETPRATCLDQCSHGHTFLP | 780 | Db | 1785 | ETSSKDDVTITNLSASGAFYTLLOQDVNRNSYIIGADGSLRLLLANGMEVALQTEPHLLA | 1844 |
| Qy | | 709 | DTGLSCDPSWTHCHDCSIBICAADCGHGVCCVGGTCRCEDGMMGAACDQACHPCABHG | 768 | Qy | 1789 | GTVPNPTVGRNVTLPIIDNGLNLVWRQKEQARGQVTVFGRRLRVHNRNLLSLDPDRVTR | 1848 |
| Db | | 781 | DTGLCNCDPSTWTHCHDCSIBICAADCGHGVCCVGGTCRCEDGMMGAACDQACHPCABHG | 840 | Db | 1845 | GTVPNPTVGRNVTLPIIDNGLNLVWRQKEQARGQVTVFGRRLRVHNRNLLSLDPDRVTR | 1904 |
| Qy | | 769 | TCRDKCEGSPGWNHEHTIAHYLDREVVKEGCPGLCNGNGRCTLIDNGWHCVCLGWGA | 828 | Qy | 1849 | TEKIYDDHRKFTLRILYDOAGRPSSLWSPSRLNGVNTYSPGGYTAGIQRGIMSRMEYD | 1908 |
| Db | | 841 | TCRDKCEGSPGWNHEHTIAHYLDREVVKEGCPGLCNGNGRCTLIDNGWHCVCLGWGA | 891 | Db | 1905 | TEKIYDDHRKFTLRILYDOAGRPSSLWSPSRLNGVNTYSPGGYTAGIQRGIMSRMEYD | 1964 |
| Qy | | 829 | GDTSMETACGSKNDGDLVDCMDPCCLQPLCHINPLCLGSPNPLDIIQETQVPSQ | 888 | Qy | 1909 | QAGRITSRIIPADGKTSYTYLEKSMVLLHSQRQYIFEFDKNDRLSSVTMPNVARQTLET | 1968 |
| Db | | 892 | GDTSMETCGGKNDGDLVDCMDPCCLQPLCHVNPCLGSPDPLDIIQETQAPVSO | 951 | Db | 1965 | QAGRITSRIIPADGKTSYTYLEKSMVLLHSQRQYIFEFDKNDRLSSVTMPNVARQTLET | 2024 |
| Qy | | 889 | QNLHSPFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNPL | 948 | Qy | 1969 | IRSVGYRNIIQOPPEGNASVIQDFTEDCHLLHTFVLGTGRBVIYKGLSKLAETLYDTT | 2028 |
| Db | | 952 | QNLHSPFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNPL | 1011 | Db | 2025 | IRSVGYRNIIQOPPEGNASVIQDFTEDCHLLHTFVLGTGRBVIYKGLSKLAETLYDTT | 2084 |
| Qy | | 949 | PGYTTSRQDGSFDLVTNGGSIILPERAPFTIQEHTLWLPWDRFFVMBETIIMRHENEI | 1008 | Qy | 2029 | KVSFTYDGTAGMLKTINLQNEGFTCTIRYROIPLIDRQIRFRFTBEGMVNARFDYNDNS | 2088 |
| Db | | 1012 | PGYTTSRQDGSFDLVTNGGSIILPERAPFTIQEHTLWLPWDRFFVMBETIIMRHENEI | 1071 | Db | 2085 | KVSFTYDGTAGMLKTINLQNEGFTCTIRYROIPLIDRQIRFRFTBEGMVNARFDYNDNS | 2144 |
| Qy | | 1009 | PSCDLSNFRPNPVPVSPSLTSPASSCAEKGPVPEIOALQBEISISGCKMRLSYLSRT | 1068 | Qy | 2089 | FRVTSQMAVINETPLPIDLYRVDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAY | 2148 |
| Db | | 1072 | PRDLSNFRPNPVPVSPSLTSPASSCAEKGPVPEIOALQBEISISGCKMRLSYLSRT | 1131 | Db | 2145 | FRVTSQMAVINETPLPIDLYRVDVSGKTEQFGKFGVIYYDINQIITTAVMTHSKHFDAY | 2204 |
| Qy | | 1069 | PGYKSVLRISLTHPTIPFNLKMHLMVAVEGRLFRKWFAPAAAPDLSSYFIWDKTDVYNQKV | 1128 | Qy | 2149 | GRMEVQYIEIIRSLMYMNTVQYDNMGRVVKELKVGYPANTTRYSEYDADGQLQTVSIN | 2208 |
| Db | | 1132 | PGYKSVLRISLTHPTIPFNLKMHLMVAVEGRLFRKWFAPAAAPDLSSYFIWDKTDVYNQKV | 1191 | Db | 2205 | GRMEVQYIEIIRSLMYMNTVQYDNMGRVVKELKVGYPANTTRYSEYDADGQLQTVSIN | 2264 |
| Qy | | 1129 | FGLSEAFVSGVEYBSCPDLLIWEKRTTVLQGYEIDASKLGWSLDKHHALNIQSGILHK | 1188 | Qy | 2209 | DKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIDRDIRLGDVQYKMDDEDGLRQGGDI | 2268 |
| Db | | 1192 | FGLSEAFVSGVEYBSCPDLLIWEKRTTVLQGYEIDASKLGWSLDKHHALNIQSGILHK | 1251 | Db | 2265 | DKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIDRDIRLGDVQYKMDDEDGLRQGGDV | 2324 |
| Qy | | 1189 | NGENQFVSQPPVIGSIMGNGRRSISCPSCNGLADGNKLLAPALTCGSDGSLYVGDF | 1248 | Qy | 2269 | FEYNASAGLLIKAYNRAGSWSVRYDGLGRVSVSSKSSHLLQFFYADLTNPTKVTHLYN | 2328 |
| Db | | 1252 | NGENQFVSQPPVIGSIMGNGRRSISCPSCNGLADGNKLLAPALTCGSDGSLYVGDF | 1311 | Db | 2325 | FEYNASAGLLIKAYNRAGSWSVRYDGLGRVSVSSKSSHLLQFFYADLTNPTKVTHLYS | 2384 |
| Qy | | 1249 | NYIRRIFFPSGNVTNILELRNKDFRHSHPAHKYLLATDPMGSAVFLSDNSRRVFKIKST | 1308 | Qy | 2329 | HSSSEITSLYDLOQHFLFAMELSSGDEFEYIACDNIPTPLAVPSGTGLMIKQLIYATYGBI | 2388 |
| Db | | 1312 | NYIRRIFFPSGNVTNILELRNKDFRHSHPAHKYLLATDPMGSAVFLSDNSRRVFKIKST | 1364 | Db | 2385 | HSSSEITSLYDLOQHFLFAMELSSGDEFEYIACDNIPTPLAVPSGTGLMIKQLIYATYGBI | 2444 |
| Qy | | 1309 | VVVKOLVKNSEVAVGTGDCQLPDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDTGM | 1368 | Qy | 2389 | YMDTNPNFQIIGYHGGLYDPLTKLVHMGRRDYLVLGRWTSPLDHELWKHLSSSNVMPFN | 2448 |
| Db | | 1365 | TVVVKDLVKNSEVAVGTGDCQLPDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDTGM | 1424 | Db | 2445 | YMDTNPNFQIIGYHGGLYDPLTKLVHMGRRDYLVLGRWTSPLDHELWKHLSSSNVMPFN | 2504 |
| Qy | | 1369 | IRRIDQNGIISTLGSNDLTARSPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDNNV | 1428 | Qy | 2449 | LYMFKNPNPISNSQDIKCFMFTDVNSWLLTFCQLHNVIIPGYPKPMDAMEPSYELIHTQM | 2508 |
| Db | | 1425 | IRRIDQNGIISTLGSNDLTARSPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDNNV | 1484 | Db | 2505 | LYMFKNPNPISNSQDIKCFMFTDVNSWLLTFCQLHNVIIPGYPKPMDAMEPSYELIHTQM | 2564 |
| Qy | | 1429 | VLOISENHQVRIIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDE | 1488 | Qy | 2509 | KTQEWDNSSKILGVQCEVQKQKAPVTILERDOLYGSTITSQOQAPKTKKPASSGSVCK | 2568 |
| | | | | | Db | 2565 | KTQEWDNSSKILGVQCEVQKQKAPVTILERDOLYGSTITSQOQAPKTKKPASSGSVCK | 2624 |

| | | | |
|--|------|---|------|
| QY | 2569 | GVKFALKGCRVTTDIIISVANEDGRRVAAAILNHAHYLENLHFTIDGVTHYFVKPGPSEGD | 2628 |
| Db | 2625 | GVKFALKGCRVTTDIIISVANEDGRRVAAAILNHAHYLENLHFTIDGVTHYFVKPGPSEGD | 2684 |
| QY | 2629 | LAILGLSGRRRLTENGVNVTYSQINTVLNGRTRRTYDLOLQYALCLNTRYGTTLDDEKA | 2688 |
| Db | 2685 | LAILGLSGRRRLTENGVNVTYSQINTVLNGRTRRTYDLOLQYALCLNTRYGTTVDDEKV | 2744 |
| QY | 2689 | RULELARQAVRQAWAREOORLREBEGELRAWTEGKQOVLSTGRVQGVYGFVVISVEQY | 2748 |
| Db | 2745 | RULELARQAVRQAWAREOORLREBEGELRAWTEGKQOVLSTGRVQGVYGFVVISVEQY | 2804 |
| QY | 2749 | PELSDSANNIHPWRQSEMGR | 2769 |
| Db | 2805 | PELSDSANNIHPWRQSEMGR | 2825 |
| RESULT 2 | | | |
| S47008 | | | |
| tenascin-like protein - fruit fly (<i>Drosophila melanogaster</i>) | | | |
| C;Species: <i>Drosophila melanogaster</i> | | | |
| C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004 | | | |
| C;Accession: S47008 | | | |
| R;Baumgartner, S.; Martin, D.; Hagios, C.; Chiquet-Ehrismann, R. | | | |
| EMBO J. 13, 3728-3740, 1994 | | | |
| A;Title: Ten(m), a <i>Drosophila</i> gene related to tenascin, is a new pair-rule gene. | | | |
| A;Reference number: S47008; MUID:94349920; PMID:8070401 | | | |
| A;Accession: S47008 | | | |
| A;Status: preliminary | | | |
| A;Molecule type: mRNA | | | |
| A;Residues: 1-2515 <BAU> | | | |
| A;Cross-references: UNIPROT:Q24551; UNIPARC:UPI00000508DE; EMBL:X73154; NID:g510505; PID | | | |
| C;Genetics: | | | |
| A;Gene: FlyBase:Ten-m | | | |
| A;Cross-references: FlyBase:FBgn0004449 | | | |
| F;298-324/Domain: EGF homology <EGF> | | | |
| F;394-421/Domain: EGF homology <EGF1> | | | |
| Query Match 25.6%; Score 3804.5; DB 2; Length 2515; | | | |
| Best Local Similarity 33.2%; Pred. No. 7e-204; | | | |
| Matches 818; Conservative 497; Mismatches 969; Indels 181; Gaps 54; | | | |
| QY | 384 | EDTASSWPPTDVSLYPSGGTGLTDPDRKGKTTEGKPSPPDFSIDSGEIDVGRAS | 443 |
| Db | 131 | EATSSAATSSQSLSLTPSLSSLANANGARTF---PARSEPPDG-TTFQGIILGQKLT | 186 |
| QY | 444 | QKIPPGTFWRQSVFIDHPVHLKFNVLGKAALVGIGYGRKGLPPSHQTFDVELLDGRLL | 503 |
| Db | 187 | KEIQPSYNNMQFYQSEPAVVKFDYTI PRGASIGVYGRNALPTHTQYHKEVLSGFAS | 246 |
| QY | 504 | TQARS--LEGTPRQSGTVPPSSHETGFIQYLDGSIWHLAFYN--DGKSEVSWFLTAT | 560 |
| Db | 247 | TRTARAHLISITREVTR-----YMEPGHMFVSLYNDGDGVQBELTFVAAAE | 292 |
| QY | 561 | ESVDNCPSCYNGDCISGTCHCFLGLPDCGRASCPVLCSGQYMKGRCLCHSGWK | 620 |
| Db | 293 | DMTQNCPCGSGNGQCLGHCCQCPFGGDDCSVCPVLCSQHGTYNGECI CNPGWK | 352 |
| QY | 621 | ABCDVPTNQDVCASNHGTCITGTICNPGYKGBSCBEVCMQDPTCSGRGVVCRGEC | 680 |
| Db | 353 | KECSLRHDECEVADCSGHGHCVCQKQMGYKGFCEBEVDCPHNCSGHGFCADGTC | 412 |
| QY | 681 | FVHGHTNCT---PRATCLDQCSGHGTFLPTDGLCSDPSTWTHDCIEICAADCGHG | 737 |
| Db | 413 | KKGWKGPDCATMDQDALQCLPDCSGHGTFLDTQTCTCEAKWSGDCSKELCDLDCG | 472 |
| QY | 738 | VCVGGTCRCEDGHWGAACDORACHPCAEHGTCTDCKSCSPGNWGEHCTIAHYLDR | 797 |
| Db | 473 | RCBGDACACDPENGGYCNTRLCVDRNCNBEHQCKNGTCLCVTGWNGKCTI | 523 |
| QY | 798 | EGCPGLCNGNGRCTLDLNG--WHCVCLQWRGAGCDTSMETACGDSKNDGDLVDMDPD | 856 |

Qy 1903 ERMEYDQAGRITSRIPADGKTWSTYILEK--SMVLLHSORQ--YIFEDKNDRLSSVTM 1958
Db 1642 EAVSFDRNGRLNEIKYDGSWTMYAFKDMFGSLPLKVTTPRRSDYLLQYDDAGALOSLT 1701
Qy 1959 P--NVARQTLETIRSVGYRNIYOPPEGNASVQDFTEDGHLHTFYLGTRGVVYKYCK 2016
Db 1702 PRGHIHAFSLQ--SLGFFKYQYSPINRHPFILLYNDEGQILAKIHPQSGKVAEVHT 1759
Qy 2017 LSKLAETLYDTTKVSFTYDTAGMLKTIINLQNEGFTCTIRYQIGPLIDRQIFRF--TERG 2075
Db 1760 AGRLETILAGLSHTHYQDTSLVKSVEQEPFELRREFKYHAGILKDEKLRFGSKNS 1819
Qy 2076 MVNARPDYNDNFRVTSQAVNETPLDILVRYDDVSGKTFQFKGVYIYDI----N 2131
Db 1820 LASARYKAYDGNARLUSGEMALDDKELPTTRIKYISQNLGOE-----VVODLKTRN 1872
Qy 2132 QIITVAMTHTKHF-----DAYGRMKEVQYEIIFRSLMYMTVQYDNMGRVVKELKVG 2185
Db 1873 AFNRTVIQDSAKOFFAIVDYDQGRVKSVLMNVKNIDVFRLELDYDLNRRIKSQKTTFG- 1931
Qy 2186 YANTTRYSEYDADGQ-LQTVSINDKPLWRYSDLNGN--LHLLSPONSARLTPLYDIRD 2243
Db 1932 -RSTAFDKINYNADGHVVEVLGNN--WKYLPDENGTGVGVVDOGEKEN---LGYDIGD 1984
Qy 2244 RITRLGDVOY-KWDEGFLRORGDIFFEYNSAGLLIKAYNRA--GSWSVRYVYDGLGRV 2300
Db 1985 RVLKVGDFENNYDARGFVVKGEQKRYNNRQLIHSFERFQSG-----YYIDRSLV 2041
Qy 2301 SSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLSYDLOCHLFAMELSSGDBFYIAC 2360
Db 2042 AMHNDKGNITQYYANPRTPHLVTHVFPKISRTMKLFYDDRDMLIALE-HEDQRYVAT 2100
Qy 2361 DNIGTPLAVSGTGLMIKQILYATAGEIYMDTNPNFQIIIGHGLYDPLTKLVHMGRR 2420
Db 2101 DQNGSPLAFDQNGSIVKEMKRTPPFRIIKDKTKPEFFVFPIDPHGGLIDPHPTKLAVTEQR 2160
Qy 2421 YDVLGRWTSPOHELWKHLSSNVMPFN--LYMFKNNPISNSQDIKCFMTDVNSWLLTF 2478
Db 2161 YDPHVGQWTP---LWETLATWMSHTDVFIRYHNNDFI--NPKNQNYMIDLSWLOIF 2216
Qy 2479 GQLHNVIPGYKPDMDAMEPSYELIHTOMKTQEWDNKS-----ILGQCEYOKQLK 2531
Db 2217 GYDLNN-----MQSRYTKLAQYTPQASIKSNLTAPDFGVISGLECIVEK--- 2261
Qy 2532 AFVTLERFDQYGTSTTSQQAPKTKKFASSG---VFGKVKFALKDGRVTTDIISVA 2587
Db 2262 ---TSEKFSDFDFVFKPLKTEPKRNLLPRVYRGVFGEGVLLSRIGGRALVSVVDGS 2318
Qy 2588 N---EDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKFPGPSEGLAILGLSGRRITLNG 2644
Db 2319 NSVQD--VVSSEFNNSYELD-LHFSIHDDQVFYFVK---DNVLKLRDDNEELRLRGGM 2371
Qy 2645 VNVTVSQINTVLNGRTRTYDLOQYALCLNTRGTTLDBEKARVLELQRAVRQAWA 2704
Db 2372 FNISTHEISDHGGSAAK---ELRLHGPDAVLIKYGVDPQEQRHRLKHAHKAVERAWE 2428
Qy 2705 RQQRLEGEELRAWTEGEKQVLSTGRVOYDGFVFVISVEOYPELSDSANNHWRQS 2764
Db 2429 LEKQLVAAGFQGRGDWTEEEKELVQHGVDVGNWIDIHSHIKYPLQADDPGNVAFQKDA 2488
Qy 2765 EMGRR 2769
Db 2489 KRKR 2493

RESULT 3

A54148

odz protein - fruit fly (Drosophila sp.)

C:Species: Drosophila sp.

C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 21-Jul-2003

C:Accession: A54148

R,Levine, A.; Bashan-Ahrend, A.; Budai-Hadrian, O.; Gartenberg, D.; Menasheerow, S.; Wide

Cell 77, 587-598, 1994
A:Title: odd Oz: a novel Drosophila pair rule gene.
A:Reference number: A54148; MUID:94243925; PMID:7514504
A:Accession: A54148
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2406 <LEV>
A:Cross-references: UNIPARC:UPI000017A1AC
C:Genetics:
A:Gene: FlyBase:Ten-m
A:Cross-references: FlyBase:FBgn0004449
F:514-540/Domain: EGF homology <EGF>
F:610-637/Domain: EGF homology <EGF1>

Query Match 23.6%; Score 3515.5; DB 2; Length 2406;
Best Local Similarity 34.0%; Pred. No. 9.6e-188;
Matches 724; Conservative 433; Mismatches 843; Indels 130; Gaps 42;

Qy 384 EDTASSWPVPTDVSLSYPSGGTGLTPDRKKGITTEGKPFSSFFPDESDSIDGEIDVGRAS 443
Db 347 EATSAATSSQSLSLTPSLSSSLANANGGARTF---PARSFPPDG-TTFGQITLQKLT 402
Qy 444 QKIPPGTFWRSQVFDIDHPVHLKFNVLGKAALGIYGRKGLPPSHTOFDVFELLDGRLL 503
Db 403 KEIQPSYWNMQFYQSEPAVYKFDYTIIPRGASIGVYGRNALPHTQYHKEVLSGESAS 462
Qy 504 TOEARS--LEGTPRQSGTVPVPSHSHETGFTIOYLDSDGIWHLAFYN-DKKESEVVSFLTAI 560
Db 463 TRTARAHLSTIREVTR-----YMEPGHWFVSLYNDGDGVQELTFYAAVAE 508
Qy 561 ESDVNCPSNCGVNGDCISGTCFLGFLGPDGCRASCPLVCSGNGOYMKGRCLCHSGWK 620
Db 509 DMTQNCNGSGNGQCULGHCCQCNPGFGDDCSVCPVLCSQHGYTNGECICNPGWK 568
Qy 621 AECDPVNTQCIDVACSNHGTCTITGTCICNPGYKGESCEEVDMDPTCSGRGVCVRGEC 680
Db 569 KECSLRHDCEVADCSGHGCHVSKQCMRGYKGFCEEVDCPHNCSGHGFCADGTIC 628
Qy 681 FVHGHTNCT---PRATCLDQCSGHGTFLPDTGLSCDSPSWTGHDCSIICAADCGHG 737
Db 629 KKGWKGPDCAITMDQDALQCLPDCSGHGTFLDITQTCTCAKWSGDDCSKELCDLDCQHG 688
Qy 738 VCVGGTCRCBDGWMGAACDORACHPRCAEHGTCDRGKCSPGWNGEHCHTIAHVLDRVVK 797
Db 689 RCEGDACADCPENGGEVCTNRLCDVRCNEHGQCNGTCLCTVTCWNGKXCTI----- 739
Qy 798 EGCPLCNGNRCITLDLNG-WHCVCQLGWRGACDTSMETACGDSKNDGDGLVDCMDPD 856
Db 740 EGCPLNSCAGHCQCRVSGEGQWECREYEGWDGPDGCIAGLELNCGDSKNDKDGVLDCEDPE 799
Qy 857 CCLQPLCHINPLCLGSPNPLDIITQETQVPSVQNLHSHFYDRIKFLVGRDSTHIIIPGENP 916
Db 800 CCASHVCKTSQLCVSAKPIDVLLRKOPPAITA---SFFERMKFLIDESSLQNYAKLET 856
Qy 917 DGGHACVIRQVMTSDGTPLVGNISFVANNPFGYITISRDGDSFDLVNTNGGISILRFR 976
Db 857 NESRSVIRGVVTSGLMGVGRVS-TTTLLEGFTLTRDDGWFGLMNGGAVTLQFGR 915
Qy 977 APITQHTLWLPDWRFFVNETIIMRHENE-----IPSCDLSNFARNPNVPSPLTS 1030
Db 916 APERPOSIRIVQVPMNWIIDLVMMSBEKGLAVTTTHTCFADHYDLMKPVVVLASWGHG 975
Qy 1031 FASSCAEKGPVPEIQALQOEISISCKMRLSVLSRTPGYKSVLRISLTHPTIPNLAK 1090
Db 976 FQACDPRSAIABESQVIESQIQTGLNLVHSSRAAGYSLTIKLTTPDVPITSLHL 1035
Qy 1091 VHLMWAVEGRLEFRKWFAPAAPDLSYYFIWDKTDVYNQKVFGLSEAFVSQYEVESCPDLIL 1150
Db 1036 IHLRITIEGILPERIEADPGIKFTVAMNRLNIYRQVVTAVVVKVGYQYTDCTD-IV 1094
Qy 1151 WEKRTTVTQGYEIDASKLGSWLDKHALNOSGILHKNGENQFVSQPPVIGSTMGNG 1210
Db 1095 WDIQTTLKLSGHDMSTSEVGGWNLDIHHRYNFHEGILQKDGSGNIYLNRNPRILTTMGDG 1154

Db 481 QWVIGFHGGLYDPLTKLVHFTQDYDVLGRWTS PDYTMKNVKGKPA - PFNLYMFKSN 539
Qy 2457 PISNQIDKCFMTDVSNSLLTFQGLHNVIPIGPKPDMAMEPSYELIHTQMKTBWDNS 2516
Db 540 PLSSELDLKNYVTDVKSLSWFMFQLSNIPIGPRAKMYFVPPYBSQSAS----ENG 595
Qy 2517 KSLIGVOCEVOKLQKAVTLERDQLYGSTITSQQAOKTKK----FASGSGVFGKVKF 2572
Db 596 QLITGVQOITERRNQAFMALE-----GQVITKHLASREKAGHWFATITPIIGKIMF 649
Qy 2573 ALKQGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVRPGPSEGLAIL 2632
Db 650 AIKEGRVTTGVSSIASIASESRKVASVLNNAYILDKMHYSIEGKDTHYFVKIGSADGDLVTL 709
Qy 2633 GLSGGRRTLENGVNVTVSQINTVLNGRTRYTDIOYCALCLNTRYG---TTLDEEKAR 2689
Db 710 GTTIGRKVLSEGVNVTVSQPTLLVNGRTRFTNIEFYSTLLSIRYGLTPDTLDEEKAR 769
Qy 2690 VLELARQARVQAWAREQORLAREGEGLRAWTEGEKQOVLSTGRVQGYDGFVVISVEQYP 2749
Db 770 VLDAQARQALGTAWAKEQKQKARDGREGSLWTEGEKQQLLSTGRVQGYEYVILPVEQYP 829
Qy 2750 ELSDSANNHFMQSEMGRR 2769
Db 830 ELADSSNNIQFLRQEMGKR 849

RESULT 5
T16743
hypothetical protein R13F6.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16743
R:Miller N.
submitted to the EMBL Data Library, April 1994
A:Description: The sequence of C. elegans cosmid R13F6.
A:Reference number: Z18570
A:Accession: T16743
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2531 <M1>
A:Cross-references: UNIPROT:Q21980; UNIPARC:UPI000017A1A8; EMBL:U00046; NID:G470358; PID
A:Experimental source: strain Bristol N2; clone R13F6
C:Genetics:
A:Gene: CBSP:R13F6.4
A:Map position: 3
A:Introns: 52/2; 113/1; 170/2; 594/1; 1009/1; 1181/1; 1547/3; 1672/3; 1890/1; 2278/1; 24

Query Match 14.2%; Score 2109; DB 2; Length 2531;
Best Local Similarity 24.5%; Pred. No. 4.8e-109;
Matches 674; Conservative 444; Mismatches 1064; Indels 568; Gaps 96;

Qy 290 GCTSPLP---CTTSQYPLTSTVYSPPRPLPRSTFARP-----AFNLK----- 332
Db 25 GAPNPTYSASTLLKYLPLAAGTNQNRQRQVGTWNGDPVAGGPMALSKKKKFPDDSD 84
Qy 333 -----PSKYCNWKAALSAIVSATILVILLAVFVAMHFLGLNHLQPMEGQWYEITETA 387
Db 85 TCSRWPSEK---WNILLAAALLVALFVICILFRAHYVY-----TQPAP-----SSDAT 130
Qy 388 SSWPPTDVSLYPSGGTGLETPDRKKGKGTTEGKSPFFPEDSFIDSGEIDVGRASQKIP 447
Db 131 SS-----AAAAASRYQDLGLRALPP-----AISLGERVDVEFF 163
Qy 448 PCTFWRQVFDHPVHLKFNYSGLKAALVIGYGRKGLPPSHTPQDFVELLDGRLL----- 503
Db 164 PKSMATTELTVKPRIRAFNATVGSQAQLVLLMSAGVHPSLSLHDALFPPIRADIRDSKS 223
Qy 504 -----TOBARLEGTPQSRGTVPSPSSHETFIQYLDSGIWHLAFYNDGKSESVS 554
Db 224 PTHIVEEGRSRRSLGASSRHRNIEILSPRSATFEQFVLEGRHYLTFINERSRVEPIS 283
Qy 555 FLTTAIE-----SVDNCPNSYGNDCISGTCHFLGLGPD 592

Db 284 FVAELQRPPTTPPKTSSSGTSGAKEHPLASVLVCESNQNGECVHGKCHCAPGTTGTC 343
Qy 593 GRASCPVLCSNGQVMKGRCLCHSGWKABCDVPTNQCIDVACSNHGTCTIT-GTICINPG 651
Db 344 DEAVCPVCSNGVPSGGICVCKSGPKGKCEMRHNCEVADCNGRGFCDDTDCRCNPG 403
Qy 652 YKGSCEBVDMDPTCSGRGVCVRGECCHCFVWGOGTNC----- 690
Db 404 WTGEACELRACPHASCCHDRGVCVNGTCYCMDGMRGNDCSVFADAIVHVPQAQSPRRQOE 463
Qy 691 -----TPRATCLDQ-----CSHGHTFLPDTGLCSC 715
Db 464 PTESSKTRKAQVKPTPTSEKKKESRELQKPIATVQVPTSESHPCSAHQQLIDD--IQCC 521
Qy 716 DPSWTGHDCSIIEICAAOCGGHGVCV-GGTCRCEDGMWGAACDQACHPRCAEHGTC-RDG 773
Db 522 ESGWDSVDCSQAC--QC-VNGDCLDDGSCQCKWGRGNSCTDKKCAIGCEDRGKCASDG 578
Qy 774 KCESPGWGHECTIAHYLDRAVKEGCPGLCNGRCRTLDLNG--WHCVCOLGHRGAGCD 831
Db 579 SKCSSGWNGENCAL-----DGCPCNOCSGKEGCMRRRSSEWSCRCQAGSTGVDCS 629
Qy 832 TSMETACGDSKDNDDGLVDCMDPDCLQLPLCHINPLCLGSPNPLDIIQETQVPVSQNL 891
Db 630 VSEVHCDDGLDNDSDGLDCCDPECCSSSCSSCVSTAASPIEVLMR-MPIFIYAN- 687
Qy 892 HSFYDRIKFLVGRDSTHIIIGENPFDDGHACVIRGQW-----TSDGTPL 936
Db 688 --FAQRVGFLIMEKSVQSYTDSQFENENLISVIRGRVMWGSPTGSDDLSTYSNKSTVPL 745
Qy 937 VGVNISFVNNPLFGYTTISRODGSFDLVNCGISIIILPERAPPITQETHLWLPDRFVM 996
Db 746 VGVVSAAHPLYGFTLTREDGYFDLTVNGARSVTLQFLRTQFOSVKKSVFVSPRQIHI 805
Qy 997 ETIIMRHEENEIPSCDLSNFARPNPVPVSPPLTSFASSCAEKGP----- 1040
Db 806 DDIVLYRQSGSP-----PASMARAKCSPTLRRIPDDVVLINWQYTSDGIE 854
Qy 1041 -----IVPEIQALQEBISIGCKRLSYLSRTPGYKSVLRISLTHPTTIPFNLMKV 1091
Db 855 TDETSDSRIVDVSRSIFESPLIQGTDVRLVYSARSAPASTMLIGLLYDRVDKELRV 914
Qy 1092 HLMVAVEGRLFRKWFAAAAPDLISYFIWDTDVNQKVFGLSEAFVSUYEVESCPDLI-- 1149
Db 915 HINIRIAGRPRDLVAPRTNLTIVFAMDKWNAVRQSEGLVPVTVRVGYETQGCRTSER 974
Qy 1150 LWKRTTVLQGYEIDASKLAG--WSLDKKHALNTQSGILHKNGENQFVSQQPVGISIM 1207
Db 975 VWQTRRSQWVG--ATARKMIGTMTWLTDIHHHLDIVNNVVMGNGGYRLITSESPRVSTFA 1032
Qy 1208 G-NGRRBSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFFNYIRIPFSGNVNTLEL 1266
Db 1033 GLDGVKRDVECLKCBGKVDSISLFRPTTVVYAQDGSIIIGDHNMIRRVSDGQVSTILT 1092
Qy 1267 RNKDFRSHSPAUKYLYLATDPMGAVFLSDNSRRVPKISTVVVKDLVKNSEVAGTGD 1326
Db 1093 GLADTSHS-----YIIVSPVDGTTAISLPLHKQWRI--SSLEPQDSRNNYDVLADGT 1145
Qy 1327 QCLPFDTRCGDGKATEATLTNPRGITVDKFLIYFVDGTMIRRIDQNGIISTLGSND 1386
Db 1146 VCASAVDS-CGDGALAQAQLIFPKGISFDMGNLVLADSRIRVIDTTGHIRSI--GET 1202
Qy 1387 LTSARPL-SCDSVMDISQVPLEMPTDLAINPMDSNLVYLDNNVVLQISENHQVRIVA-GR 1444
Db 1203 TPQHPIRTCAQITKLVDLQMEWPTSLTIDPITGSLVLDTNVVYDEIVDVVDTTIALGS 1262
Qy 1445 PMHCQVPGIDHFLLSKVAIHA--TLESATALAVSHNGVLYIAETDEKINRIQVTTG-G 1501
Db 1263 PTTCDLANATSSASAKSLDHRHLIQNARDITVGTGAIYVVEDSGRLNVOVKLSDDRS 1322
Qy 1502 EISLVAGAPSGCDCKNDANCDG---PSGDDGYAKDAKLNTPSSLAVCAOGELYVADLGN 1558

Db 1323 TFSILTGGKSPCSC-DVAACGCDDAVSLRDVAASQAHLSPYAVCVSPSGDVIADSGNS 1381
Qy 1559 RIRFI-RKNKPFPLNTQNWYELSSPIDOELYLFDTTGKHLYTQSLPTGDYLYNFTYTGDGD 1617
Db 1382 KIKKVSARMARKYDGRSTYEVDAERKEKTYTFNRHGHQSHSTVSLITRTFFNFYSQYDWP 1441
Qy 1618 ITLITDNNGNVNRDRDSTGMLVLPVDPDGVVVTWGTNSALKSVTTQOGE--LAMMTY 1675
Db 1442 ISMISE-----IRNAS-----GVVLRLVRKNDLSLPDLTTLTGRTTLTWSAY 1483
Qy 1676 HG-----NSGLIATKSNENGWTTTYEYDSPORLNTVPTPTQVQS 1714
Db 1484 DGTLEQVSKRDSATSRDATKLFYKKGILL-TSRIDVATAVGFYDEYGRAIGL----- 1534
Qy 1715 SFRSDTSSVHVQVETSSKDDVTITTNLSAGAPYTLTQQVRSYYIIGADGSLRLLLAN 1774
Db 1535 --KKDRB-YWRLGSETISMG--SVNTEVLNGQRF--QQVR-----LG-EGNLAVHSTN 1580
Qy 1775 GME---VALQTEPHLLAGTV-NPTVGKRNVTLPIDNGLNLVEMRQRKEQA-----RQVVT 1825
Db 1581 GATTRLISLRNEGYSLASPLGTSTLYDKSSIPDSNGEPLISRRRTKVPALGNPQRRELT 1640
Qy 1826 V-----FGRL-----RVNRNLLSLDFRVRTTEKI-----YDDH 1856
Db 1641 TRMDWRHVARRGDDSDGSLGRKVAEVRFRPRINGVNMFMSEYDVKSNQDTLRIGSTTDD 1700
Qy 1857 RKFTLRILYDOAGRPSSLWS--PSSRLNGVNVYSPGGYIAGIQGINSERMEYDOAGRIT 1914
Db 1701 AQALLFDYTSNGIRIRISAPEDSQMAEMNITWDGAGRKSEVTWGSWKIRLTVDNSNRLT 1760
Qy 1915 SRIPADGK---TWSYTYLEKSMVLLHSORQYIFEDPKNDRLSSVTMPNVVAROTLETIR 1970
Db 1761 EHAI-DGARVPKMSYAGASRRPNEIQHDGAKWNIQYDNYDRIKEIVLSKQEATSPSSI- 1818
Qy 1971 SVGYRNIYQPEGNASVIOFTEDGHLHTFYLGTRRVYIKYKGLSKLAETLYDTTKV 2030
Db 1819 ALG-----GDEWLKRTS-----LNSKPSLV-----RLSREGKVLSTTPD 1855
Qy 2031 SFTY-----DETAGMLKTINLQNGFCTIYRQIGPLIDRQIFRPFTEEGVNAARFDNY 2085
Db 1856 ENHWLBERKDPITG--RTTEILNDEETVTVCWS-----PEEPSITSSFTYFY 1901
Qy 2086 DNSPRVTSQMAVINETPLPIDLYDYDVSGKTEQFGKFGVIYDINQIITAVNTHTKHF 2145
Db 1902 DDMURVTIIPVIEQSULETSQSYDERRGHVAINGF-----KWADASTSRC 1950
Qy 2146 DAYGRMKEV-----QYEIFRSLMYW-----MTVOYDNMGVRWKVKELV---GPYANTR 2191
Db 1951 QGHGLMYETSANDHRQVVERKLIIFGDARASIKIIRDKAGRASBSHLEISSSGTQRN-QK 2009
Qy 2192 YSYEYDADGQLOTYSINDKP---LWRYSYDLNGLNLHLLSPGNSARLTPLRYDIRDITR 2247
Db 2010 ITRTFDAAGRVASVEQNDQEPVRIIW-----NSDARVE---KINDARVE 2050
Qy 2248 -----LGDVOYKMDDEDFLRQRG-DIFEYNSAGLLIKAYNRAGSWRVRYDGLG 2297
Db 2051 WNRGALKTFQDISYQVDSIGWVKVRDNTTVFGDGGKRLVSA--RSQRLRINIFYRED 2108
Qy 2298 RRVSSKSHSHHLOFFYADLTNPTKVTYHLVNHSSSEITSLYYDLOQHLFAMELSSGDEFF 2357
Db 2109 RVVQIQNS-KDFIHFYGYIDTPKLVSHF--SKNGKISTLFYDDSDVPFAMQSDGTRYA 2165
Qy 2358 IACDNIGTPLAVFGSGTGLMIKQILYATAGEIYMDTNFNFIIL-IGYHGGI-YDPLTKLVH 2415
Db 2166 LLTDETSTIKAIL-GDSNVLRILIDRSVFGALLPSSSSSHPLPIGYLGGIEISEISVIL 2224
Qy 2416 MGRDYDVLACRWTSPOHLEKHLSSNVMPFNLYMFKNNPIINSODIKCF----- 2467
Db 2225 NNGRPLDYSERYMS-----ISPFAVRLELNKFNISIDLMALELTDROPFR 2271
Qy 2468 ----MTDVNSWLLTFGQLHNVIP-----GYPKPDMADAMEPSYELIHTQMTQEMDNSKSI 2519
Db 2272 VENVPEDFTWFSLAGLS-PNLLPSAHLGLP-----ASSAIVHRLSS----- 2313

Qy 2520 LGVQCEVQKQKAFVTLERFDQLYGSTITSCQQA-----PKTKKFPASSGSVFGKGVKF 2572
Db 2314 -----FPRKLRPLTHL-----TTVLPTRLASDISLTSPTSETSWSIDDVGFNSNLLI 2359
Qy 2573 ALKD---GRVTTDIIISVANEDGRRVAAILNHAIYLENLHPTIDG-VDTHYFVFKPGPSGD 2628
Db 2360 LNE DATTTGVMVEMLSDLKSEEREVISKLFDG--VKSLDPATWGLVPTPTRLHWRAPNSKLE 2417
Qy 2629 LAILGLSGGRRITLNGVNVTVSQINTVLNGRTRRYTDIOLOYGALCLNTRYGTTLDDEKA 2688
Db 2418 LS-----STFSHFTMAVN-----KOSVELRNKSKLIVHFSENKAEIVK 2457
Qy 2689 RVLELARQRAVROAWAREQORREGEGBEGLRAWTEGEKQVQLSTGRVQGYD 2738
Db 2458 KIVELEKLTRENIJAVWRAERKAEAGEKTWRQSDRETRELTSGKSVSYGD 2507
RESULT 6
A61625
tenascin-like protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C:Accession: A61625; S28463
R:Baumgartner, S.; Chiquet-Ehrismann, R.
Mech. Dev. 40, 165-176, 1993
A:Title: Ten(a), a Drosophila gene related to tenascin, shows selective transcript loca
A:Reference number: A61625; MUID:93264270; PMID:7684246
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-782 <BAU>
A:Cross-references: UNIPROT:Q24550; UNIPARC:UPI000017A1AB; EMBL:X68794
C:Genetics:
A:Gene: ten-a
A:Cross-references: FlyBase:FBgn0004446
C:Keywords: tandem repeat
F:1-62/Domain: signal sequence #status predicted <SIG>
F:63-782/Product: tenascin-like protein #status predicted <MAT>
F:497-524/Domain: EGF homology <EGF>

Query Match 7.9%; Score 1175.5; DB 2; Length 782;
Best Local Similarity 31.4%; Pred. No. 1.2e-57;
Matches 243; Conservative 101; Mismatches 240; Indels 191; Gaps 17;
Qy 301 PGYPLTSS-TVYSPRPRLPRSTFAPAFNLKXPSKY-CNWKCAALSAIVSATLVILLA 358
Db 2 PGFPLRNHSAHAPHYSP-----YSPSRPHIDKRCQHRCSWKCLSLALIFVSVVLTAWLA 56
Qy 359 YFVAMEHLFGLNWH-----LQPMEGQWYEI-----TEDTASSWP-----VPTDVSLYP 400
Db 57 YFAAVSSMKPNMDSTNCILVDYKSPHDLHGGLAKSNEKGVATAFTTESIQSTSDHG 116
Qy 401 SGGTGLETPDRKQKGTTEG-----KPSFFPEDSFID----- 432
Db 117 QNGHGLMNPAGSGGSGNSGIIQQQLVQQQPHSINQPLTPLDATNTLQDHHQLTYGAL 176
Qy 433 -----SGEIDVG-----RRASQ----- 444
Db 177 PGVGVGIGMSGGGMGGLNGGLGQMQOPGGGLNGHHQALQPOLGGVVELKEFNAY 236
Qy 445 --KIPGCTFWRSOVFDHPVHLKFNVSIGKAAVLGYIGRKLPPSPHTQFDVELLDGRR 502
Db 237 HATIPAYQFTWLEFRNKHGPAIFRNFPLPWGAHFVYSRNVAPSVTQHDVFVEIKGRL 296
Qy 503 LT--QEARSLEGTPROSR----- 518
Db 297 DSHLRHRRSSANFPOLGKIWSCIARTETRVNRNLIRNTRNTRVAVSIPANRTWHRPSI 356
Qy 519 -----GTVPSSH-----ETGFIQYLDSDGIWHLAFNDCKES 550
Db 357 RPNISICNGLASPKVHWYWNKRSAGDGLPALDWDAMTVNVSLQLQYLDLTGLWFIISVYNDELVA 416

A: Molecule type: mRNA
A: Residues: 1-1746 <NIS>
A: Cross-references: UNIPROT: Q29116; UNIPARC: UPI0000136BBB; EMBL: X61599; NID: g2124; PIDN: C; Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type C; Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracellular
F: 1-22/Domain: signal sequence #status predicted -SIG>
F: 23-1746/Product: tenascin #status predicted <NAI>
F: 346-372/Domain: EGF homology <EGF>
F: 377-403/Domain: EGF homology <EGF2>
F: 622-703/Domain: fibronectin type III repeat homology <FN3A>
F: 711-793/Domain: fibronectin type III repeat homology <FN3B>
F: 802-884/Domain: fibronectin type III repeat homology <FN3C>
F: 892-976/Domain: fibronectin type III repeat homology <FN3D>
F: 984-1064/Domain: fibronectin type III repeat homology <FN3E>
F: 1073-1155/Domain: fibronectin type III repeat homology <FN3F>
F: 1164-1246/Domain: fibronectin type III repeat homology <FN3G>
F: 1254-1335/Domain: fibronectin type III repeat homology <FN3H>
F: 1343-1423/Domain: fibronectin type III repeat homology <FN3I>
F: 1431-1511/Domain: fibronectin type III repeat homology <FN3J>
F: 1526-1734/Domain: fibrinogen beta/gamma homology <FBG>
F: 38,166,184,327,788,1034,1079,1121,1354/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 4.4%; Score 652; DB 1; Length 1746;
Best Local Similarity 21.2%; Pred. No. 8.2e-28;
Matches 342; Conservative 204; Mismatches 558; Indels 512; Gaps 72;

QY 566 CPSCYNGDCISGTCFLGFLGPDGCRASCVPVLCSGNGQYMKGRCLCHSGWKGAEC- 624
DB 315 CPKDCPRGRCINGTCYCDGFEGBDGLACPHGRCGRCEGQVCDEGFAGADCS- 374
QY 625 --VPTNOCIDVACSNHGTCTGTICNPGYKGBSCBEVDCMDPTCSGRGVGVGECHCFV 682
DB 375 RRCPSD-----CHNRGRCLDGRCECDGFEGBDGLAC- PGCSGHRGVNGQVCDE 427
QY 683 GWGTCETPRATCLDQCSGHGFTLPDTGLCSDDPSWTGHDCEIETCAADCGHGVCGV 742
DB 428 GRTGEDCSQL--CPNDCHGRGCV--QGRCECEHGFQYDCSEMSCPDCHQHGRGVNG 483
QY 743 TCCEGDMGAAACDQACRACRCAEHGTCRDGRCECSFGNGHECTIAHLDVRVVEGCPG 802
DB 484 MCVDDGYTDCRELRCPGDCSQRCVDRGRCVCHGFGAGPDC-----ADLACFS 534
QY 803 LCNGNGRCLLDLNGMHCVQLGWRGAGC-----DTSMETACGDSK--DNDGDGLVDCM 853
DB 535 DCHGRGRC--VNG-QVCHEGFTGDKCQRCPGDCGCHGQRCVDCGQVCCHGFTGLDCG 590
QY 854 DPDC-----CLQPLCHINPLCLG-----SPNPLDIIQETQVPVVSQQNLHFSFYDR- 897
DB 591 QRSCLPNDSCNMGQCVSGRCICNEGYSGEDCSQVSP-PKDLI---VTEVTEETVNLAWDNE 646
QY 898 ---IKFLVGRDSTH-----IIPGNFPDGHACVIRGQVMTSDGTPLGVN-----I 941
DB 647 MRVTEYLIVTPHEDGLEMQFRVPCD-----QISTIRELEPGVEYFIRVF 693
QY 942 SFVNNPLFGYTISSRQGSFDLVNNGGISILRPERAPFITOBHTLWLPMDFVFMETIIM 1001
DB 694 AILENKK-SIPVSARVATY-LPTPEG---LKFKSIIK-ETSVEVEWDLPIAFETWEIIF 746
QY 1002 RHEENIIPSCDLSNFAFPNVPVSPPLTSFASCAEKGPIVEIQALQEEIISICKMRL 1061
DB 747 RNNKDEGEITKSLRPE-----TTYROTGLAPG-----QVEYIS---LHI 785
QY 1062 SYLSSRTPGYKSVLRISLTHPTIPFNLKMLMVAVEGRFLFRKFAAAPPDLSYFIWDKT 1121
DB 786 VKNNTGRGPKLVTTTRLDAPS-----QIEAKDVTDTTALITWPKPLAEID----- 831
QY 1122 DVYNQKVFGLSFAFVSGVEYSSCPDLILWEKRTTVLQGYEIDASKLGWSLDKGHANI 1181
DB 832 -----GIELTYGIDKDFG-----DRTTIDLTHERNQYSIGNLKPDPTEYEVSL 873
QY 1182 QSGILHKGNGEQFVSQQPPVIGSIMGNRRRISCPSCNGIADGNKLLAPVALTCGSDG 1241
DB 874 IS-----RR-----ADMSSNPAKETFTTGLDA 895

QY 1242 SLVYGVDFNYIRRIFFSGNVTNILELRNKDFRSHSHSPAHHYYLATDPMGSAVFLSDSNRR 1301
DB 896 P-----NRLRRISQTSNITL-----EMWNGKAAADTYRIKYAPISGG----- 933
QY 1302 VPKIKSTVVVKDLVKNSEVAVAGTGQCLPFDTRCGDGGKATEATLTPNPRGITVDKPGLI 1361
DB 934 -----DHAEEVEPRSPQ-----TTTKATLTGLRPGT--EYGI- 963
QY 1362 YFVDGTMIRRIDONGIISTILGSDNLTLSARPLSCDSVMDISOVLEWPTDLA-----IN 1415
DB 964 ----GVSNAVGKDSDPATINAAATDLPDPKDFRVSLEKE--SSLTLLWRTPLAKDFRYL 1018
QY 1416 -----PMDNSLYVLNNVQVISENHQVRIVRAGRPMHCQVPG----- 1452
DB 1019 YGLPFGQVQVQLPRNATSYILRG---LEPGQEYITILLTAEKGRHKSPARVAKASTAGEP 1075
QY 1453 -----IDHFLLSKVAIHATLSATALAVSHNGVLYIAETDEKKNRI-RQVTT 1500
DB 1076 EIGNLSVSDITPESFSLSWTATEGAFETFTTIIIDSNRFL---ETMEYNISGAERTAHIS 1132
QY 1501 G-----EISLVAGAPSGCCDKNDANCDGSGDGYAKDAKLNTPSSILAVCADGE----- 1549
DB 1133 GLRPNDGFIYVLSGLAPGIQTK-----PISATATTEAEPEVDN 1170
QY 1550 LYVADLGNIRIRFIRKKNKPFINTQMYELSPIDQELY-----LFDTTGKHLTYQSULT 1603
DB 1171 LLVSDA-----TPDGFRLSWTADEGVDSFVLKIRDTK-----KQSEPL 1209
QY 1604 GDLYLVFTYTGDDGITLITDNNGMNVNRDSTGMPMLWLVPDQGVVMTGNTSALKSV 1663
DB 1210 -----EITLASERTRDITGLREATEYEI-----ELYGISGGRKS----- 1244
QY 1664 TTOGHELAMMTYHGNSGLLATKSNENGMWTFYEDSFGRLTNVTFFPTQGVSSPSRSDTSS 1723
DB 1245 -----QPVSAIATTAMGSPKEITFSDITENSATVSMWVPTAQVESPR-----I 1287
QY 1724 VHVQVETSSKDDVTITNLSASGAFYTLLOQOVNSYIIGADGSLRLLLLANGMEVALQTE 1783
DB 1288 TYVPITGAPSVVTVGDTKTQTLRLRL-----PGVEYLVSVIAVKGFE---ESE 1334
QY 1784 PHLLAGTVNPTVGRKRVTLPTDNGNLNVEMRQRKEQARGQVTVFGRRLRVHNRLLSLDF 1843
DB 1335 P--VSGT-----LTTALDGPGLVT----- 1352
QY 1844 DRVTRTKIYDHRKFTLRILYDQAGRPSLWSPS-SRLNGVNVYSPGGYIAGIQRGIMS 1902
DB 1353 ANITDSEAL-----AMQPAIAPVDHVVISYT-GDRVPEITRTVSG 1392
QY 1903 ERMEY----DQAGRITSRIFAD-GKTWSVYLEKSMVLLHRSORQVIFEFDKNDRLSSV 1956
DB 1393 NTVEYALTNLEPATEYTLRIFAEKPKOKSSTITTK-----FTTDL-DSPRDL 1438
QY 1957 TMPNVARQT-LETIR-----SVGYRNIIQPPEGNASVI-----QDFTEDGHLHTPYLG 2005
DB 1439 TATEVQSEETALLTRPPRASVTGVLVYVESVDGTLKEVVVGPETTSVLSGLSPSTHYTA 1498
QY 2006 TGRVITYKGL-SKLAETLYDTTKVSFTY-----DETAGMLKNTINIQNE 2049
DB 1499 ---RIQALNGPLRSKMSQTVFTTIGLLYPPPRDCSQALMNGDITSG-LYTIYVND 1550

RESULT 10
A32160
tenascin-C - human
N: Alternate names: hexabrachion
C: Species: Homo sapiens (man)
C: Date: 31-Jul-1989 #sequence revision 12-Apr-1996 #text change 09-Jul-2004
C: Accession: I38337; A32160; S14015; S16166; S50208; S49754
R: Gherzi, R.; Carnemolla, B.; Siri, A.; Ponassi, M.; Balza, E.; Zardi, L.
J. Biol. Chem. 270, 3429-3434, 1995
A: Title: Human tenascin gene. Structure of the 5'-region, identification, and character:
A: Reference number: A55974; MUID: 95155442; PMID: 7531707

A:Accession: J38337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2201 <RES>
A:Cross-references: UNIPROT:P24821; UNIPARC:UPI0000034A0E; EMBL:X78565; NID:G556844; PID:R:Gulcher, J.R.; Nies, D.E.; Marton, L.S.; Stefansson, K.
Proc. Natl. Acad. Sci. U.S.A. 86, 1588-1592, 1989
A:Title: An alternatively spliced region of the human hexabrachion contains a repeat of Nucleic Acids Res. 19, 525-531, 1991
A:Reference number: A32160; MUID:89160821; PMID:2466295
A:Accession: A32160
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 431-538, 'R', 540-1065, 'H', 1067-1599, 'LWLHPRASN', 1609-2054, 'L' <GUL>
A:Cross-references: UNIPARC:UPI000016AAC6; GB:M24630; NID:G514363; PIDN:AAA52703.1; PID:R:Siri, A.; Carnemolla, B.; Saginatti, M.; Leprini, A.; Casari, G.; Baralle, F.; Zardi, I.
Nucleic Acids Res. 19, 525-531, 1991
A:Title: Human tenascin: primary structure, pre-mRNA splicing patterns and localization
A:Reference number: S14015; MUID:91187670; PMID:1707164
A:Accession: S14015
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-243, 245-369, 'V', 371-679, 'R', 681-1676, 'I', 1678-2139, 'TR', 2142, 2144-2201 <ST>
A:Cross-references: UNIPARC:UPI0000155D15; EMBL:X56160; NID:G37226; PIDN:CAA39628.1; PID:R:Nies, D.E.; Hemesath, T.J.; Kim, J.H.; Gulcher, J.R.; Stefansson, K.
J. Biol. Chem. 266, 2818-2823, 1991
A:Title: The complete cDNA sequence of human hexabrachion (tenascin). A multidomain protein
A:Reference number: S16166; MUID:91131572; PMID:1704365
A:Accession: S16166
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-538, 'R', 540-1065, 'H', 1067-1599, 'LWLHPRASN', 1609-2054, 'LH', 2055-2201 <NIE>
A:Cross-references: UNIPARC:UPI000016AAC5; EMBL:M55618; NID:G184483; PIDN:AAA88083.1; PID:R:Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A:Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by RT-PCR
A:Reference number: S50206; MUID:95035091; PMID:7524681
A:Accession: S50206
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 46-125 <GUJ>
A:Cross-references: UNIPARC:UPI0000177AF4; EMBL:X80280
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Gene: GDB:HXB
A:Cross-references: GDB:120073; OMIM:187380
A:Map position: 9q33-9q33
C:Superfamily: tenascin; EGF homology; fibronogen beta/gamma homology; fibronectin type 3; Superfamily: alternative splicing; extracellular matrix
F:408-434/Domain: EGF homology <EGF>
F:622-703/Domain: fibronectin type III repeat homology <FN3A>
F:711-794/Domain: fibronectin type III repeat homology <FN3B>
F:892-976/Domain: fibronectin type III repeat homology <FN3C>
F:1437-1519/Domain: fibronectin type III repeat homology <FN3D>
F:1619-1701/Domain: fibronectin type III repeat homology <FN3E>
F:1709-1780/Domain: fibronectin type III repeat homology <FN3F>
F:1798-1878/Domain: fibronectin type III repeat homology <FN3G>
F:1886-1966/Domain: fibronectin type III repeat homology <FN3H>
F:1981-2189/Domain: fibronogen beta/gamma homology <FBG>

Query Match 4.4%; Score 649.5; DB 2; Length 2201;
Best Local Similarity 22.3%; Pred. No. 1.7e-27;
Matches 310; Conservative 166; Mismatches 492; Indels 423; Gaps 64;

Qy 545 NDGKESEVSEFLTAIESVDNCPNCGNGCISGTCHCFLGFLPGDCGRASCPVLCS-G 603
Db 208 DDGFTGDCSOLA-----CPSDNDQKGVGVCICFEGYAGADCSREICFVPCSEE 259
Qy 604 NGQYKGCCLCHSGWKGAECDVPTNQCIDVACSHGTCITCTCNPGYKGCSEVDQCM 663
Db 260 HGTCVDGLVCVCHDGFAGDDCNKPL--CLN-NCYNRGRVENEVCDEGFTGDCSELICP 316
Qy 664 DPTCSGRGVCVRGECHCFVGVGGTNCETPRATCLDQCSGHGTFPLPDTGLCSCDPSWTGHD 723

Db 317 N-DCFRGRRCINGTCYCEBEGFTGEDCKP--TCPHACHTQGR--EBGQCVCDEBGFAGLD 371
Qy 724 CSIEICAADCGHGVCGVGGTCRCEDGMMGAACQQRACHPRCAEHGTCDRGKCECSPGWNG 783
Db 372 CSEKRCPADCHNRGRCVDRGCECDGFTGADCGELKCPNGCSGHRGCVGQCDEGVTG 431
Qy 784 EHTC-----IAHYLDKRVKKG-----CPGLCNGRCRTLDLNGHVCV 820
Db 432 EDCSQRPCNDCHSRGRVC-EGKVCVCEQFGKYDCSDMSCPNDCHQHGRC---VNGM-CV 486
Qy 821 COLGWRGAGC-----DTSMETACGSKDNDGDGLV--DCMDPDC-----CL-Q 860
Db 487 CDDGYTGEDCRDRCQPRDCSNRGLCVGQCVCEDEGFTGPDCAELSCNDCGQRCVNGQ 546
Qy 861 PLCH--INPLCLGSPNPLDIIIOETVPVVSQQNLHSHFYDRIKFLVGRDSTHIIIPENPFD 917
Db 547 CVCEGFMGDKCEQRCPSCHGQRCVDCQICHEGF-----TGLDC----- 589
Qy 918 GGHAC-----VIRQVMTSDGTPLVGVNLSFVNNPLFGYTIISQDGSFDLVNNGI 968
Db 590 GQHSFCPSDCNGLGQCVSGRCICNEG--YSGEDCSEVSPK-----DLV----- 630
Qy 969 SIILPERAFPIQ--EHTLWLPND-RFFVMTIIMRHEENIPSCDLSNFAENPVVSP 1025
Db 631 -----TVEVTEETVNLAWDNEMRVTEYL-----VTP 658
Qy 1026 SPLTSPASSCAEKGPIVPEIQALQEEISISGCKMRLSYLSRTPGYKSVLRISL---THP 1082
Db 659 T-----HEGGLMQFRVPGDQTS-----TIOLEFGVEYFRVFAILENKK 700
Qy 1083 TIPFNLKVLHMAVEGRLPKRFKFAAPDLSSYYPIMDKTV-----YNOKVFG- 1130
Db 701 SIPVSARVATYLPAPGLKPKF---SIKETSVEWMDPLDIAPETWEIIFRNMNKEDEGE 756
Qy 1131 -----LSEAFVSGVSEYSECPDLI-----LMEKRTVLOG---YEI---D 1164
Db 757 ITKSLRRPETSRYQTGLAPGQGEYELSHIVKNNTRGPKLRKVTTLRDAPSQIEVKDVTD 816
Qy 1165 ASKLGW--SLDKHHALNIQSGI-----LHKNGENQFVSQQPPVIGSINGNGRRR 1213
Db 817 TTALITWFKPLAIEDGIELTYGKDVPGDRTTIDLTEDENQY-----SIGNLKP-TEY 869
Qy 1214 SISPCSCNGLADGNKLLAPVALTCGSDGSLYVGDFNIRIFPFGSVNTNILELRNKDPRH 1273
Db 870 EVSLISRRGDMSSNP--AKETFTTGLDAP-----RNLRRVSQTDNSITL-----EWRN 915
Qy 1274 SHSFAHYLYATDPMSCAVFLSDSNSRRPKIKSTVVVKLVKNSEVAVGTGDCQLPDD 1333
Db 916 GKAAIDSYRIKYAPISGG-----DHAEDVDVPKSOQA----- 946
Qy 1334 TRCGDGGKATEALTNPRTGIVDKFGLIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPL 1393
Db 947 -----TTKTLTGLRPGT--EYGI-----GVSAYKEDKESNPATINAATLTPKDL 991
Qy 1394 SCDSVMDISOVRLEWPTDLA-----IN-----PMDNSLYVLNNVVLQISE 1434
Db 992 QVSETAETS-LTLWLKTPAKFDRYLRNLSLPTGQWGVQLPRNTTSYVLRG---LEPGQ 1047
Qy 1435 NHQVRIVAGRPMC-----QVPGIDHFLSKVAIHAHTLESATAL--AVSHNGVL 1481
Db 1048 EYNVLLTAERGRHKSKPARVAKSTEQAPELENLTFTVEGMDGLRLNMTAADQAYEH----- 1103
Qy 1482 VIAETDE-KKINRITROVTTSGEISLVAGAPSGCDCKNDANCDSCGDDGYAKADAKLNTPS 1540
Db 1104 FIIOVQANKVEARNLTVPG--SLRAVDIPGLKAATPYTVSYIGVYQGY-----RTPV 1155
Qy 1541 SLAVCADGELYADLGNIRIFIRKKNKPFLLNTQMYELSSPIDQELYLFDTTGKHLTQS 1600
Db 1156 LSAEASTGE--TPNLGEVVVAEVGWDALKLN-----WT 1186
Qy 1601 LPTGDYLYNFTYTGDDGIIITLITDNNGNMNVRRDSTGMPLWLVPDQGVYVWVTGHSAL 1660
Db 1187 APEGAYEYFFIQOEADTVEAAQN-----LTVPGLRLSTDLPLGLKAAT 1229

Qy 1341 KATEATLTPRGIITVDFGLIYFVDGTMIRRIDQNGIISTLGSNDLTSARPILSCDSVMD 1400
Db 920 -TTRATLTGLRP-----GTEYGGVTAVRQ-DRESAPATINAGTDLNDPKDLEVSPT 971
Qy 1401 ISQVRLSWPTDLA-----INPMNSLYVLNNVVLQISENHQVRIV 1441
Db 972 -TTLSLRWRFPAKFDYRLTYVSPGKQNEMEIPVDSTFILRG---LDAGTEYTTISLV 1027
Qy 1442 AGRPMHCQVP-----GIDHPLLKVAIHATLESATALAVSHNGV 1480
Db 1028 AEGRHKSPTTKGSTEERPELGNLSVETGWDGFLQWTWADGAYE-----NFV 1078
Qy 1481 LYIAETDEKINIRQVTTSGEISLVAGAPS---GDCCKNDANCDFSGDGGYAKDAKL 1536
Db 1079 IQVQSDNPE-----ETWNIIVPGQHSVNVTLKANTPNVNTLYGVIRYTRKPLY 1130
Qy 1537 NTPSSLAVCADGELYVADL-----GNIRIRPKNK---PF-----L 1570
Db 1131 VETTTGAHPEVGELTVSDITPESFNLSWTTTNGDFAFTIEIDSNRLLEPFMEFNISGNS 1190
Qy 1571 NTQNMVELSPIDQELYLFDTTGKHLX-----TQSLPTGDVLYNFTYTGDDITL 1620
Db 1191 RTAHISGLSPSTDFIVLYGIS---HGFRTOAISAAATEAPEVDNLLVSDATPDGPRLT 1248
Qy 1621 ITDNNG-----NMNVNRDSTGMPLWLVP-----DQVYVWVTMGT 1656
Db 1249 WTADDGVDFSVLKIRDTKRSD--PLELIVPGHERTHDITGLKEGTEYEIELYGVSSGR 1306
Qy 1657 NS-ALKSVTTQGHBLAMWYHGN-SGLLATYKSNEN---GWTTPYEYDSFGRLTNNVTFPT 1710
Db 1307 RSQPINSVAT-----TVVGSFKGISFSIDITENSARVSWTP-----PR 1343
Qy 1711 GOVSSFRSDTSSVHVQVETSSKDDVTITNLSAGAFYTLQDOVENSYYIGADGSLRL 1770
Db 1344 SRVDSYRVS-----YVPTGTGPNVTVDGSKTR-----TKLVKLV-----GVDYVNNI 1388
Qy 1771 LLANGMEVALQTEPHLAGTVNPTVGRKN--VTLPIDNGLNMLVWR-----QRK 1817
Db 1389 ISVKGFE---ESEP--ISGILKALTALDSPGLVWNNITDSEALATWQPAIAAVDNYIVSYS 1443
Qy 1818 EQARGQVT--VFGRRLRHNRLNLSLDFDRVTRTEKIYDHRKFTLILYDQA--GRPSL 1873
Db 1444 SEDEPEVTOMVSGNTVE-YDLNGLRPATEVTLRVHAVKDAQKSETLSTQFTGLDAPKDL 1502
Qy 1874 WSPSRRLNGVNTYSPGYIAGIQRGIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSM 1933
Db 1503 SATEVQSETAVITWRPP-----RAPVTDYLLTYESIDGRVKEVILDPETTSYTLTE--- 1553
Qy 1934 VLLHSQRQYIFEDKNDRLSSVTMPNVARQTLTETIRSVGYRNIYQPPENASVIOQFT 1993
Db 1554 ---LSPSTQYTVKQLALSR-----SMRSKMIOQTVTTTGLLY-----PYPKDCSQALLANGEV 1602
Qy 1994 EDGHLHTFYLGTCR 2008
Db 1603 TSG--LVTIYLANGDR 1615

RESULT 12
T09070
probable tenascin X - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09070
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09070
A>Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 1-4006 <ROW>
A:Cross-references: UNIPROT:O35452; UNIPARC:UPI0000002A159; EMBL:AF030001; NID:G2564945;
C:Genetics:

A:Gene: TNX
A:Map position: 17
A:Introns: 124/1; 735/1; 773/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 1440/1;
019/1; 3115/1; 3208/1; 3405/1; 3517/1; 3558/1; 3606/1; 3646/1; 3694/1; 3737/3;
C:Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin ty
C:Keywords: extracellular matrix
F:422-448/Domain: EGF homology <EGF>
F:826-906/Domain: fibronectin type III repeat homology <3FR>
F:3789-3997/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 4.2%; Score 626; DB 2; Length 4006;
Best Local Similarity 22.4%; Pred. No. 9e-26;
Matches 359; Conservative 163; Mismatches 585; Indels 498; Gaps 77;

Qy 566 CPSCNYGNGDCISGTCHCFLGFLGPCGRASCVPVLCSGNGQYMKGRCLCHSGMKGABCDV 625
Db 422 CPDRCGRGCEGVCVCHAGYSGEDCGVRSFCGDCRGCNCSGRCVCPWGYTGRDGG- 480
Qy 626 PTNQCIDVACSNHGTCTITGTCICNPYKSGESBEVDCMDPTCSGRGVCVVGECHCFVGMG 685
Db 481 -TRAC-PGDCRGRGRCVDRGVCNPGFTGBDCGSRRC-PGDCRGGHGCENGVCVCAVGS 537
Qy 686 GTNCEPTRATCLDQCSGHGTFPDTGLCSDPSTWGHDCSIEICAAACDGGHGVCGVGTCTR 745
Db 538 GDDCST--RSCPBDRCRGQCL--NGLCEDEGYSGBEDCGIRRCPRDCSHGVQCQDGLCM 593
Qy 746 CEDGMMGAACDQACHPRCAEHGTCRDGKCECSPGWNGEHCTIAHYLDRVVVKEGCPGLCN 805
Db 594 CHAGYAGEDCSITPCADCRRRRCRCDGRCVCPNGYTGPAAC-----ATRTC PADCR 644
Qy 806 GNGRCITLDLNGMHCVCQGLGWRGAGCDTSMETA-----CGDSKNDGDGLVDCMD---P 855
Db 645 GRGRCVQGV---CMCVGYSGEDCGQEBPPASACPGCG-PRELCRAGQCVCVEGRFGP 699
Qy 856 DCLQLP---CHINPLCL-----P-----GS 872
Db 700 DCAIOTCPGDCRGERGICQRCVCQEGYAGDCGEEIPAIONMRMHLETTVTRTEWTRA 759
Qy 873 PNPDLIIQETQVPVSQNLHSFYDRIKFLVGR-DSTHIIIPGENPFDGGHACVIRGQWMTS 931
Db 760 PGVDAYEIQFIPTGEGVSPPTARVPSSASAVDQRLAQD-----YQVTVRALRGTS 814
Qy 932 DGTPLVGVNTSYFNNPLFGYTIISRDGSDFLVNTGGISIIILRPERAPPTQEHTLWLPW- 990
Db 815 WGPASAKTITMIDGP-----QDLRVAVT-----PTTLDLSWL 848
Qy 991 -----DRFPVMTETIMRHEEN-EIPSCDLSNFARNPNPVVSPSPLTSP----- 1031
Db 849 RPOAEVDRFVYVSAGNQVRLEVP-----PEADRTQLTDLMPGEVYVTVTA 897
Qy 1032 -----ASSCAEKGPIVPEIQALQEEIISGCKMRLSVLSRTPGYKSVLRISLTHP 1082
Db 898 ERGHAVSYPAIRANTGSLSPGLEATDEPPPG-----PSTTQGAQAPILILEHH- 948
Qy 1083 TIFPNLMKVLHVMVAVEGRFRKFAAADLSYTF-----IWDKTDV----- 1123
Db 949 --PLGELKV-LGRDKAGRLSVAN-TAQPDSDFAHQLRMQVAEGPWAHEELLPDGVQALV 1004
Qy 1124 -----YNQVFGJSE-AFVSVGVEYESCPDLILWEKRTTVLQGYEIDASKLGGHSLD 1174
Db 1005 PPPPPGAPYKXLFHLGITPPGKISVPITYQIMD-----RAEQPGKPSVQPRGELTVT 1058
Qy 1175 KHALNATQSGILKHKNGENOFVS-----QQPPVIGSIMGNRRRSISCPSCNGLADGN 1227
Db 1059 ---GLTSDSLHLHWTPVEGDFDSFLQYKDKQGPQALISVSGPQSTFIS-----GLPEGR 1110
Qy 1228 K-----LLAPVALTCGSD-----GSLYVGD-----FNYIRR 1253
Db 1111 KYKFILYGLIGKKRHGFLMAEAKILIQSDPDGSPRPLGELWVTDPTPHSLHLSWTVLGG 1170
Qy 1254 IPFSGNVNTILELRNKDPR-----HSHSPAHHY-----LA 1284
Db 1171 QFDS----FVVQVRDEKQPRVVPVEGPRDSRVVISPLDPNRYKFRYTLFLGIANKKRYGFLT 1226

Db 4441 AGCCACCGCTTTGGCTGTTTTCACACAATGGGGTCTGTATATTGCTGAGACTGATGAGAA 4500
Qy 4501 AAGATCAACCGCATCAGGCAGGTCAACCACTAGTGAGAGATCTCACTGTTGCTGGGC 4560
Db 4501 AAGATCAACCGCATCAGGCAGGTCAACCACTAGTGAGAGATCTCACTGTTGCTGGGC 4560
Qy 4561 CCCAGTGGCTGTGACTGTAAATAATGATGCCAACTGTGATTTGTTTCTGGAGACGATGG 4620
Db 4561 CCCAGTGGCTGTGACTGTAAATAATGATGCCAACTGTGATTTGTTTCTGGAGACGATGG 4620
Qy 4621 TTATGCCAAGATGCAAAAGTTAAATAACCCATCTTCCCTGGCTGTGCTGATGGGA 4680
Db 4621 TTATGCCAAGATGCAAAAGTTAAATAACCCATCTTCCCTGGCTGTGCTGATGGGA 4680
Qy 4681 GCTCTACGTGGCGGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAAACAAGCCTTT 4740
Db 4681 GCTCTACGTGGCGGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAAACAAGCCTTT 4740
Qy 4741 CCTCAACACCCAGAACATGTATGAGCTGTTTCAACCAATTGACCAGGAGCTCTATCTGTT 4800
Db 4741 CCTCAACACCCAGAACATGTATGAGCTGTTTCAACCAATTGACCAGGAGCTCTATCTGTT 4800
Qy 4801 TGATACACCGGCAAGCACTGTACACCAAGCGCTGCCCAAGAGACTACTGTACAA 4860
Db 4801 TGATACACCGGCAAGCACTGTACACCAAGCGCTGCCCAAGAGACTACTGTACAA 4860
Qy 4861 CTTTCACTACCTGCGGACGAGACTACTGAGATGCCCTCTGGCTGTGGTCCAGATGGCCAGGT 4920
Db 4861 CTTTCACTACCTGCGGACGAGACTACTGAGATGCCCTCTGGCTGTGGTCCAGATGGCCAGGT 4920
Qy 4921 AAATGTCCGCGAGACTACTGAGATGCCCTCTGGCTGTGGTCCAGATGGCCAGGT 4980
Db 4921 AAATGTCCGCGAGACTACTGAGATGCCCTCTGGCTGTGGTCCAGATGGCCAGGT 4980
Qy 4981 GTACTGGGTGACCATGGGCACCAACAGTGCACTCAAGAGTGACACACAAGAGACAGA 5040
Db 4981 GTACTGGGTGACCATGGGCACCAACAGTGCACTCAAGAGTGACACACAAGAGACAGA 5040
Qy 5041 GTTGGCCATGATGACATACCATGGAATTCGGGCTTCTGGCAACCAAAAGCAATGAAA 5100
Db 5041 GTTGGCCATGATGACATACCATGGAATTCGGGCTTCTGGCAACCAAAAGCAATGAAA 5100
Qy 5101 CGGATGGAACAATTTATGATGACAGACTTTGGCCGCTTGACAAATGTGACCTTCCC 5160
Db 5101 CGGATGGAACAATTTATGATGACAGACTTTGGCCGCTTGACAAATGTGACCTTCCC 5160
Qy 5161 TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTGATGTCAGGTAGA 5220
Db 5161 TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTGATGTCAGGTAGA 5220
Qy 5221 GACCTCCAGCAAGGATGATGTCACCAATACCAACCTGCTGCTCAGGCGCTTCTA 5280
Db 5221 GACCTCCAGCAAGGATGATGTCACCAATACCAACCTGCTGCTCAGGCGCTTCTA 5280
Qy 5281 CACACTGCTGGAAGCAAGTCCGGAACAGCTACTACATCGGGGCCGATGCTTCTGCG 5340
Db 5281 CACACTGCTGGAAGCAAGTCCGGAACAGCTACTACATCGGGGCCGATGCTTCTGCG 5340
Qy 5341 GCTGCTGCTGGCCAAAGCATGGAGTGGCGCTGACAGACTGAGCCCCACTGCTGGCTGG 5400
Db 5341 GCTGCTGCTGGCCAAAGCATGGAGTGGCGCTGACAGACTGAGCCCCACTGCTGGCTGG 5400
Qy 5401 CACCGTCAACCCCAACCGTGGGCAAGGAAATGTCAACGCTGCCCAACCAAGCGCTCAA 5460
Db 5401 CACCGTCAACCCCAACCGTGGGCAAGGAAATGTCAACGCTGCCCAACCAAGCGCTCAA 5460
Qy 5461 CTTGTTGAGATGGCCGACGCAAGAGCAAGGCTCGGGCCAGGTCACTGTCTTTGGCG 5520
Db 5461 CTTGTTGAGATGGCCGACGCAAGAGCAAGGCTCGGGCCAGGTCACTGTCTTTGGCG 5520
Qy 5521 CCGGCTGCGGGTGCAACCCGAAATCTCTATCTCTGACCTTTGATCGGTAAACCGCAC 5580
Db 5521 CCGGCTGCGGGTGCAACCCGAAATCTCTATCTCTGACCTTTGATCGGTAAACCGCAC 5580

Qy 5581 AGAAGATCTATGATGACCAACCGCAAGTTTCAACCTTCGGATTTCTGTACGACGAGCGGG 5640
Db 5581 AGAAGATCTATGATGACCAACCGCAAGTTTCAACCTTCGGATTTCTGTACGACGAGCGGG 5640
Qy 5641 CGCGCCCAAGCTCTGGTCAACCCAGCAGCAGCTGAAATGGTGTCAACCTGTACATACTCCCC 5700
Db 5641 CGCGCCCAAGCTCTGGTCAACCCAGCAGCAGCTGAAATGGTGTCAACCTGTACATACTCCCC 5700
Qy 5701 TGGGGGTTAATTTGCTGGCATCCAGAGGGGATCATGCTCTGAAAGAATGGAATACGACCA 5760
Db 5701 TGGGGGTTAATTTGCTGGCATCCAGAGGGGATCATGCTCTGAAAGAATGGAATACGACCA 5760
Qy 5761 GCGCGGCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT 5820
Db 5761 GCGCGGCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT 5820
Qy 5821 AGAAGTCCATGCTGCTGTACTACACAGCCAGAGGAGTATATCTTTGAGTTTCGACAA 5880
Db 5821 AGAAGTCCATGCTGCTGTACTACACAGCCAGAGGAGTATATCTTTGAGTTTCGACAA 5880
Qy 5881 GAATGACCGGCTCTCTTCTGTGACGATGCCAAACGTTGGCGGCGGACACCTAGAGACAT 5940
Db 5881 GAATGACCGGCTCTCTTCTGTGACGATGCCAAACGTTGGCGGCGGACACCTAGAGACAT 5940
Qy 5941 CCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCCTCAGTCAT 6000
Db 5941 CCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCCTCAGTCAT 6000
Qy 6001 ACAGGACTTCACTGAGGATGGGCACTCTTTCACACCTTACCTTGGGCACTGGCCGCGAG 6060
Db 6001 ACAGGACTTCACTGAGGATGGGCACTCTTTCACACCTTACCTTGGGCACTGGCCGCGAG 6060
Qy 6061 GGTGATATACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACAA 6120
Db 6061 GGTGATATACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACAA 6120
Qy 6121 GGTCAAGTTTCACTATGACGAGACGCGGATGCTGAAAGCATTCAACCTACAGATGA 6180
Db 6121 GGTCAAGTTTCACTATGACGAGACGCGGATGCTGAAAGCATTCAACCTACAGATGA 6180
Qy 6181 GGGCTTCACTGACCACTCCGCTACCGTCAAGATTTGGGCCCTTGAITGACGACAGATCTT 6240
Db 6181 GGGCTTCACTGACCACTCCGCTACCGTCAAGATTTGGGCCCTTGAITGACGACAGATCTT 6240
Qy 6241 CCGCTTCACTGAGGAAGGCATGCTCAACGCGCTTTTGACTACAACTATGACAAACAGCTT 6300
Db 6241 CCGCTTCACTGAGGAAGGCATGCTCAACGCGCTTTTGACTACAACTATGACAAACAGCTT 6300
Qy 6301 CCGGTTGACCAAGCATGTCAGCTGTGATCAACGAGACCCCACTGCCATTGATCTCTATCG 6360
Db 6301 CCGGTTGACCAAGCATGTCAGCTGTGATCAACGAGACCCCACTGCCATTGATCTCTATCG 6360
Qy 6361 CTATGATGATGTCTCAGGCAAGACAGAGAGTTTGGGAAGTTTGGTGTCAATTTACTATGA 6420
Db 6361 CTATGATGATGTCTCAGGCAAGACAGAGAGTTTGGGAAGTTTGGTGTCAATTTACTATGA 6420
Qy 6421 CATTAACCAAGATCATCACCACAGCTGTGATGACCCACCAAGCAATTTGATGATCATG 6480
Db 6421 CATTAACCAAGATCATCACCACAGCTGTGATGACCCACCAAGCAATTTGATGATCATG 6480
Qy 6481 CAGGATGAAGGAAGTGCAGTATGAGATCTTCGCTCGCTCATGTACTGGATGACCGTCCA 6540
Db 6481 CAGGATGAAGGAAGTGCAGTATGAGATCTTCGCTCGCTCATGTACTGGATGACCGTCCA 6540
Qy 6541 GTATGATAACATGGGCGAGTAGTGAAGAGGAGCTGAAGGTAGGACCTTACGCCAATAC 6600
Db 6541 GTATGATAACATGGGCGAGTAGTGAAGAGGAGCTGAAGGTAGGACCTTACGCCAATAC 6600
Qy 6601 CACTCGCTACTCTATGATGATGATGCTGACGCGCCAGCTGACAGACAGTCTCCATCAATGA 6660
Db 6601 CACTCGCTACTCTATGATGATGATGCTGACGCGCCAGCTGACAGACAGTCTCCATCAATGA 6660

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|-----------------------|-----------------|--|-------------------|--------------|
| Query Match | 42.4%; | Score 3542.2; | DB 9; | Length 8362; |
| Best Local Similarity | 65.5%; | Pred. No. 0; | | |
| Matches 5458; | Conservative 0; | Mismatches 2683; | Indels 186; | Gaps 12; |
| QY | 33 | CCATGGACGTGAAGGAGAGCAAGCCTTACCGCTCGCTGACCGCGGC---- | CGGACGCGC | 89 |
| Db | 69 | CCATGGATGTGAAGAAGCGCAGGCTTACTGCTCCCTGACCAAGACGACAGAGAAG | 128 | |
| QY | 90 | AGCGCCGCTACACACAGCTCTGTCGCGGACAGCAGGAGGGCAAG---- | CCCCCGCAGAAAT | 146 |
| Db | 129 | AACGGCGCTACACAAATTCCTCCGACACAATGAGGAGTCCGGGTACCCACACAGAGT | 188 | |
| QY | 147 | CGTACAGCTCCAGCGAGACCTGAAAGCCTACAGACAGAA----- | CGCCCGCTTAGCCTATG | 203 |
| Db | 189 | CCTACAGTTCAGGCGAGACATTGAAGCTTTTGATCATGATTCCTCGCGGCTGCTTTACG | 248 | |
| QY | 204 | GCAGCGCGGTCAAGGACATTTGTGCGGAGGAGGCCAGGAATTTCTGCGCACAGGTGCCA | 263 | |
| Db | 249 | GCAACAGAGTGAAGATTTGGTTACAGAGAGCAGACAGGTTTCACTAGACAGACAGACA | 308 | |
| QY | 264 | ACTTCACCTTCGGGGAGCTGGGGCTGGAAGAAGTAAACGCCCTCAACGGGACCCCTGTACC | 323 | |
| Db | 309 | ATTTTACCTTAAGGCAGTTAGGAGTTTGTGAACAGCAACTCGAAGAGGACTGGCATTTT | 368 | |
| QY | 324 | GGACAGACATTTGGCTTGCSCCAATGGGCTACTCCATGGGGCTGGCTCTGATGCCGACA | 383 | |
| Db | 369 | GTGCGGAATGGGGCTCCCTCACAGAGTTACTCTATCAGTGCAGGGTCAGATGCTGATA | 428 | |
| QY | 384 | TGAGGCTGACACGGTGTCTGCCCTGAGCACCCCTGGCTCTGTGGGGCGGAGCACAC | 443 | |
| Db | 429 | CTGAAATGAAGCAGTGTATGTGCCAGAGCATGCCATGAGACTTTTGGGGCAGGGGGTCA | 488 | |
| QY | 444 | GGTCAGGGCGAGCTCTGCTGTCCAGCGGGCCAAATTCGAATCTCACTCAACCGACA | 503 | |
| Db | 489 | AATCAGGCCGAGCTCTGCTGTCAAGTCGGTCCAACTCAGCCCTCAACCTGCACAGATA | 548 | |
| QY | 504 | CCGAGCATGAAAACACTGAGACTGATCATCCGGGGCGCTGCAGAACCAACGCGCGGCTCC | 563 | |
| Db | 549 | CGGAGCACGAAAAACAAGTCCGACAGTGAAGTAGCAACCTGCAAGCAATCAAGGCCAGT | 608 | |
| QY | 564 | GGACGCGCGCGCGCGCTCTCGCACGCCCCAACACCCCAACGACGACGCGGCTCCA | 623 | |
| Db | 609 | CTACCTCTGCAGCCCTTGCGCCCTTCCCATAAAGCAGCACTCTGCACAGCATCATCCATCCA | 668 | |
| QY | 624 | TTAACTCCCTGAACCGGGGCACTTCAAGCGGAGAGCAACCCAGCGCGGCGCCCAAG | 683 | |
| Db | 669 | TCACTTCTCTCAACAGAACTCCCTGACCAATAGAAGGAACCAAGTCCGCGCGCGCGCGG | 728 | |
| QY | 684 | ACCACCTCGCTCTCGGAGAGCCCTTGCAGGGCGGCGCCAGGAGCTGCCCAACGCCCAGG | 743 | |
| Db | 729 | CTGCTTTGCGCGCGAGCTGCAAC-----CACACCGAGTCCGTCAGCTGCAGG | 779 | |
| QY | 744 | AGAACTGGCTGTCAACAGCAACATCCCGCTGGAGACAGGAACCTAGGCAAGCAGCCAT | 803 | |
| Db | 780 | ACAGCTGGGTCTTGGCAGTATGTATACCACTGGAAGCAGGCATTT----- | 825 | |
| QY | 804 | TCCTAGGAGCATTTGCAGGACAACTCATTTGAGATGGACATTTCTCGGCGCCTCCCGCCATG | 863 | |
| Db | 826 | ----- | 825 | |
| QY | 864 | ATGGGGCTTACAGTGACGGGCACTTCTCTTCAAGCCTGGAGGACCTTCCCGCTCTTCT | 923 | |
| Db | 826 | -----CCTATTCAAAACAGGAAACAGGTACAAACGCCACTGTTCAC | 863 | |
| QY | 924 | GCACCATCACCAAGGTATCCCACTGAGTCCAGCACAGTGTACTCTCTCCCGCCCGCAC | 983 | |
| Db | 864 | GTACTGCAACCCACAGATACAAATGGCATCTGGGTCTGTTTATTACCACTACTCTCGGC | 923 | |
| QY | 984 | CCCTGCGCGCGAGCACCTTTCGCGCGCGCGCTTTTAACTCAAGAGCCCTTCCAAGTACT | 1043 | |
| Db | 924 | CATTCTATGAACACCCCTATCAAGAAGTGCTTTTAAATTCAGAAAGTCTTTAAAGTACT | 983 | |

| | | | | |
|----|------|--|--|--|
| Qy | 1044 | GTAACCTGGAAGTGGCGAGCCCTGAGCGCCATCGTCATCTCAGCACTCTGTGTCATCTCTGC 1103 | | |
| Db | 984 | GTAGCTGAAATGCACATGCATGTGTGCGGTAGGGTCTCGGTCTCTCTGCAATACTCTCC 1043 | | |
| Qy | 1104 | TGGCATACTTTTGTGGCCATGCACCTGTTTGGCCTTAACTTGGCACCTGCGCCGATGAGG 1163 | | |
| Db | 1044 | TGTCTTATTTTATAGCAATGCATCTCTTGGCCTCAACTGGCAGCTACAGCAGACTGAAA 1103 | | |
| Qy | 1164 | GGCAGATGTATGAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACACCACTCT 1223 | | |
| Db | 1104 | ATGACACATTTGACA-----ATGGAAGTGAATTTCTGATACCATGCTGCCAACAACTG 1157 | | |
| Qy | 1224 | CCCTATATCCCTCAGGGGGCACTGGCTTTAGAGACCCCTGACAGGAAAGGCAAGAACCA 1283 | | |
| Db | 1158 | TGTCATTACCTTCTGGAGACA----- 1178 | | |
| Qy | 1284 | CAGAAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAGTTTTCATAGATTCTGGAGAAATTG 1343 | | |
| Db | 1179 | ---ATGGAATAATTAGTGGATTTTACGCAAGAAATAACACATAGATTCCGGAGAACTTG 1235 | | |
| Qy | 1344 | ATGTGGAAAGCGAGCCCTCCAGAAATTCCTCCTGGCACTTTCTGGAGATCTCAAGTGT 1403 | | |
| Db | 1236 | ATATTGCCGGAAGAGCAATTCAGAGATTCTCCCGGATCTTCTGGAGATCACAGCTCT 1295 | | |
| Qy | 1404 | TCATAGACCATCTGTGCATCTGAATTTCAATGTGTCTCTGGGAAAGGCAAGCCCTGGTTG 1463 | | |
| Db | 1296 | TCATTGTATCAGCCACAGTTTCTTAAATTCATATCTCTCTCAGAAGGATGCAATTGATTG 1355 | | |
| Qy | 1464 | GCATTATGCGAGAAAGGCTCCCTCTTTCACATACACAGTTTGTACTTTGTGGAGCTGC 1523 | | |
| Db | 1356 | GAGTATATGCGGAAAGGCTTACCGCTTCCCATCTCAGTATGACTTCTGCGAGCTCC 1415 | | |
| Qy | 1524 | TGATGSCAGAGGCTCTTAACCCAGAGGCGCGAGCCCTAGAGGGACCCCGCGCAGT 1583 | | |
| Db | 1416 | TGGATGSCAGAGCTGATTGTCAGAGAGCAGCGGAGCTGCTTGAGACGAGAGAGCCG 1475 | | |
| Qy | 1584 | CTGGGGAACTGTGCCCCCTCCAGCGCATGAGACAGCTTCATCCAGTATTGGATTCAG 1643 | | |
| Db | 1476 | GGCGGACAGCGAGATCCGTGAGCTTTTATGAGGCCGCTTTATCCAGTACTTGGATTCTG 1535 | | |
| Qy | 1644 | GAATCTGGCACTTGGCTTTTAAATGACGGAAGGAGTCAGAACTGGTTTCTCTTCTCA 1703 | | |
| Db | 1536 | GAATCTGGCATCTGGCTTTTATAATGATGGGAAATAATGCAGACAGAGTGTCTTTTAATA 1595 | | |
| Qy | 1704 | CACTGSCATTTAGTCTGGTGAATACTGCCCCAGCAACTGCTATGCAATGGTGACTGCA 1763 | | |
| Db | 1596 | CCATTGTTATAGAGTCTGTGGTGAATGTCCCGAAATTGCCATGGAATGGAAATGGCAATGCG 1655 | | |
| Qy | 1764 | TCTCTGGGACCTGCGCACTGCTTCTCGGTTCCTGGGCCCGGACTGTGGCAGAGCCTCCT 1823 | | |
| Db | 1656 | TTTCTGGAATCTGCCATTTGTTTTCAGGATTTCTGGGTCCGGATTTGTTCAAGAGCCGCT 1715 | | |
| Qy | 1824 | GCCCGTGTCTGTAGCGGAAATGGCCAAATACATAAGAAAGGACAGATCTTGTGCCACAGTG 1883 | | |
| Db | 1716 | GTCCAGTGTATGATAGTGGCAACGGGCACTACTCCAAAGGCGGCTGCTGCTGTTTTCAGCG 1775 | | |
| Qy | 1884 | GCTGGAAGGCGCTGAGTCCGATGTGCCCAACCAACAGTGTATTCGATGTGGCTCGCAGCA 1943 | | |
| Db | 1776 | GCTGGAAGGCGCACCGAGTGTGATGTGCCGACTACCCAGTGTATTGACCCACAGTGTGGGG 1835 | | |
| Qy | 1944 | ACCATGGCACTGCAATCACGGGCACTGCATCTGCAACCCCTGCTTACAAGGGCGAGAGCT 2003 | | |
| Db | 1836 | GTGCTGGGATTTGTATCATGGGCTCTTGTGCTTGGCACTCAGATACAAGAGAGAAAGTT 1895 | | |
| Qy | 2004 | GTGAGGAAGTGAATGTCATGGACCCCAATGTTTACGGCCGGGTGTCTCGGTGAGAGCGG 2063 | | |
| Db | 1896 | GTGAAGAACTGACTGTATAGACCCCTGGGTGTTCTAAATCATGCTGTGTATATCCACGGGG 1955 | | |
| Qy | 2064 | AATGCCATTGCTTTGTGGATGGGAGGACCAACTGCGAGACCCCGAGGGCCACATGCT 2123 | | |
| Db | 1956 | AATGTCACCTGCACCTCAGGATGGGAGGTAGCAATTTGTGAAATACTGTAAGACCATGTGTCT 2015 | | |

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|----|------|---|------|
| Qy | 2124 | TAGACGAGTGTTCAGGCCACGGAAACCTTCTCTCCCGGACACCGGGCTTTGCAGCTGTGACC | 2183 |
| Db | 2016 | CAGACCAAGTGTCTCCGGCCACGGAAACGTATCTTCAAGAAAGTGGCTCTCTGCACGCTGTGACC | 2075 |
| Qy | 2184 | CAAGCTGGACTGGACACGACTGTCTTATTCAGAGATCTGTCTGCCGACTGTGGTGGCCATG | 2243 |
| Db | 2076 | CTAACTGGACTGGCCCCAGACTGCTCAACAGAAATATGTCTCTGGAGACTGTGGCTCACAGC | 2135 |
| Qy | 2244 | CGCTGTGCTAGGGGGCACCTGCCCGCTCCGAGAGATGGCTGGATGGGGGCGAGCCTCGGACC | 2303 |
| Db | 2136 | CGCTTGTGATGGGGGGGACGTGTCTGCTGTGAAGAGGCTGGAACGGGCCAGCCTGTAATC | 2195 |
| Qy | 2304 | AGCGGGCTTGCCACCCCGGCTGTGCCGAGCATTTGGGAACTCTGCCGCGGACGGCAAGTGCAGT | 2363 |
| Db | 2196 | AGAGAGCTTGCCACCCCGCTGTGCCGAGCACGGGACCTGCAAGGATGGCAAGTGTGAAAT | 2255 |
| Qy | 2364 | GCAGCCTGGCTGAATGGCGGAACACTGCAACATCGCTCACTATCTCGATAGAGTACTGTA | 2423 |
| Db | 2256 | GCAGCCAGGGCTGGAATGGAGAGCACTGCATCTCTGCTCACTATTGGATAAGATAGTGA | 2315 |
| Qy | 2424 | AAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTACCTTAGACCTCGAATGGTT | 2483 |
| Db | 2316 | AAGAGGGTTGTCCTGGTCTGTGCAACAGCAATGGAAGATGTACCTCGGACCAAAATGGCT | 2375 |
| Qy | 2484 | GGCACTCGCTTGCACAGCTGGGCTGGAGAGGAGCTGTGTCACATTTCCATGGAGACTG | 2543 |
| Db | 2376 | GGCATTTGTGTGCCAGCCTGGATGGAGAGGAGCAGCTGTGACCTAGCCATGGAGACTC | 2435 |
| Qy | 2544 | CCTCGGCTGACAGCAAAAGACAATCATGGAGATGGCCTGGTGGACTGTCATGGACCCCTGACT | 2603 |
| Db | 2436 | TTTGCAAGATAGCAAGAGACAATGAAGGAGATGGACTCAATTGACTGTGATGACCCCGAATT | 2495 |
| Qy | 2604 | GCTGCCTCCAGCCCTGTGCCATATCAACCCGCTGTGCTTGGCTCCCTTAAACCCCTCTGG | 2663 |
| Db | 2496 | GCTGCCTACAGAGTTCTGCGCAGAAATCAGCCCTATTGTCCGGGACTGCGGACCCCTCAGG | 2555 |
| Qy | 2664 | ACATCATCCAGGAGACACAGTCCCTGTGTCCACAGCAGAAACCTACACTCTCTTTATGACC | 2723 |
| Db | 2556 | ACATCATTTAGCCAAAGCCTTCAATCGCCTTCTCAGCAAGCTGCCAAATCTCTTTTATGATC | 2615 |
| Qy | 2724 | GCATCAAGTTCTCTGTGGCAGGACAGCAGCAGACATAAATCCCGGGGAGAACCCCTTTG | 2783 |
| Db | 2616 | GAATCAGTTTCTTATAGGATCTCATAGCACCCCATGTTATACCTTGGAGAAAGTCTTTTCA | 2675 |
| Qy | 2784 | ATGGAGGCGATGCTGTGTATTCTGTGGCCAAAGTGATGACATCAGATGGAAACCCCTCTGG | 2843 |
| Db | 2676 | ATAAGAGCCTTGCACTCTGTCTATCAGAGCCAAAGTACTGACTGCTGTATGGAACTCCATT | 2735 |
| Qy | 2844 | TTGGTGTGAACATCAGTTTTGTCAATAACCCCTCTCTTTTGGATATACAATCAGCAGGCAAG | 2903 |
| Db | 2736 | TTGGAGTAAATGCTCTCGTTTTTCCATTACCCAGAAATATGGATATACTATTACCCGCCAGG | 2795 |
| Qy | 2904 | ATGGCAGCTTTGACTTTGTGTGACAAATGGCGGCATCTCCATCATCTCTGGGTTTCGAGCGG | 2963 |
| Db | 2796 | ACGGAAATGTTTGACTGTGTGGCAAAATGGTGGGGCTCTCTAACTTTGGTATTTGAAACGAT | 2855 |
| Qy | 2964 | CACCTTTTCATCACACAGGAGCACACCTGTGGCTGGCATGGGATGCGTCTTTTGTTCATGG | 3023 |
| Db | 2856 | CCCAATTCCTCACTCAGTATCATACTGTGTGGATTCATGAAATGTCTTTTATGTGATGG | 2915 |
| Qy | 3024 | AAACCATCATCATGAGACATGAGGAGAAATGAGATTTCCAGCTGTGACTGAGCAAAATTTTG | 3083 |
| Db | 2916 | ATACCCCTAGTCAATGAAGAAAGAGAGAAATGATATTCCCGAGCTGTGATCTGAGTGGATTCG | 2975 |
| Qy | 3084 | CCCGCCCCAACCCGAGTCTCTCCATCCCACTGACGTCCTTTCGCCAGCTCCTGTGCGAC | 3143 |
| Db | 2976 | TGAGGCCAAATCCCATCAATTGTGTCTATCCACCTTTATCCACCTTTTTCAGATCTTCTCCTG | 3035 |
| Qy | 3144 | AGAAAGGCCCATTTGTGCGGAAATTCAGGCTTTTGCAGGAGGAAATCTCTATCTCTGGCT | 3203 |
| Db | 3036 | AAGACAGTCCCATCAATCCCGAAACACAGGATCTCCACGAGGAAACTCAAAATTCAGGAA | 3095 |
| Qy | 3204 | GCAAGATGAGGCTGAGCTACCTGTGAGCAGCCGGAACCCCTGGGCTACAAATCTCTCTGAGGA | 3263 |

[illegible]

Db 4176 TGGATAATCCATTATATGCTCTGGATAAATAATAGTAGTTTTACAGATCACTGAAATCGTC 4235
Qy 4344 AGGTGCGCATTTGTCCCGGGAGGCCCATGCACTGCCAGAGTCCCTGGCAATTTGACCACTTCC 4403
Db 4236 AAGTTTCGCAATTTGCTGTGGAGCGGCCCATGCACTGTCTAGGTTCCCGAGTGG---AATATC 4292
Qy 4404 TGCTAAGCAAGGTGCCATTCACCAACCCCTGGAGTCAGCACCGCTTTTGGCTGTTTTCAC 4463
Db 4293 CTGTGGGAAGACACGCGGTGCAGACACACTGGNATCAGCCATGCTTGTGTCTT 4352
Qy 4464 ACAATGGGCTCTGTATATTGCTGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAG 4523
Db 4353 ACAGTGGGGTCCCTGTACATTACTGAAACTGATGAGAGAAAAATTAACGGGATAAGCCAG 4412
Qy 4524 TCACCACTAGTGGAGAGATCTCACTCGTCTGGGGCCCCAGTGGCTGTGACTGTGATAAAA 4583
Db 4413 TCACCAACAGATGGAGAAATCTCTTAGTGCCCGGAATACCTTCAGAGTGTGACTGCAAAA 4472
Qy 4584 ATGATGCCAATCTGTGATTTTCTTGGAGACGATGGTTATGCAAGGATGCAAAATTAA 4643
Db 4473 ATGATGCCAATCTGTGACTGTTTACAGAGTGGAGATGGCTACGCCAAGGATGCCAACTCA 4532
Qy 4644 ATACCCCATCTTCTCTGGCTGTGTCTGATGGGAGCTCTACGTGGCGCAGCTTTGGGA 4703
Db 4533 GTGCCCCATCTCTCCCTGGCTGCTTCTCCAGATGGTACACTGTATATTGCAGATCTAGGA 4592
Qy 4704 ACATCCGAATTCGGTTTATCCGGAAGAAACAAGCCTTTCTCAACACCCAGACATGTATG 4763
Db 4593 ATATCCGGATACGGGCTGTCTAAGANATAAGCCTTTACTTATCTATGAACTTCTATG 4652
Qy 4764 AGCTGTCTTCCAAATGACAGGAGCTCTATCTGTTTGATACCAACCGCAAGCACTGT 4823
Db 4653 AAGTTGCGTCTCCAACTGATCAAGAACTCTACATCTTTGACATCAATGGTACTCAACAA 4712
Qy 4824 ACACCAAGCCCTGCCACAGGAGACTACCTGTGCNACTTCACTACACTGGGGAGCGG 4883
Db 4713 ATACTGTAGTTAGTCACTGGTGATTACCTTTACAAATTTTAGCTACAGCAATGACAA 4772
Qy 4884 ACATCACTCAATCACAGACAACAATGGCAACATGGTAAATGTCGCGCGAGACTCTACTG 4943
Db 4773 ATATTACTGTGTGACAGACAGCAATGGCAACACCTTTAGANATTAGACGGNACCAATC 4832
Qy 4944 GGATGCCCTCTGGCTGGTCCAGATGGCCAGGTGATCTGGGTGACCATGGGCACCA 5003
Db 4833 GCATGCCAGTTGAGTGGTGTCTCTGTGATAACCAAGTGATATGGTTGACAAATAGGAA 4892
Qy 5004 ACAGTGCATCAAGAGTGTGACCACACAGGACACAGTTGGCCATGATGACATACCATG 5063
Db 4893 ATGGATGTTTGAAGAAGCATGACTGCTCAAGGACTGGAAATAGTTTGTGTACTTACCATG 4952
Qy 5064 GCATTTCCGGCTTTCTGGCAACAAAGCAATGAAACGGATGGACAAACATTTTATGAGT 5123
Db 4953 GCAATAGTGGCTTTTAGCCACTAAAGAGTGATGAAACTGGATGGACACGTTTTTGTACT 5012
Qy 5124 ACACAGCTTTTCGCGCCCTGACAAATGTGACCTTCCCTACTGCGCAGGTGAGCAGTTTCC 5183
Db 5013 ATGACAGTGAAGTGTCTGCAAAATGTACGTTTCCAACTGGAGTGGTCAACAACTGCG 5072
Qy 5184 AAGGTGATACAGACAGTTTCACTGTCATGTCAGGTAGAGACCTCCAGC---AAGCATGATG 5240
Db 5073 ATGGGACATGACAAAGGCTATCACAGTGGACATTTAGTCACTTAGCCGAGAAAGATG 5132
Qy 5241 TCACCAATACCAACCACTGTCTGCTCAGGGCTCTTACACACTGCTGCAAGACCAAG 5300
Db 5133 TCAGCATCACTTCAAACTGTGCTCGATCGATTTCTTTCTACACCATGCTTCAAGATCAGT 5192
Qy 5301 TCCGGAACAGCTACTACATCGGGCCGATGCTCCTTGGCTGGCAGCGCTCAACCCACCGTGG 5360
Db 5193 TAAGAAACAGCTACAGATTGGTTATGACGCTCCCTCAAGATTAATCTACGCCAGTGGCC 5252
Qy 5361 TGGAGTGGCGTGCAGACTGAGCCCACTTGTGGCTGGCAGCGCTCAACCCACCGTGG 5420
Db 5253 TGGACTCACTACCAACAGAGCGGACGCTTCTGTGCTGGCAGCGCTTAATCCGACGGTTG 5312

Qy 5421 GCAGAGGAATGTCACTGCTGCCCATCGAACACGCGCTCAACCTGTGTGAGTGGCGCCAGC 5480
Db 5313 CCAAAAGAAACATGACTTTTGGCTGGCGAGAACGCTCAAACTTGTGGATGGAGATTCC 5372
Qy 5481 GCAAAGACAGCTCGGGGCCAGGTCACTGTCTTTTGGCGCGCGCTCGGGGTGCACAACC 5540
Db 5373 GAAAAGCAAGCCAAAGGGAAGTCAATGTCTTTTGGCCGCAAGCTCAGGTTAATGGCA 5432
Qy 5541 GAAATCTCTATCTCTGACTTTTGCATCGCGTAAACACACACAGAGAAGATCTATGATACC 5600
Db 5433 GAAACCTCTTTTCACTTGTGACTTTGATCGAACAAAGACAGAAAAGATCTATGACGACC 5492
Qy 5601 ACCGCAAGTTTCACTTGGATTTCTGACACAGCGGGCGCGCCAGCCCTCTGTGTAC 5660
Db 5493 ACCGTAAATTTCTACTGAGGATCGCTTACGACAGCTCTGGGACCCGACTCTCTGGCTGC 5552
Qy 5661 CCAGCAGCGCTGAAATGGTGTCAACGTGACATCTCCCTGGGGGTTAATTTGTCTGGCA 5720
Db 5553 CAACGACAGAGCTGATGGCGGTCAATGTCTACCTATTTCATCCACAGGTCAAAATGGCCAGCA 5612
Qy 5721 TCCAGAGGGGATCATGTCTGAAAAGAAATGGAATACGACACAGCGGGCGCGCATCACATCCA 5780
Db 5613 TCCAGCGAGGACCACTAGCGAGAAAGTAGATTATGACGACAGGGAGGATCGTGTCTC 5672
Qy 5781 GGATCTTTCGTGATGGGAAGACATGAGGCTACACATCTTTAGAGAAAGTCCATGGTGTGC 5840
Db 5673 GGGTCTTTTGTGATGGTAAACATGGAGTTACACATATTTAGAAAAAGTCCATGGTCTTC 5732
Qy 5841 TACTACACAGCAGAGCAGTATATCTTTGAGTTCCGACAGAAATGACCGCTCTCTCTCTG 5900
Db 5733 TGCTTCAAGCAGCGCAGTACATCTTCGATACGATATGTGGGACCGCTCTGTCTGCCA 5792
Qy 5901 TGACGATGCCCACAGTGGCGCGCAGACACTAGAGACCATCCGCTCAGTGGGCTACTACA 5960
Db 5793 TCACCATGCCCAGTGGCTCGCCACACCATGACAGACCATCCGATCCATTGGCTACTACC 5852
Qy 5961 GAAACATCTACGCGCCCTGAGGGCAATGCCCTCAGTCAACAGGACTTCACTGAGGATG 6020
Db 5853 GCAACATATACAAACCCCGGAAAGCAACGCTCCATCATACGGACTACAAACGAGGAAG 5912
Qy 6021 GGCACTCTCTTACACACTTCTACTCTGGGCACTGGCGCGAGGTGATATACAAAGTATGGCA 6080
Db 5913 GGCTGCTCTACAAACAGCTTTCTTGGGTACAGTGGAGGGTCTTATTTCAAATACAGAA 5972
Qy 6081 AACTGTCAAAGCTGGGAGAGACGCTCTATGACACCAAGGTCACTTCACTATGACG 6140
Db 5973 GGCACTAGGCTCTCAGAAATTTTATATGATGATGACAAAGAGTCACTTACCTATGATG 6032
Qy 6141 AGACGGCAGGCATGCTGAAGACCATCAACCTACAGAAAGAGGGCTTCACTGACCACTCC 6200
Db 6033 AAACAGCAGGAGTCTTAAAGACAGTAACCTCCAGAGTATGGTTTATTTGCAACATTA 6092
Qy 6201 GCTACCGTCAGATTTGGGCCCCCTGATTTGACCGCAGACAGATCTTCCGCTTCACTGAGGAAGCA 6260
Db 6093 GATACAGGCAATTTGCTCCCTGATTTGACAGCAGATTTTCCGCTTTAGTGAAGATGGGA 6152
Qy 6261 TGGTCAACCGCTTTTGAATCAAACTATGACAAAGCTTCCGGGTGACCGCATGCGAGG 6320
Db 6153 TGGTAAATGCAAGATTTTGACTATAGTATGACAAAGCTTTCCAGTGTGATGATGATGATG 6212
Qy 6321 CTGTGATCAACAGAGACCCCACTGCTTCTCTATGCTATGATGATGATGATGATGATGATG 6380
Db 6213 GTGTGATCAATGAAAGCCACTGCTTATTTGATCTGTATCTGTATCAGTTTGAATGACATTTCTGGCA 6272
Qy 6381 AGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATTAACAGATCAATCAACA 6440
Db 6273 AAGTTGAGCAGTTTGGGAAGTTTGGAGTTATATATATGATATTAACAGATCAATTTCTA 6332
Qy 6441 CAGCTGTCAATGACCCACAGCAATTTTGTATGATATGGCAGGATGAGAGTGCAGT 6500
Db 6333 CAGCTGTAAATGACCTATACGAAGCAGCTTTTGTATGCTCATGGCCGCTTATCAAGGAGATTTCAAT 6392

| | | |
|------|--|------|
| 6501 | ATGAGATCTTCCGCTCGCTCATGTACTGGAATGACCGTGCAGTATGATAACATGGGCGCAG | 6566 |
| Qy | | |
| 6393 | ATGAGATATTCCAGCTCGCTCATGTACTGGAATTAACAATTCAGTATGATAACATGGGTCGGG | 6452 |
| Db | | |
| 6561 | TAGTGAAGAGGAGCTGAAGGTAGGACCCCTACGCCAATACCACCTCGCTACTCTCTATGAGT | 6620 |
| Qy | | |
| 6453 | TACCAAGAGAGAGATTAAATAGGGCCCTTTGCCAACACCCAAATATGCTTTATGAAT | 6512 |
| Db | | |
| 6621 | ATGATCTGACGCCAGCTGCAGACAGTCTCCAATCAATGAACAAGCCACTCTGCGCTACA | 6680 |
| Qy | | |
| 6513 | ATGATGTTGATGGACAGCTCCAAACAGTTTACCTCAATGAANAAGATAATGTCGCGGTACA | 6572 |
| Db | | |
| 6681 | GCTACGACCTCAATGGGAACCTGCATTTACTAGAGCCCTGGGAACAGTGCACGCTCACAC | 6740 |
| Qy | | |
| 6573 | ACTACGATCTGAATGGAAACCTCCATTTACTGAACCAAGTAAACAGTGGCGCTCTGACAC | 6632 |
| Db | | |
| 6741 | CACTACGGTATGACATCCGGACCGGATCACTCGGCTGGGTGACGTGCAATCAAGATGG | 6800 |
| Qy | | |
| 6633 | CCCTTCGCTATGACCTGCGAGACAGAAATCACTCGACTGGGTGATGTTCAATATCGGTTGG | 6692 |
| Db | | |
| 6801 | ATGAGATGGCTTCCTGAGGCACGGGGCGGTGATATCTTTTGAGTACAACTCAGCTGGCC | 6860 |
| Qy | | |
| 6693 | ATGAAATGGTTTCCTACGTCAAAAGGGCACGGAATCTTTGAAATAGATCTCCAAGGGC | 6752 |
| Db | | |
| 6861 | TGCTCATCAAGGCTTAAACCGGGCTGGCAGCTGGAGTGTACGGTACCGCTACGATGGCC | 6920 |
| Qy | | |
| 6753 | TTCTAACTCGCTTTACAGTAAAGGGCAGTGGCTGGACAGTGATCTACCGTTATGACGGCC | 6812 |
| Db | | |
| 6921 | TGGGGCGGCGTGTCCAGCAAGCAGCAGCCACAGCCACACCTCGAGTCTCTATGTCAG | 6980 |
| Qy | | |
| 6813 | TGGGAAGGGCGTGTCTAGCAAAACCAAGTCTAGCAGACACCTGCGAGTTTTTTATGCTG | 6872 |
| Db | | |
| 6981 | ACCTGACCAACCCACCAAGGTCAACCACCTGTACAACCACTCCAGCTCTGAGATCACCT | 7040 |
| Qy | | |
| 6873 | ACTTAACTTATCCACTAGAGTTACTCATGTCTACAACCATTCGAGTTCAGAAATTAACCT | 6932 |
| Db | | |
| 7041 | CCCTCTACTACGACTTGCAAAGGACACCTCTTTGCCATTGGAGCTGAGCAGTGGTGTAGT | 7100 |
| Qy | | |
| 6933 | CCCTGTATTATGATCTCCAAGGACATCTTTTGGCATGGAAATCAGCAGTGGGGATGAAT | 6992 |
| Db | | |
| 7101 | TTTACATAGCTTGTGACAAACATCGGGACCCCTCTTGCTGTCTTTAGTGGAAACAGGTTGA | 7160 |
| Qy | | |
| 6993 | TCTATATTGCATCGGATAACACAGGGACACCATCGGCTGTGTTCAGTAGCAATGGGCTTA | 7052 |
| Db | | |
| 7161 | TGATCAAGCAAAATCTGTATACACAGCCTATGGGAGATCTACATGGATACCAACCCCAACT | 7220 |
| Qy | | |
| 7053 | TGCTGAACAAGATTCAGTACACTGCATATGGGGNAATCTATTTTGACTCTTAATTTGACT | 7112 |
| Db | | |
| 7221 | TTGAGATCATCATTAGGCTACCATGGTGGCCCTCTATGATCCACTCAACAGCTTGTCCACA | 7280 |
| Qy | | |
| 7113 | TTCAACTGGTAAATTGGATTTTCATGGTGGCCCTGTATGACCCACTCACCAATTAATCCACT | 7172 |
| Db | | |
| 7281 | TGGGCGCGCAGATTATGATGTGCTTGCCCGGACGCTGGACTAGCCAGACCAAGAGCTGT | 7340 |
| Qy | | |
| 7173 | TTGGAGAAAGAGATTATGCAATTTTGGCAGAGCGGTGGACAACACCTGACATAGAAATCT | 7232 |
| Db | | |
| 7341 | GGAAAGCACTTAGTAGCAGCAACGTATGCTTTTAATCTTATCTTATCTTCAAAAAACAAC | 7400 |
| Qy | | |
| 7233 | GGAAAAATGGGAAGGACCCAGCTCTTTTTAACTTTGTCATGTTTAGGNAATACA | 7289 |
| Db | | |
| 7401 | ACCCCATCAGCAACTCCCGAGCATCAAGTGTCTTCATGACAGATGTTTAAACAGCTGGCTG | 7460 |
| Qy | | |
| 7290 | ACCTGCAAGCAAAAATCCATGACGTGAAGATTTACATCACAGATGTTTAAACAGCTGGCTG | 7349 |
| Db | | |
| 7461 | TCACCTTTTGAATTCAGGTTACAAACGTGATTCCTGTTTATCCAAACCAAGACATGATG | 7520 |
| Qy | | |
| 7350 | TGACATTTGGTTTCCATCTGCACAAATGCTATTCTCTGGATTCCTCTGTTTCCCAAAATTTGAT | 7409 |
| Db | | |
| 7521 | CCATGGAAACCTCTCTACGAGCTCATCCACACAGATGMAAACCGCAGGATGGGACAACA | 7580 |
| Qy | | |
| 7410 | TAAACAGAACCTTCTTACGA-----ACTTGTGAAGAGTCAAGAGTGGGATGATA | 7457 |
| Db | | |
| 7581 | GCAAGTCTATCTCTCGGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGGCTTTGTGTACCT | 7640 |
| Qy | | |

RESULT 3

RESULT 3
US-11-096-051-9

US-11-098-031-2
; Sequence 9, Application US/11096051

Publication No. US20050244868A1

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; TITLE OF INVENTION: Ten-M3 Polypeptides and

FILE REFERENCE: Attorney Docket No. Cura 967

; CURRENT APPLICATION NUMBER: US/11/096,051

; CURRENT FILING DATE: 2005-03-30

; PRIOR APPLICATION NUMBER: 10/038,854

; PRIOR FILING DATE: 2001-12-31
PRIOR PUBLICATION NUMBER: 10/

;; PRIOR APPLICATION NUMBER: 10/455,712
; PRIOR FILING DATE: 2003-06-04

; PRIOR FILING DATE: 2003-06-04
 ; PRIOR APPLICATION NUMBER: 60/557 978

;; PRIOR APPLICATION NUMBER: 60/557,978
: PRIOR FILING DATE: 2004-03-30

; PRIOR FILING DATE: 2004-03-30
 ; NUMBER OF SEQ ID NOS: 38

; NUMBER OF SEQ ID NOS: 38

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|----|------|---|------|
| Qy | 2006 | GAGAACTGGACGTGCATGGACCCACACATGTTTCAGCGCGGGTGTCTCGTGGAGAGCGGAA | 2066 |
| Db | 1978 | GAAGAACTGACTGTATAGACCCCTGGGTGTTCTAAATCATGGTGTGTATATCCACGGGGAA | 2037 |
| Qy | 2066 | TGCCATTGCTTTGTGGGATGGGGAGGCACCAACTGCGAGACCCCGAGGGCCACATGCTTA | 2125 |
| Db | 2038 | TGTCACCTGCAGTCCAGGATGGGAGGTAGCAATTTGTGAATACTCTGAAGACCATGTGTCCA | 2097 |
| Qy | 2126 | GACCAAGTGTTCAGGCCACGGAACCTTCCTCCCGACACCGGGCTTTTGCACTGTGACCCA | 2185 |
| Db | 2098 | GACCAAGTGTCTCCGCGCACGGAACTATCTTCAGAAAGTGGCTCTGCACTGTGACCCCT | 2157 |
| Qy | 2186 | AGCTGGACTGGAACGACACTGTTTATCGAGACTGTGCTCGCGACTGTGTGTGGCCATGCG | 2245 |
| Db | 2158 | AACTGGACTGGCCCCAGACTGCTCAACGAAATATGTTCTGTGGACTGTGGCTCACACGGC | 2217 |
| Qy | 2246 | GTGTGCGTAGGGGGCACCTCCGCTGCGAGGATGGCTGGATGGGGGAGAGCCTCGGACCG | 2305 |
| Db | 2218 | GTTTGGCATGGGGGGAAGTGTGCTGTGAAGAAGGCTGGACGGGCCAGGCTGTAAATCAG | 2277 |
| Qy | 2306 | CGGGCTTGCCACCCGCGCTGTGCCAGCACTGGGACCTGCCGCGACGGCAAGTGCAGATGC | 2365 |
| Db | 2278 | AGAGCTTGCCACCCCGCTGTGCGAGCACGGACCTTGCAAGGATGGCAAGTGTGATGC | 2337 |
| Qy | 2366 | AGCCTTGGCTGGAAATGCGAAACACTGCACCATCGCTCACTATCTGGATAGGGTAGT--- | 2421 |
| Db | 2338 | AGCCAGGGCTGGAAATGAGAGCACTGCACATCGCTCACTATCGCTCACTATTTGGATAAGATGTAAA | 2397 |
| Qy | 2422 | -----TAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGCGACAGATGTACC | 2467 |
| Db | 2398 | GACAAGATAGGATATAAAGAGGGTTGTCTGTGTCGCAACAGCAATGAAGAGATGTACC | 2457 |
| Qy | 2468 | TTAGACTCGAATGTTGGCACTCGCTCTGCCAGCTGGGCTGGAGAGAGCTGTGCTGTGAC | 2527 |
| Db | 2458 | CTGGAACCAAAATGGCGGACATTGTGTGCCAGCTGGAATGGAGAGGACGAGCTGTGAC | 2517 |
| Qy | 2528 | ACTTCCATGGAGACTGCTCGGTGACAGCAAGAACAAATGATGAGAGATGGCTGTGTTGGAC | 2587 |
| Db | 2518 | GTAGCCATGGAGACTCTTTGACAGATAGCAAGGACAAATGAAGGGGATGGACTCATTTGAC | 2577 |
| Qy | 2588 | TGCATGGACCTTGACTGCTGCTCCAGCCCTGTGGCCATATCAACCGCTGTGCTCTGGC | 2647 |
| Db | 2578 | TGCATGATCCCGAATGTGCTGCTACAGATTCCTGSCAGAAATCAGCCCTATTTGTGCGGGA | 2637 |
| Qy | 2648 | TCCCTTAACCTCTTGGACATCATCCAGGAGACACAGGTCCCTGTGTGCACAGCAGAACCTA | 2707 |
| Db | 2638 | CTGCGGATCTCTAGGACATCATTTAGCCAAAGCCTTCAATGCGCTTCTCAGCAAGCTGCC | 2697 |
| Qy | 2708 | CACCTCTTTATGACCGCATCAAGTTCTCTGTGGCGAGGAGACGACACGACATAATCCCC | 2767 |
| Db | 2698 | AAATCCTTTTATGATCGAATCAGTTTCTCTTATAGGATCTGATAGCACCCATGTTATACCT | 2757 |
| Qy | 2768 | GGGAGAAACCCCTTTGATGGAGGCGATGCTGTGTTATTCTGTGGCCCAAGTGAACACATCA | 2827 |
| Db | 2758 | GGAGAAAGTCTCTTCAATAAGAGCCTTGCATCTCATCAGAGGCCAAGTACTGACTGCT | 2817 |
| Qy | 2828 | GATGGAACCCCTCTGTTGGTGTCAACATCAGTTTGTCTAATAACCCCTCTCTTTGGATAT | 2887 |
| Db | 2818 | GATGGAATCCACTATTGGAGTAAATGTCTCGTTTTTCCATTACCCAGAATATGGATAT | 2877 |
| Qy | 2888 | ACAATCAGCAGGCAAGATGGCAGCTTTTGACTTTGTGTGACAAATGGCGGCATCTCCATCATC | 2947 |
| Db | 2878 | ACTATTACCCGCCAGGACGGAAATGTTTGACTTTGGTGGCAATGGTGGGGCTCTCTAACT | 2937 |
| Qy | 2948 | CTGGGTTTCGAGCGGGACCTTTTCAATCAACAGAGACACCCCTGTGGCTGCCATGGGAT | 3007 |
| Db | 2938 | TTGGTATTTGAACGATCCCCATCTCTCACTCAGTATCATACTGTGTGTGGAATTCCTATGAAAT | 2997 |
| Qy | 3008 | CGCTTCTTTGTTCATGGAAACCATCATCATGAGACATGAGGAGAAATGAGATTTCCCGCTGT | 3067 |
| Db | 2998 | GTCCTTTATGTGATGGATACCTCTAGTCAATGAGAGAAAGAGAGAAATGATCTCCCGCTGT | 3057 |
| Qy | 3068 | GACCTGAGCAATTTTGGCCGCGCCCAACCCAGCTGCTCTCATCCCCACCTGACGTCTCTC | 3127 |

| | | | |
|----|--|--|------|
| Db | | GATCTCAGTGGAAATTCTGAGGCCAAATCCCATCA TTGTGTCATCACTTTATCCACTTTT | 3117 |
| Qy | | GC CAGCTCCTGTGCGAGAAAAGCCCCCATTTGTGCCGGAATAATT CAGCGTTTTGCAGGAGGAA | 3187 |
| Db | | TT CAGATCTTCTCCTGAACAGAGCTCCCATCA TTTCCCGAAAAACACAGGTACTCCACGAGGAA | 3177 |
| Qy | | ATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACTGAGCAGCCGGAGCCCCTGCGCTAC | 3247 |
| Db | | ACTACAATTTCCAGGAAACAGATTTTGAAACTCTCCTACTTTGAGTTTCCAGAGCTGCAGGGTAT | 3237 |
| Qy | | AAATCTGTCTGAGGATCAGCCTCACCCACCGACCATCCCTTTCAACCTCATGAAGGTG | 3307 |
| Db | | AAGTCAGTTCTCAAGATCACATGACCAGTCTA TTTATTTCCATTTAATTTAATGAAGTT | 3297 |
| Qy | | CACCTCATGTGATCGGTGAGGGCCGCTCTTCAGGAAGTGGTTGCTGCGAGCCCCAGAC | 3367 |
| Db | | CATCTTATGTAAGTCTAGTAGGAAGACTCTTCCA AAGTGGTTCTCGCTCACCAAAC | 3357 |
| Qy | | CTGTCTCTATTA TTTCA TTTGGGACAAGACAGAGCTCTAC AACAGAAGTGTTTGGGCTT | 3427 |
| Db | | TTGGCCTATACTTT CATATGGGATAAAACAGATGCA TATAATCAGAAAGTCTATGTCCTA | 3417 |
| Qy | | TCAAGAGCCTTTGTTTCCGTGGGTATGAATGA ATCCTGCCACAGATCTAACTCTGTGG | 3487 |
| Db | | TC TGAAGCTGTGTGTGCTGGATATGAGTATG AGTCTGTGTTTGAACCTGACTCTGTGG | 3477 |
| Qy | | GA AAAAGAACAAACAGTGTG CAGGGCTATGAAAT TGACGCGTCCAAGCTTGAGGAGTGG | 3547 |
| Db | | GA AAAGGACTGCCATTTCTG CAGGGCTATGA NTGGATGCGTCCAACATGGGTGGCTGG | 3537 |
| Qy | | AGCCTAGACAAACATCATG CCTCAACAT TC AAAGTGGTATCTCTGCACAAGGGAATGGG | 3607 |
| Db | | ACATTAGATAAA CATCACGTCTGGATGTACAG ACGGTATACTGTACAAGGGAAACGGG | 3597 |
| Qy | | GAGAACGAGTTTGTGCTCAGACAGCTCTCTGT CATTTGGGAGCATCATGGGCAATGGCGC | 3667 |
| Db | | GA AAACCGATTCATCTCCACAGAGCTCCAGT CGTAGTAGCATCATGGGCANTGGCGGA | 3657 |
| Qy | | CGGAGAAGCATCTCTGCCCCAGCTGCAAC GGGCTTTGCTGACGGCCAAACAGCTCTCGGCC | 3727 |
| Db | | AGCGCAGCATTTCTCTGCCCCAGTTGCAAT GGTC AAGTGTAAACAGTTTACTTGGCC | 3717 |
| Qy | | CCAGTGGCCCTACCTGTGGCTCTGAC GGGAGGCTCTATGTGGGTGNATTTCAACTACATT | 3787 |
| Db | | CCAGTGGCGTAGCTGTGTGGGATCGATGG CAGTCTGTACGTAGGCGGATTTCAACTACGTG | 3777 |
| Qy | | AGAAGGATCTTCCCTCTGGAATGTG CACCAACATCTC TAGAGCTGAGGAATAAAGATTTC | 3847 |
| Db | | CGCGGAGATTCCTCTTGGAATGTAA CAAGTGTCTTAGACTTAGAATAAAGATTTT | 3837 |
| Qy | | AGACATAGTCA CAGTCCAGCACAAAT ACTACCTGGCCA CAGACCCCATGAGTGGGGCC | 3907 |
| Db | | AGACATAGCAGCAACCCAGCTATAGAT CTACTCTTGC AAGGATCCAGTCA CGGGAGAT | 3897 |
| Qy | | GTCTTCCTTTCTGACAGCAACAGCGGCGGGTCTTT AAAATCAAAGTCCACTGTGGTGGTG | 3967 |
| Db | | CTGTACGTTTCTGACACAAACACCGCAGAA TTTATCGCCCAAAGTCACTTACGGGGGCA | 3957 |
| Qy | | AAGGACCTTGTCAAGACTCTGAGGTGGTTG CCGGGACAGTGCACAGTGCCTCCCTTTT | 4027 |
| Db | | AAAGACTTGACTAAAATG CAGAAGTCTGTCGAGGGA CAGGGAGCAANTGCCCTTCGGTTT | 4017 |
| Qy | | GATGACACTCGCTCGCGGGATG GTGGAGAGGCCACAGAAGCCACACTCCACAAATCCCAGG | 4087 |
| Db | | GACGAGCGAGATGTGGGATGGAGGAAAGCCGT GGAAGCCACACTCATGAGTCCCAAA | 4077 |
| Qy | | GGTATTACAGTGACAAAGTTTGGGCTGATCTA CTCGTGTAATGGCCACCATGATCAGACGC | 4147 |
| Db | | GGAATGCGAGTTGATAGAATGGATTAA TCTACTTTTGTGATGGAAACCATGATTAGGAAA | 4137 |
| Qy | | ATCGATCAGAAATGGGATCATCTCCACCTGCT CGGCTCTAATGATCTCAGATCAGCCCGG | 4207 |

Db 4138 GTTGACCAAAATGGAATCATATCAACTCTTCTGGGCTCTAAACGATTTGACTTCAGCCAGA 4197
QY 4208 CCACTCAGCTGTGAATCTGTCTATGATATTTCCAGGTAAGA CTGGAGTGGCCACAGAC 4267
Db 4198 CCTTTAACTTGTGACACCAAGCATGACATCAGCCAGGTACGTCTGGAATGGCCCACTGAC 4257
QY 4268 TTAGCCATCAACCAATGACAACTCAGTTTATGTCCTCGACAAACAAATGTGTCTCGNA 4327
Db 4258 CTAGCCATTTAACCTTATGATTAATCTCCATTTATGTCCTGGATTAATTAATGATTTTACAG 4317
QY 4328 ATCTCTGAAACCAACAGGTGGGCATTTGTGCGGGAGGCCCATGCACTGCCAGGTCCCT 4387
Db 4318 ATCACTGAAATTCGTCAAGTTCGCAATTTGCTGTGGAGGCCCATGCACTGTGAGTTCCC 4377
QY 4388 GGCATTGACCACTTCTCTGTAGCAAGGTGGCCATCCAGGAAACCTCTGGAGTCAAGCCACC 4447
Db 4378 GAGGTGG---AATATCTCTGTGGGAGACACGGGGTGCAGACAACTCTGGAATCAGCCACT 4434
QY 4448 GCTTTGGCTGTTTACACAAATGGGGTCTGTATATTTGCTGACACTGATGAGAAAGATC 4507
Db 4435 GCCATTGCTGTCTTACAGTGGGGTCTGTACATTTACTGAAACTGATGAGAGAAATTT 4494
QY 4508 AACCCGATCAGCAGGTCAACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGCCGCCAGT 4567
Db 4495 AACCCGATTAAGGCAGGTCAACAACAGATGGAGAAATCTCCTTAGTGGCCGGAATACCTTCA 4554
QY 4568 GCGTGTGACTGTAAAATGATGCCAACTGTGATTTGTTTCTGGAGACGATGGTTATGCC 4627
Db 4555 GAGTGTGACTGCAAAAATGATGCCAACTGTGACTGTACCAAGAGTGGAGATGGCTTACGCC 4614
QY 4628 AAGGATGCAAAATGAAATACCCCATCTCTCTTGGCTGTGTGCTGATGGGGAGCTCTAC 4687
Db 4615 AAGGATGCCAACTCAGTGGCCCATCTCTCTGGCTGTCTTCCAGATGGTACACTGTAT 4674
QY 4688 GTGGCGACTTGGGAAACATCGAAATTCGGTTTATCCGGAAGAACAAAGCCCTTTCTCAAC 4747
Db 4675 ATTGAGATCTAAGGAATATCCGATCCGGGTGTGTCAAGAAATGAGCCCTTTACTTAAAC 4734
QY 4748 ACCGAGACATGATGAGTGTCTTCCAAATTTGACAGGAGCTCTATCTGTTTGATACC 4807
Db 4735 TCTATGAATCTTATGAAGTTGCGTCTCCAACTGATCAAGAACTCTACATCTTTGACATC 4794
QY 4808 ACCGCAAGCACCTGTACACCCAAAGCCTGCCCCAGGAGACTACTGTACAACTTCAAC 4867
Db 4795 AATGTTACTACCAATATAC TGTAGTTTAGTCACTGGTGTATCTTCAATTTAGC 4854
QY 4868 TACACTGGGAGCGGACATCACACTCATACAGACAA CAATGGCAACATGGTAAATGTC 4927
Db 4855 TACAGCAATGCAATGATATTA TCTGCTGTGACAGACAGCAATGGCAACACCCCTTAGAAT 4914
QY 4928 CGCCGAGACTCTACTGGGATGCCCTCTGCTGGTGGTGGTCCCCAGATGGCCAGGTGACTGG 4987
Db 4915 AGACGGGACCCAAATTCGATGCCAGTTCGAGTGGTGTCTCTGTATTAACAAAGTATATGG 4974
QY 4988 GTGACCATGGGCACCAACAGTGCATCAAGAGTGTGACCAACAGGACACAGAGTTGGCC 5047
Db 4975 TTGACAAATAGGAACAAATGGATGTTTGAAGGCATGACTGTCAAGGACTGGAATTAGTT 5034
QY 5048 ATGATGACATACCATGGCAATTCGGCTTCTGGCAACCAAAAGCAATGAAAACGGATGG 5107
Db 5035 TTGTTTACTTACCATGGCAATGATGGCCCTTTTAGCCATAAAGTATGAACTGGATGG 5094
QY 5108 ACAACATTTTATGATGACACAGCTTTTGGCGCCTGACAAATGTGACCTTCCCTACTGGC 5167
Db 5095 ACNAGTTTTTGTACTATGACAGTGAAGTTCGTCTGACAAATGTTACGTTTCCAACTGGA 5154
QY 5168 CAGGTGACAGTTTCCGAAGTGATACAGACAGTTTCAAGTGCATGTCCAGGTAGAGACCTCC 5227
Db 5155 GTGGTCAAAAACCTGCAATGGGGAATGGAACAAGCTATCACAGTGGACATTTGAGTCACT 5214
QY 5228 AGC---AAGGATGATGTCACCATTAACCAACCACTGTCTGCTCAGGGCCCTTCTACACA 5284
Db 5215 AGCCGAGAAAGATGTGAGCATCACTTCAAACTCTGCTCGATCGATTCGATCTTTCTACACC 5274

QY 5285 CTGCTGCAAGACCAAGTCCGGAAACAGCTATCTACATCGGGCCGATGCTCTTTCGGGCTG 5344
Db 5275 ATGTTCAAGATCAGTTTAAAGAAAACAGCTACAGATTTGTTTATGACGGCTCCCTCAGAATT 5334
QY 5345 CTGCTGGCCCAACGCATGGAGGTGGCGCTCAGACTCAGACCCCACTTTGCTGTGGCGCAC 5404
Db 5335 ATCTACGCCATGGCTTGGACTCACACTACAAACAGAGCGGCACGTTCTTGGCTGGCAC 5394
QY 5405 GTCAACCCCAACCGTGGCCAAAGAGAAATGTCACTGCTGCCATCGCAACAGCGCTCAACCTG 5464
Db 5395 GCTAATCCGAGGTGGTCCAAAAGAAACATGACTTTGCTCGCGAGAACGCTCAAACTTG 5454
QY 5465 GTGAGTGGCGCCAGCAAGAGCAGGCTCGGGGCCAGGTCTCACTGTCTTTTGGCGCGCG 5524
Db 5455 GTGGAATGAGATTTCCGAAAAGAGACGCAAGCCCAAGGGAATCAATGTCTTTTGGCGCAAG 5514
QY 5525 CTGCGGGTGCACAACCGAAATCTCCTATCTCTGACCTTTGATCGCGTAAACACGACAGAG 5584
Db 5515 CTAGGGTTAATGGAGAAACCTCCTTTTCACTGAGGATCGCTTACGACACGCTCTGGGCAC 5574
QY 5585 AAGATCTATGATGACCAACCAAGTTTCAACCTTTCCGATTTCTGTACGACCAAGCGGGCGG 5644
Db 5575 AAGATCTATGACGACCAACCGTAAATTTCTACTGAGGATCGCTTACGACACGCTCTGGGCAC 5634
QY 5645 CCAGCCTCTGGTCAACGACGACAGGCTGAATGGTGTCAACGTGACATCTCCCTGGG 5704
Db 5635 CCGACTCTCTGGCTGCCAAGCAAGCTGATGGCCCTCAATGTCACTTATTCATCCACA 5694
QY 5705 GGTATACATCTCGCATCCAGAGGGGCATCATGTCTCTGAAAGATGGAATACGACACGAGCG 5764
Db 5695 GGTCAATTCGACGATCCAGCGAGGCAACA CTAGCGAGAAAGTATGATGAGGACAG 5754
QY 5765 GGCAGCATCATCTCCAGGATCTTTCGTGATGGGAAGACATGGAGCTACACATCTTAGAG 5824
Db 5755 GCGAGGATCGTGTCTCGGTCTTTGCTGATGGTAAACATGGAGTTACACATATTTAGAA 5814
QY 5825 AAGTCCATGCTGTCTACTACACAGCAGAGGAGTATATCTTTGATGTCGACAGAAAT 5884
Db 5815 AAGTCCATGTTCTTCTGTCTTCAAGCCAGCGAGTACATCTTTGGAATACGATATGTGG 5874
QY 5885 GACCGCTCTTCTGTGAGATGCCCAAGCTGGCGGGCAGACACTAGAGACCATCCGC 5944
Db 5875 GACCGCTCTGTGCCATCACCATGCCAGTGTGGCTCGCCACACCATGCGACCTCCGA 5934
QY 5945 TCACTGGGCTCTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCTCTCAGTCATACAG 6004
Db 5935 TCCATTTGGCTACTACCGCAACATATACAACCCCGGAAAGCAACGCTCTCCATCATCAG 5994
QY 6005 GACTTCACTGAGGATGGGACCTCTTCACTTACACTTCTACTGGGCACTGGCGCAGGGTG 6064
Db 5995 GACTACAGAGGAAGGGCTGCTTCTACAAACAGCTTTCTTGGGTACAAGTCGAGGGTG 6054
QY 6065 ATATACAAGTATGGCAAACTGTCAAAAGCTGGCAGAGACGCTCTATGACACCAACAAGGTC 6124
Db 6055 TTATTCAAATACAGAGGACAGACTAGGCTCTCAGAAATTTTATATGATAGCAACAGATC 6114
QY 6125 AGTTTCACTATGACAGAGCGGAGGATGCTGGAAGACCATCAACCTACAGAAATGAGGGC 6184
Db 6115 AGTTTACCTATGATGAAAACAGCAGGAGTCTTAAAGACAGTAAACCTCCAGAGTGTAGT 6174
QY 6185 TTCACCTGCACCATCGCTACCGTACAGTTGGGCCCCCTGATTTGACCGACAGAGATCTTCCGC 6244
Db 6175 TTTATTTGACCACTTAGATACAGGCAANTGGTCCCTGATTTGACAGGCGAGATTTTCCGC 6234
QY 6245 TTCCTGAGGAAGGCATGGTCAACGCCCCGTTTGTGACTACAACTATGACAAACAGCTTCCGC 6304
Db 6235 TTTAGTGAAGATGGGATGTTAAATGCAAGATTTGACTATAGCTATGACAAACAGCTTTCCGA 6294
QY 6305 GTGACAGCATGCGAGCTGTGATCAACGAGACCCCACTGCCATTTGATCTCTTATCGCTAT 6364
Db 6295 GTGACAGCATGCGAGGGTGTGATCAATGAAACGCGCACTGCCCTATTGATCTGTATCAGTTT 6354

| | | | |
|----|------|--|------|
| Qy | 6365 | GATGATGTGTCAGGCAAGACAGACGAGCTTTGGGAGTTTCGGTGTCACTTTACTATGACATT | 6424 |
| Db | 6355 | GATGACATTTCTGGCAAAAGTTTGACGATTTGGAAAGTTTCGGAGTTATATATATTATGATATT | 6414 |
| Qy | 6425 | AACAGAGATCATCACACGAGTGTTCATGACACCCACACCAAGCATTTTGGATGCATATGCGAGG | 6484 |
| Db | 6415 | AACAGAGATCATTTCTCAGCTGTATGACCTATACGAAGCACATTTTGATGCTCATGGCCGT | 6474 |
| Qy | 6485 | ATGAAGGAAGTGCAGTAGTAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCAGTAT | 6544 |
| Db | 6475 | ATCAAGGAGATTCAATATGAGATATTACAGTTCGCTCATGTACTGGATTACAAATTCAGTAT | 6534 |
| Qy | 6545 | GATTAACATATGGGCGAGTAGTGGAAGAAGAGCTGAAGGTAGGACCTTACGGCAATATCCACT | 6604 |
| Db | 6535 | GATAACATATGGTTCGGGTAAACCAAGAGAGAGATTAAATAAGGGGCCCTTTGCGCAACCCACC | 6594 |
| Qy | 6605 | CGCTACTCTATAGTAGTAGTAGTGTGACGGCCAGCTGCAGACAGTCTCCATCAATATGACAAG | 6664 |
| Db | 6595 | AAATATGCTTATGAATATGATGTTTGAATGGACAGCTCCAAACAGTTTACCTCAATGAAGAAG | 6654 |
| Qy | 6665 | CCACTCTGGGGCTACAGCTACGACCTCAATGGGAACCTGCACTTACTTGAGCCCTCGGGAAC | 6724 |
| Db | 6655 | ATAATGTGGCGGTACACTACGATCTGAATGGAAACCTCCATTTACTTGAACCCAGTAAC | 6714 |
| Qy | 6725 | AGTGACGGGTACACACCTACGATATGACATCGCGACCGCATCACTCGGCTGGGTGAC | 6784 |
| Db | 6715 | AGTGGCGTCTGACACCCCTTCGCTATGACCTGCGAGACAGAACTCACTGACCTGGGTGAT | 6774 |
| Qy | 6785 | GTGCAATACAAAGATGGATGAGGATGGCTTCTTGAGGCAGCGGGCGGTGATATCTTTTGA | 6844 |
| Db | 6775 | GTTCAATATCGGTTTGGATGAAGATGGTTTCTACGTCAAAGGGGCGACGGAATATCTTTGAA | 6834 |
| Qy | 6845 | TACAACTCAGCTGGCCTGCTCATCAAGGCCCTACAAACCGGCTGGCAGCTGGAAGTGTGAGG | 6904 |
| Db | 6835 | TATAGCTCCAAAGGGCTTCTAACTCGAGTTTACAGTAAAGGCAGTGCCTGGAAGTATC | 6894 |
| Qy | 6905 | TACCGCTACGATGGCCTGGGGCGCGGTGTCAGCAAGAGACGCCACAGCCACCACTG | 6964 |
| Db | 6895 | TACCGTTATGACGGCCTGGGAAGCGGTGTTCTAGCAAAACCAAGTCTAGGACAGCACCTG | 6954 |
| Qy | 6965 | CAGTTCTTATGACAGACTTGACCAACCCACCAAGGTCAACCCACTGTGTACAAACCACTCC | 7024 |
| Db | 6955 | CAGTTTTTTATGCTGACTTAACCTTATCCCACTAGGATTACTCATGCTCTACAAACCACTCG | 7014 |
| Qy | 7025 | AGCTCTGAGATCACTCCCTCTACTACGACTTGAAGGACACCTCTTTGGCATGGAGCTG | 7084 |
| Db | 7015 | AGTTCAAGAAATTAACCTCCCTGTATTATGATCTCCAGGACATCTTTTGGCATGGAAATC | 7074 |
| Qy | 7085 | AGCAGTGGTGTATGATGTTTATCATAGCTTTGTGACAAACATCGGGACCCCTCTTGTGCTCTT | 7144 |
| Db | 7075 | AGCAGTGGGATGAATTTCTATATTGCATCGSATAAACAGGGACACCACTGGCTGTGTTCT | 7134 |
| Qy | 7145 | AGTGGAAACAGGTTTGTATGATCAAGCAAAATCTCTGTACACAGGCTATGGGAGATCTACATG | 7204 |
| Db | 7135 | AGTAGCAATGGGCTTATGCTGAAACAGATTCAAGTACACTGCATATGGGGAATATCTATTTTT | 7194 |
| Qy | 7205 | GATACCAACCCCACTTTTCAGATCATCATAGGCTACCATGCTGGGCTCTTATGATCCACTC | 7264 |
| Db | 7195 | GACTCTAATATPTGACTTTTCAACTGGTAAATGGATTTTATGTTGGTGGCTGTATGACCCACTC | 7254 |
| Qy | 7265 | ACCAAGCTTTGCCACATGGGCGCGAGATTATGATGTGCTGGCGGACGCTGGACTAGC | 7324 |
| Db | 7255 | ACCAATTAATCCACTTTGGAGAAGAGATTATGACATTTTGGCAGGACGCTGGACAACA | 7314 |
| Qy | 7325 | CCAGACCAAGAGCTGTGTGAAGCACTTATGATAGCAAGCAAGTCAATGCTTTTAACTCTAT | 7384 |
| Db | 7315 | CCTGACATAGAAATCTGGA---AAAGAAATTTGGGAAGGACCCAGCTCCTTTTAACTTGTAC | 7374 |
| Qy | 7385 | ATGTTCAAATAACAAACCCCATCAGCAACTCCAGGACATCAAGTGTCTTCATGACAGAT | 7444 |
| Db | 7372 | ATGTTTTAGGAATAACAACCCCTGCAAGCAAAATTCATGACGTGAAGAATATACATCACAGAT | 7434 |
| Qy | 7445 | GTTAACAGCTGGCTGTCCACTTTTGGATTTCCAGCTACACAAAGTGTATCCCTGGTTATCCC | 7504 |

| | | | |
|----|------|---|------|
| Db | 7432 | GTAAACAGCTGGCGTGGTGAACATTTGGTTTCCATCTGCACAAATGCTATTCCTGATTTCCCT | 7491 |
| Qy | 7505 | AAACCCAGACATGGATGCATGGAAACCCCTCTCAGAGCTCATCCACACACAGATGAAACAG | 7564 |
| Db | 7492 | GTTCCCAAATTTGATTTAAACAGAAACCTTCTTACGA-----ACTTGTGAAGAGT | 7539 |
| Qy | 7565 | CAGAGTGGGACACACAGCAAGTCTATCTCCGGGGTACAGTGTGAAGTACAGAGACGAGCTC | 7624 |
| Db | 7540 | CAGCAGTGGGATGATATATACCGCCCATCTTCGGAGTCCAGCAGCAAGTGGCGCGCAGGCC | 7599 |
| Qy | 7625 | AAGGCCCTTTGTACCTTTAGAACGGTTTGAACAGCTCTATGGCTCCAAATTCACCAAGCTGC | 7684 |
| Db | 7600 | AAGGCCCTTCGTGCTGGGGAAGATGGCCGAGTGCAGGTGAGCGCGCGCCGGCCGGC | 7659 |
| Qy | 7685 | CAGCAGGCTCAAGACCAAGAAAGTTTGGATTCAGCGGCTCAGTCTTTTGGCAAGGGGGTC | 7744 |
| Db | 7660 | ---GGCGCGCAGTCTCTGGCTGTGGTTTCGCCACGGTCAAGTCTGATTCGGAACAGGGCGTC | 7716 |
| Qy | 7745 | AAGTTTCCCTTTGAAGATGCGCAGTGCACACAGACATCATCAGTGTGGCCAAATGAGGAT | 7804 |
| Db | 7717 | ATGCTGGCCGTACGCCAGGCGCGGTGCAGACCAACGTGCTCAACATCGCCACAGGAC | 7776 |
| Qy | 7805 | GGCGAAGGGTGTGTCGCATCTTTGAACCATGCCCACTACCTAGAGAACTTCGCACTTCACC | 7864 |
| Db | 7777 | TGCATCAAGTGGCGCGCGTGCTCAACAAACGCTTCTACCTGGAGAACCTTCGCACTTCACC | 7836 |
| Qy | 7865 | ATTGATGGGTGGATACCCATTTACTTTGTGAACACAGGACCTTCAGNAGTGACCTGGCC | 7924 |
| Db | 7837 | ATCAGGGGCAGGACACGCACTACTTTCATCAAGAACCAACCGCCGAGAGCGACCTGGGC | 7896 |
| Qy | 7925 | ATCCCTGGGCGCTCAGTGGGGGCGCGAAACCTTGAGAAATGGGTCAACGTCACCTGTGCTCC | 7984 |
| Db | 7897 | ACGCTGCGTTGACACAGCGCGCGCAAGCGCTGGAGNACGCGATCAACGTGACGGTGTCTG | 7956 |
| Qy | 7985 | CAGATCAACACAGTATTAAATGGCAGGACTAGACGCTTACACAGACATCCAGTCCAGTAC | 8044 |
| Db | 7957 | CAGTCCACCACCGTGTGTGAACCGGCAGGACCGCAGGTTTCGCGGACGTGGAGATGCACTTC | 8016 |
| Qy | 8045 | GGGGCATGTGCTTTGAACACACGCTACGGGACACGTTTGGATGAGGAGAGGCAACGGTCC | 8104 |
| Db | 8017 | GGCGCGTGGCGCTGCACGTGCGCTACGCGCATGACCTTGAACGAGGAGAGGCGCGCATC | 8076 |
| Qy | 8105 | CTGAGCTGGCCCGGCAGAGACGCGTGGCGCAAGCGTGGCGCCGCGCAGCAGCAGAGACTG | 8164 |
| Db | 8077 | CTGAGCAGGCGCGGCGACGCGCGCTCGCCCGGCGCTGGCGCGCAGCAGCAGCGCGTG | 8136 |
| Qy | 8165 | CGGAAAGGGAGGAAGCGCTCGCGGCGCTGACAGAGGGGAGAGCAGCAGGTGCTGAGC | 8224 |
| Db | 8137 | CGCAGCGCAGGAGGGCGCGCGCTCTGGACGAGGCGGAGAGCGCGCAGCTGCTGAGC | 8196 |
| Qy | 8225 | ACGGGCGGTGCAAGGCTACGAGCGCTTTTTCGTGATCTCTGTCGAGCAGTATCCACGAA | 8284 |
| Db | 8197 | GCCGGCAAGGTTCAGAGGCTACGACGGGTACTACGTACTCTCGGTGGAGCAGTATCCCGAG | 8256 |
| Qy | 8285 | CTGTTCAGACAGCGCCAAACACATCCACTTTCATGAGACAGACGAGATGGGCCGAGGTGA | 8344 |
| Db | 8257 | CTGCCGACACGCGCAACACATCCAGTCTCTGCGGCAGAGCGAGATCGCGCAGGAGTAA | 8316 |
| Qy | 8345 | C | 8345 |
| Db | 8317 | C | 8317 |

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RESULT 4
US-11-036-051-7
; Sequence 7, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Verne, Corine

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1814 AGAGCCTCTGCGCCGCTCTGTAGCGGAAATGGCCAAATACATGAAAGGCAGATGCTTG 1873
1798 AGAGCGCCTGTCCAGTGTATGTAGTGGCAACGGGAGTACTTCCAAAGGCGCCTGCCTG 1857
1874 TGCACAGATGGCTGGAAAGCGGTGAGTGCATGTGCCCAACCAACAGTGTATCGATGTG 1933
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1934 GCCTGCAGCAACCATGGCACTGCATCCATCAGCGGCACCTGCATCTGCAACCTGCTGCTACAAG 1993
1918 CAGTGTGGGGTCTGTGGGATTTGTATCATGGGCTCTGTGCTTGCAGCTCAGGATACAA 1977
1994 GGGCAGAGCTGTGAGGAAGTGGACTGCATGGAACCCACATGTTTCAGGCCGGGTGTCTGC 2053
1978 GGAGAAAGTTGTGAAGACTGACTGTATAGACCTGGGTGTTCTAATCATGTGTGTGT 2037
2054 GTGAGAGCGAAATGCCANTCTGTTGTGGGATGGGAGGCAACCACTGCGAGACCCCAAG 2113
2038 ATCCACGGGGAATGTCACTGCAGTCCAGGATGGGAGGTAGCAATTTGTGAAATACTGAAG 2097
2114 GCCACATGTTAGACCAAGTGTTCAGGCCACGGAACTTCTCTCCGGACACCGGGCTTTC 2173
2098 ACCATGTGTCCAGACCAAGTCTCGGCCACGGAACTGTTCTTCAAGAAAGTGGCTCTCTGC 2157
2174 AGCTGTGACCAAGCTGGAACAGACTGTTCTATCGAGATCTGTGCTGCGGACTGT 2233
2158 AGTGTGACCTTAATGGAATGCGCCAGACTGTCTCAACGAAATATGTTCTGTGGACTGT 2217
2234 GGTGGCCATGGCGTGTGCTGAGGGGCACTGCGCTGCGAGGATGGCTGGATGGGGGCA 2293
2218 GGCTCACACGGCGTTTGCATGGGGGGAAGTGTGCTGTGAAGAGGCTGGAACGGGCGCA 2277
2294 GCCTGGACACGGGGCTCCACCCGCTGTGCGGAGCATGGGACCTGCCCGAGCGC 2353
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2398 AAGATAGTTAAAGACAAGATAGGATAAAAGAGGGTTGCTGCTGTGCAACAGCAAT 2457
2456 GGCAATGTACCTTAGACCTGAATGGTTGGCACTGGCTGCCAGCTGGGCTGGAGAGGA 2515
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2516 GCTGGCTGTGACACTTCCATGGAGACTGCTGCGGTGACAGCAAGACAATGATGGAGAT 2575
2518 GCAGGCTGTGACGTAGCCATGGAGACTCTTTGCAAGATAGCAAGCAATGAAGGGAT 2577
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2578 GGAATCATTGACTGATGGATGCCGATTTGCTGCCCTACAGAGTTCTTCCAGAAATCAGCCC 2637
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3058 ATTCAGAGCTGTGATCTGAGTGGATTTCTGTAGGCCAAATCCCATCATTTGTGTATCACCT 3117
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Db 5995 TCCATCATCAGGACTACAAACGAGGAAGGCTGCTTCTACAAACAGCTTCTTGGGTACA 6054
Qy 6053 GGGCGAGGGTGAATATCAAGTATGCGAAATCTGTCAAAGCTGGCAGAGCGCTCTATGAC 6112
Db 6055 AGTCGGAGGGTCTTATTCAAATACAGAAGGCAAGCTAGGCTCTCAGAAATTTTATATGAT 6114
Qy 6113 ACCACCAAGGTTCAGTTTTCACCTTATCAGCAGCGGAGGATGCTCTGAAGACCATCAACCTA 6172
Db 6115 AGCACAAGGTTCAGTTTTCACCTTATGATGAACAGCAGGAGTCTTAAAGACATGAACCTC 6174

| | | | |
|----|------|--|-------|
| Qy | 6173 | CAGAAATGAGGGCTTTCACCTCGACAACATCCGCTACCGTCAGATTTGGGCCCCCTGTGATTGACCGA | 62323 |
| Db | 6175 | CAGAGTGATGGTGTTTATTGTCACCATTAGATACAGGCAAAATTTGGTCCCTCGATTGACAGG | 62334 |
| Qy | 6233 | CAGATCTTCCGCTTCACTGAGGAAGGCATCGTCAACGCCCGTTTTCGACTACAACTATGAC | 6292 |
| Db | 6235 | CAGATTTTCGCTTTTAGTGAAGATGGGAATGGTAAATGCAAGATTTGACTATAGCTATGAC | 6294 |
| Qy | 6293 | AACAGCTTTCGGGTGACACGACATGCAGGCTGTGATCAACAGAGACCCCACTGCCCATTTGAT | 6352 |
| Db | 6295 | AACAGCTTTCGAGTGACAGCATGACGGGTGTGATCAATCAAGAACGCCACTGCCTATTGAT | 6354 |
| Qy | 6353 | CTCTATCGCTAATGATGATGTGTAGGCAAGACAGAGCAGTTTGGGAAGTTTGTGTGTCATT | 6412 |
| Db | 6355 | CTGTATCAGTTTGATGATCAATTTCTGGCAAAAGTTTGAGCAGTTTGGAAAGTTTGGAGTTATA | 6414 |
| Qy | 6413 | TACTATGACATTAACCCAGATCAACACAGCTGTGCATGACCCACCAACCAAGCAATTTTGAT | 6472 |
| Db | 6415 | TATTATGATATTAAACAGATCAATTTCTACAGCTGTGAATGACCTATATCGAAGCACTTTGAT | 6474 |
| Qy | 6473 | GCATATGGCAGGATGAAGGAAGTGCAGTATGAGATCTTTCGCTCGCTCATGTACTTGGATG | 6532 |
| Db | 6475 | GCTCATGGCCGTATCAAGGAGATTCAATATGAGATATTACAGTTCGCTCATGTACTTGGATT | 6534 |
| Qy | 6533 | ACCGTCCAGTATGATAACATGGGCGGAGTGTAGTGAAGAAAGGAGCTGGAAGGTAGGACCCCTAC | 6592 |
| Db | 6535 | ACAAATCAGTATGATAACATGGGTGGGTAAACCAAGAGAGAGATTAATAATAGGGCCCCTTT | 6594 |
| Qy | 6593 | GCCAAATACCACTCCGTACTCTATGAGTATGATGCTGACGCCGAGCTGCAGACAGTCTCC | 6652 |
| Db | 6595 | GCCAAACCAACCAATATGCTTTATGAAATATGATGTTGATGGACAGCTCCCAACAGATTTC | 6654 |
| Qy | 6653 | ATCAATGACAAGCCACTCTGGCGCTACAGCTTACGACCTCAATGGGAACCTTGCATCTTACTG | 6712 |
| Db | 6655 | CTCAATGAAAGATTAATGTGGCGGTACAACTACGATCTGTAATGAAACCTCCATTTACTG | 6714 |
| Qy | 6713 | AGCCCTGGGAACAGTGCAGCGCTCACACCACTACGGTATGACATCCCGGACCGCATCACT | 6772 |
| Db | 6715 | AACCCAAAGTAACAGTGGCGGTCTGCACACCCCTTCGCTATGACCTGCAGACAGAAATCACT | 6774 |
| Qy | 6773 | CGGCTGGGTGACGTGCAATACAAAGATGGATGAGATGGCTTCTGTAGGCGACGGGGCGGT | 6832 |
| Db | 6775 | CGACTGGGTGATGTTTCAATATPCGTTGGATGAAGATGGTTCTCTACGTCAAGGGGGCAGC | 6834 |
| Qy | 6833 | GATATCTTTTGAGTACAACCTCAGCTGGCTGTCTCATCAAGGCCTTACAACCCGGGCTGGCAGC | 6892 |
| Db | 6835 | GAAATCTTTGAAATATAGCTCCAGGGGGTCTTACTCGAGTTTACAGTAAGGCAGTGGC | 6894 |
| Qy | 6893 | TGGAGTGTCAAGTACCGTACGATGGCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCAC | 6952 |
| Db | 6895 | TGGACAGTGATCTACCGTTATGACGGCTGGGAAGGGCGTGTTCGTAGCAAAACCAAGTCTA | 6954 |
| Qy | 6953 | AGCCACACCTCGAGTTCCTTATGACAGACCTGACCAACCCCAACCAAGGTCACCCACTG | 7012 |
| Db | 6955 | GGACAGCACCTTCGAGTTTATTTATGCTGACTTAACTTATCCCACTAGAGTTACTCATGTC | 7014 |
| Qy | 7013 | TACAACCACTCCAGCTCTGAGATCAACCTCCCTCTACTACGACTTTCGAAGGACACCTCTTT | 7072 |
| Db | 7015 | TACAACCACTTCAGTTTCAGAAATACCTCCCTGTATTATGATCTCCAAAGNACATCTTTTT | 7074 |
| Qy | 7073 | GCCATGGAGCTGAGCAGTGGTGATGAGTTTTATCATAGCTTGTGTGACAACTCGGGAACCCCT | 7132 |
| Db | 7075 | GCCATGGAAATCAGCAGTGGGGATGAAATCTATATTTGATCGGATTAACACAGGGACACCA | 7134 |
| Qy | 7133 | CTTGCTGTCTTTAGTGGAAACAGTTTGTATGATCAAGCAAAATCCCTGTACACAGCCTATGGG | 7192 |
| Db | 7135 | CTGGCTGTGTTTCAGTAGCAATGGGGCTTATGCTGAAACAGATTCAGTACACTGCAATATGGG | 7194 |
| Qy | 7193 | GAGATCTACATGGATACCAACCCCAACTTTCAGATCATCATAGGCTACCATGGTGGGCTC | 7252 |
| Db | 7195 | GAAATCTATTTTGACTCTAAATATTGACATTTCACTGGTAAATTTGATTTCACTGGTGGCTG | 7254 |
| Qy | 7253 | TATGATCCCACTCACCAAGCTTGTCCACATGGGCCGGCGAGATTTATGATGTGCTGGCCCGGA | 7312 |

| | | | |
|----|------|---|------|
| Db | 7255 | TATGACCCACTACCAAAATTAATCCACTTTGGGAAGAGATTATGACATTTTGGCAGGA | 7313 |
| Qy | 7313 | CGCTGGACTAGCCAGACCAACGAGCTGTGGAGACACCTTAGTAGCAGCAACGTCATGCCT | 7372 |
| Db | 7315 | CGGTGGACAACACCTGCACATAGAAATCTGSA--AAAGAAATGGGAAGGACCCAGCTCCT | 7371 |
| Qy | 7373 | TTTAAATCTCTATATGTTTCAAAAACAACACCCCATCAGCAACTCCAGAGACATCAAGTGC | 7432 |
| Db | 7372 | TTTAACTTGTACATGTTTATAGGAATATCAACCCCTGCAAGCAAAATTCATGACGTGAAGAT | 7431 |
| Qy | 7433 | TTTCATGACAGATGTTAAACAGCTGCCTGCTCACCTTTGGATTTCCAGCTTACACAAACGTCATC | 7492 |
| Db | 7432 | TACATCACAGATGTTAAACAGCTGCCTGGTGACATTTGGTTTCCATCTGCACATGCTATT | 7491 |
| Qy | 7493 | CTTGGTTATCCAAAACCAAGACATGGAATGGAACCCCTCTTACGAGCTCATCCACACA | 7552 |
| Db | 7492 | CCTGGATTCCTGTTCCCAAATTTGATTTAAACAGAACCTTCTTTACGA-----A | 7539 |
| Qy | 7553 | CAGATGAAACGAGAGTGGGACAACAGCAAGTCTTCTCTCGGGGTACAGTGTGAAGTA | 7612 |
| Db | 7540 | CTTTGGAAGAGTCAGCAGTGGGATGATATACCCGCCATCTTTCCGAGTCCAGCAGCAAGTG | 7599 |
| Qy | 7613 | CAGACGAGCTCAAGGCTTTGTGCACCTTAGAACGGTTTGACACGAGCTCTATGGCTCCACA | 7672 |
| Db | 7600 | GCAGGAGGCCAAGGCTTCTGTCTGCTGGGAAGATGGCCGAGGTGAGGTGAGCCGG | 7659 |
| Qy | 7673 | ATCACCAGCTGCAGCAGGCTCCAAAAGCAAGAAGTTTGATCTCAGCGGCTCAGTCTTT | 7732 |
| Db | 7660 | CGCCGGGCGGC--GSCGCGCAGTCTGGCTGTGGTTGCCCACGGTCAAAGTCGCTGATC | 7716 |
| Qy | 7733 | GGCAAGGGGTCAAGTTTGGCTTTGAAGATGGCCGAGTGACACAGACATCATCAGTGTG | 7792 |
| Db | 7717 | GGCAAGGGCTCATGCTGGCCGTGAGCCAGGGCGGTGAGAACCAACGCTGCTCAACATC | 7776 |
| Qy | 7793 | GCCAAATGAGCATGGCGAAGGGTTGTGCCATCTTGAAACCATGCCCACTACCTAGACAAC | 7852 |
| Db | 7777 | GCCAAACGAGACTGCATCAAGTGTGGCGGCGTCTCNAACAAACGCTTCTACCTGGAGAC | 7836 |
| Qy | 7853 | CTGCATCTTCAACATGTATGGGTGGATACCCATTTACTTTGTGTGAACACAGGACCTTCAAGAA | 7912 |
| Db | 7837 | CTGCATCTTCAACATCGAGGGCAAGGACACGCATCTTCTATCAAGACCAACCAACCCCGAG | 7896 |
| Qy | 7913 | GGTGACCTGGCCATCTCTGGGCTCAGTGGGGGGCGGCAACCTTGGAGAAATGGGCTCAAC | 7972 |
| Db | 7897 | AGCGACCTGGGACAGCTGCGGTTTGACACAGCGGCGCAAGGCGCTGAGAAACGGCATCAAC | 7956 |
| Qy | 7973 | GTCACTGTGCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATC | 8033 |
| Db | 7957 | GTGACGCTGTGCGAGTCCACACCGTGGTGAACGGCAGGACGCGAGTTTCGCGACGTA | 8016 |
| Qy | 8033 | CAGCTTCAGTACGGGGCACTGTGCTTGAACACACGCTACGGGACAACTTTGGATGAGGAG | 8092 |
| Db | 8017 | GAGATGAGTTTCGGCGGCTGGCGCTGCACGTGCGCTACGGCATGACCTTGGACGAGGAG | 8076 |
| Qy | 8093 | AAGGCAACGGGTCTGTGAGCTGGCCGCGCAGAGACCGTGGCCACAGCGTGGGCCCGCGAG | 8152 |
| Db | 8077 | AAGCGCGCATCTCTGAGCAGGCGCGCAGCGCGCTCGCCCGGGGCTTGGGCGCGGAG | 8136 |
| Qy | 8153 | CAGCAGAGCTGGGGAAGGGAGGAGGCTTCGGGCGCTGGACAGAGGGGGAAGCAG | 8212 |
| Db | 8137 | CAGCAGCGCTGCGCGACCGGAGGAGGGCGCGGCTCTTGGACGGAGGGCGAGAGCGG | 8196 |
| Qy | 8213 | CAGGTCTGAGCACAAGGCGGGTGCAAGGCTTACGACGGCTTTTTCGTGATCTCTGTGCGAG | 8272 |
| Db | 8197 | CAGCTGTGAGCGCGGCAAGGTGACGGGCTACGACGGGTACTACGTACTCTCGGTGAG | 8256 |
| Qy | 8273 | CAGTACCCAGAACTGTGCAGACAGCGCCAAACATCCACTTTCATGACAGAGCGAGATG | 8332 |
| Db | 8257 | CAGTACCCCGAGCTGGCGGACAGCGCCAAACATCCAGTTTCTTGGCGGACAGCGAGATC | 8316 |
| Qy | 8333 | GGCCGGAGGTGAC | 8345 |

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|--|------|--|------|--|
| Db | 8317 | GGCAGGAGGTAAC | 8329 | |
| RESULT 5 | | | | |
| US-11-096-051-3 | | | | |
| ; Sequence 3, Application US/11096051 | | | | |
| ; Publication No. US20050244868A1 | | | | |
| ; GENERAL INFORMATION: | | | | |
| ; APPLICANT: Kekuda, Ramesh | | | | |
| ; APPLICANT: MacLachlan, Timothy K | | | | |
| ; APPLICANT: Rastelli, Luca | | | | |
| ; APPLICANT: Vernet, Corine | | | | |
| ; APPLICANT: Eitenberg, Seth | | | | |
| ; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use | | | | |
| ; FILE REFERENCE: Attorney Docket No. Cura 967 | | | | |
| ; CURRENT APPLICATION NUMBER: US/11/096,051 | | | | |
| ; CURRENT FILING DATE: 2005-03-30 | | | | |
| ; PRIOR APPLICATION NUMBER: 10/038,854 | | | | |
| ; PRIOR FILING DATE: 2001-12-31 | | | | |
| ; PRIOR APPLICATION NUMBER: 10/455,772 | | | | |
| ; PRIOR FILING DATE: 2003-06-04 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/557,978 | | | | |
| ; PRIOR FILING DATE: 2004-03-30 | | | | |
| ; NUMBER OF SEQ ID NOS: 38 | | | | |
| ; SOFTWARE: CuraseqList version 0.1 | | | | |
| ; SEQ ID NO 3 | | | | |
| ; LENGTH: 7786 | | | | |
| ; TYPE: DNA | | | | |
| ; ORGANISM: Homo sapiens | | | | |
| ; FEATURE: | | | | |
| ; NAME/KEY: CDS | | | | |
| ; LOCATION: (476)..(7603) | | | | |
| US-11-096-051-3 | | | | |
| Query Match 40.7%; Score 3396.4; DB 9; Length 7786; | | | | |
| Best Local Similarity 68.1%; Pred. No. 0; | | | | |
| Matches 4809; Conservative 0; Mismatches 2231; Indels 24; Gaps 5; | | | | |
| Qy | 1287 | AAGGAAAGCCAGTAGTTCTTTTCCAGAGGACAGTTTCATAGATTCTCGAGAAATTGATG | 1346 | |
| Db | 567 | ATGGAAATTAGTGATTTCGCAAGAAATAACACCATAGATTCCGGAGAACTTGATA | 626 | |
| Qy | 1347 | TGGGAAGGCGAGCCTCCCAAGAAAGATTCTCTGGCACTTCTTGGAGATCTCAAGTGTTC | 1406 | |
| Db | 627 | TTGGCCGAAGAGCAATTCAAGAGATTCTCCCGGATCTCTCGAGATCAAGCTCTCA | 686 | |
| Qy | 1407 | TAGACCATCTCTGTCATCTGAATTCATGTCTCTGGAAAGCAGCCCTGGTTGGCA | 1466 | |
| Db | 687 | TTGATCAGCCACAGTTTCTTAAATTCAATATCTCTCTTCAGAAAGGATGCATTGATTGGAG | 746 | |
| Qy | 1467 | TTTATGGCAGAAAGGCTCCCTCTTCACATACACAGTTTGACTTTTGTGGAGCTGCTGG | 1526 | |
| Db | 747 | TATATGGCCGGAAGGCTTACCGCTTCCCATCTCAGTATGACTTTCGGAGCTCTCTGG | 806 | |
| Qy | 1527 | ATGGCAGAGGCTCTTAACCCAGAGGCGCGAGCCTTAGAGGGACCCCGCGCAGTCTC | 1586 | |
| Db | 807 | ATGGCAGCAGGCTGATTGCCAGAGCAGCGAGCCTCTTGGAGAGAGAGCCCGGC | 866 | |
| Qy | 1587 | GGGGAACGTGCCCCCTCCAGCCATGAGCAGGCTTCATCAGTATTGGATTGAGAA | 1646 | |
| Db | 867 | GCGAGGAGATCCGTGACGCTTCATGAGCGCGCTTATCCAGTACTTGGATTCTGGAA | 926 | |
| Qy | 1647 | TCGGCACTTGGCTTTTACAAATGACGGAAGGAGTCAGAAAGTGGTTTCTCTCAACA | 1706 | |
| Db | 927 | TCGGCACTTGGCTTTTATATGATGGGAAATGAGAGCAGGTGCTTTTAAATACCA | 986 | |
| Qy | 1707 | CTGCCATTGATCGGTGATTAATGCCCCAGCAACTGCTATGGCAATGGTGAATGCT | 1766 | |
| Db | 987 | TTGTTATAGAGTGTGTGTGAATGTCCCCGAAATTCGCAATGGAATGGAAATGCGTTT | 1046 | |
| Qy | 1767 | CTGGACCTGCCACTGCTCTCTGGGTTTCTGGGCGCGGCTGAGGAGCCCTCTGCC | 1826 | |
| Db | 1047 | CTGNACTTGCCATTGTTTCCAGGATTTCTGGGTCGGATTGTTCAAGAGCCGCTGTC | 1106 | |
| Qy | 1827 | CCGTGCTCTGTAGCGGAAATGGCCCAATACATGAAAGGCAGATGCTTGTGCCACAGTGGCT | 1886 | |
| Db | 1107 | CAGTGTATTATGTAGTGGCAACGGGCAGTACTCCAGGGCCGCTGCTGTGTTTCAGCGCT | 1166 | |
| Qy | 1887 | GAAAAGGCGCTGAGTGGATGTGCCCAACCAACAGTGTATCGATGTGGCCTGCAAGAAC | 1946 | |
| Db | 1167 | GGAAGGCGACCGAGTGTGTGCGGACTACCCAGTGTATTGACCCACAGTGTGGGGTC | 1226 | |
| Qy | 1947 | ATGGCACCTGCATCAGCGGACCTGCATCTGCACCTCTGCAACCTGCTACAAAGGGAGAGCTGTG | 2006 | |
| Db | 1227 | GTGGATTGTATCATGGGCTCTTGTCTTGCAACTCAGGATACAAAGGAGAAAGTTGTG | 1286 | |
| Qy | 2007 | AGGAAGTGGACTGCATGGACCCCAATGTTTCAGGCCGGGTGTCTGCGTGAGAGCGCAAT | 2066 | |
| Db | 1287 | AAGAAGCTGACTGTATAGACCTTGGGTGTTCTTAATCATGTGTGTATCCACGGGAAT | 1346 | |
| Qy | 2067 | GCCATTGCTTTGTGGGATGGGAGGACCAACTGCGAGACCCCGCAGGCCACATGCTTAG | 2126 | |
| Db | 1347 | GTCACCTGAGTCCAGGATGGGAGGTAGCAATTGTGAATTACTGAAGACCATGTGTCCAG | 1406 | |
| Qy | 2127 | ACCAGTGTTCAGGCCACCGAACCTTCTCCCGACACCCGGCTTTTGAGCTGTGACCCAA | 2186 | |
| Db | 1407 | ACCAGTGTTCGGCCACCGAACCTTCTTCAAGAAAGTGTGCTCTGACGCTGTGACCTTA | 1466 | |
| Qy | 2187 | GCTGGACTGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGTGGCCATGGCG | 2246 | |
| Db | 1467 | ACTGGACTGGCCAGACTGCTCAAGCAATATATGTTCTGTGGACTGTGGCTCACAGGCG | 1526 | |
| Qy | 2247 | TGTGCGTAGGGGACCTGCGCTGGAGGATGGCTGGATGGGGGAGCTTGGACCGAC | 2306 | |
| Db | 1527 | TTTGATGGGGGGAGCTGTGCTGTGAAGAGGCTGGAGCGGCCAGCCCTGTAATCAGA | 1586 | |
| Qy | 2307 | GGGCTGCCACCCCGCTGTGCCAGCATGGGACCTGCGCGCAGCGCAAGTGGAGTGCA | 2366 | |
| Db | 1587 | GAGCTGCCACCCCGCTGTGCCGACGACCGGACCTTCAAGGATGGCAAGTGTGAATGCA | 1646 | |
| Qy | 2367 | GCCCTGGCTGGAATGGGAAACACTGCACCATCGCTCACTATCTGGATAGGGTAGTTAAAG | 2426 | |
| Db | 1647 | GCCAGGCTGGAATGGAGAGCACTGCACATCGCTCACTATCTTGGATAAGATGTTAAAG | 1706 | |
| Qy | 2427 | AGGTTTGGCTGGTGTGCAATGGCAACGGCAGATGTACCTTTCAGACCTGAAATGTTGGC | 2486 | |
| Db | 1707 | AGGTTTGTCTGTGTCGACAGCAATGGAAAGATGTACCTTGGACCAAAATGGCTGGC | 1766 | |
| Qy | 2487 | ACTGGCTTGCACAGTGGGCTGGAGAGGAGTGGCTGTGCACACTTCCATGGAGACTGSCCT | 2546 | |
| Db | 1767 | ATTGTGTGCCAGCCTGGATGGAGAGGAGGAGCTGTGACGTAGCCATGGAGACTCTTT | 1826 | |
| Qy | 2547 | GCGGTGACAGCAAGCAATGATGGAGTGGCTGTGTGACTGTCATGGAGCCCTGACTGCT | 2606 | |
| Db | 1827 | GCAAGATGCAAGGCAATGAAGGAGATGGACTCAATTGACTGGAACCCGATTTGCT | 1886 | |
| Qy | 2607 | GCCTCAGGCCCCCTGTGCCATATCAACCCGCTGTGCTTGGCTCCCCCTAACCCCTCTGACA | 2666 | |
| Db | 1887 | GCCTACAGAGTTCTTGCAGAAATCAGCCCTATTGTGGGGACTGCGCGACCTCAGACA | 1946 | |
| Qy | 2667 | TGATCCAGAGACACAGTTCCTGTGTGCAGAGAACTCACTCTCTTCTATGACCGCA | 2726 | |
| Db | 1947 | TCATTAGCCAAAGCCCTTCAATCGCCCTTCTCAGCAAGCTGCCAAATCCTTTTATGATCGAA | 2006 | |
| Qy | 2727 | TCAAGTTCTCTGTGGGACGAGCAGCACAATATCCCGGGGAGAACCCCTTTGATG | 2786 | |
| Db | 2007 | TGATTTCTTATAGATCTGTAGACCCATGTATACCTGGAGAAAGTCTCTTCAATA | 2066 | |
| Qy | 2787 | GAGGCACTTGTGTATTTCGTGGCCAGTGAATGACATCAGATGGAACCCCTCTGGTTG | 2846 | |
| Db | 2067 | AGAGCCTTGCATCTGTATCAGAGGCCAAGTACTGCTGCTGATGGAATCCCACTTATTG | 2126 | |
| Qy | 2847 | GTGTGAACATCAGTTTGTCAATAACCCCTCTCTTTGGATATACATCAGAGCGCAAGATG | 2906 | |
| Db | 2127 | GAGTAAATGCTCTCTGTTTTCATTTCCATTTACCCAGAAATAGGATATATCTATTATCCCGCCAGGAG | 2186 | |

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|------|---|------|
| 2907 | GCAGCTTTGACTTGGTGACAAAATGGCGGCATCTCCATCATCTCTGCGGTTGCGAGCGGGCAC | 2966 |
| 2187 | GAATGTTTGACTTGGTGGCAAAATGGTGGGGCCTCTCTAACTTTTGGTATTTGAAACGATCCC | 2246 |
| 2967 | CTTTTCATCACACAGGAGCACAACCTCTGGCTGCATGGGATCGCTTCTTTGTTCATCGAAA | 3026 |
| 2247 | CATTCTCCACTCAGTATCATACTGTGTGGATTTCCATGGAATGTCCTTTATTTGTGATGATGA | 2306 |
| 3027 | CCATCATCATGAGACATGAGGAGAAATGAGATTTCCAGACTCTGACCTGAGCAAAATTTTGGCCC | 3086 |
| 2307 | CCCTAGTCATGAGAAAGAGAAATGATATTTCCACGCTGTGATCTGAGTGGATTCGTGA | 2366 |
| 3087 | GCCCCAACCCAGTTCGTCTCTCCATCCCACTGAGAGTCTTCCTGGCAGCTCTCTGTGCAGAGA | 3146 |
| 2367 | GGCCAAATCCCATCATTTGTGTGTCATCACCTTTATCCACCTTTTTTCAGATCTTCTCTCGAAG | 2426 |
| 3147 | AAGGCCCAATGTGCGCGAAATTCAGAGCTTTGCAGGAGGAAATCTCTATCTCTGGCTGCA | 3206 |
| 2427 | ACAGTCCCATCATTTCCCGGAAACACAGGTACTCCACAGAGGAAACTACAAATTTCCAGGAACAG | 2486 |
| 3207 | AGATGAGGCTGAGTCACTCTGAGCAGCGGACCCCTGGCTACAAATCTGTCTCTCCTGAGGATCA | 3266 |
| 2487 | ATTTGGAACCTCTCTACTTTGAGTTCAGAGCTGCAGGGTATAGTCAGTTCCTCAAGATCA | 2546 |
| 3267 | GCCTCACCCACCCGACCATCCCTTTCAACCTCATGAAAGTGCACCTCATGGTACGCGTGG | 3326 |
| 2547 | CCATGACCCAGTCTATTATTCCATTTAATTTAATGAAAGTTTCATCTTATGTTAGTCTGTAG | 2606 |
| 3327 | AGGCGCGCTCTTCAGGAAGTGGTTCCGTGCAGCGCCCGAGACCTGTCTTATTTATTTCAATTT | 3386 |
| 2607 | TAGGAAGACTCTTCCAAAGTGGFTTCTCGCTCACCAAACTTGGCCCTATACATTTTTCATAT | 2666 |
| 3387 | GGGACAGACAGACGCTCTACAACACAGAAGTGTTTTGGGCTTTTCAGAAAGCCTTTGTTTCCG | 3446 |
| 2667 | GGGATAAACAAGTGCATATATACGAAAGTCTATGTCTCTATCTGAAGCTGTTGTGTCTAG | 2726 |
| 3447 | TGGGTTATGAATATGAATCTCTGCCAGATCTAATCTGTGGGAAAAAGAACACAGTGC | 3506 |
| 2727 | TTGGATATAGTATGAGTTCGTGTGTGGACCTGACTCTGTGGAAAAAGAGACTGCCATTCT | 2786 |
| 3507 | TGCAGGCTATGAATTTGACGCGTCCAGCTTTGGAGATGGAGCTTAGACAAACATCATG | 3566 |
| 2787 | TGCAGGGCTATGAATGGATGCGTCCAAACATGGGTGGCTGAGCAATTAGATAAAGATCAGC | 2846 |
| 3567 | CCCTCAACATTTCAAAGTGGTATCTCTGCACAAAGGGAATGGGGGAAACGAGTTTGTGTCTC | 3626 |
| 2847 | TGCTGGATGTACAGAAACGGTATATCTGTACAGGGAACGGGGAAAAACGATTTCATCTCCC | 2906 |
| 3627 | AGCAGCTCTCTGTCTATTGGGAGCATCATGGGCAATGGGCGCCGGAGAGCATCTCTCTGCC | 3686 |
| 2907 | AGCAGCTCCAGTCTGTAGTAGCATCATGGGCAATGGGCGAATGGGCGAAGCGCAGCATTTCTCTGCC | 2966 |
| 3687 | CCAGCTGGAACGGCTTGTGTGACGGCAACAGCTCTTGGCCCGCAGTGGCCCTCACCTGTG | 3746 |
| 2967 | CCAGTTGCAATGGTCAAGCTGATGGTAACAGTTTACTTGGCCCCAGTGGCGCTAGCTTGTG | 3026 |
| 3747 | GCTCTGAGGGAGGCTCTATGTGGTGATTTTCAACTACATTTAGAAGGATCTTCTCCCTCTG | 3806 |
| 3027 | GGATCGATGGCAGTCTGTACGTAGGCAATTTCAACTATGTGGCGCGGATATTTCCCTTCTG | 3086 |
| 3807 | GAATGTCAACCAACATCTTAGAGCTGAGGAATAAGATTTTCAGACATAGTCAACAGTCCAG | 3866 |
| 3087 | GAATGTAAACAAGTGTCTTAGAACTTAAGAAATAAAGATTTTAGACATAGCAGCAACCCAG | 3146 |
| 3867 | CACACAAATACTACTCTGGCCACAGACCCCATGAGTGGGGCGGTCTTCTCTTTCTGACAGCA | 3926 |
| 3147 | CTCATAGATACTACTCTTGCACACGACCCAGTCAACGGGAGATCTGTGACGTTTCTGACAAA | 3206 |
| 3927 | ACAGCGCGGGTCTTTTAAAAATCAAGTCCACTGTGGTGGTGAAGGACCTTGTCAAGAAGT | 3986 |
| 3207 | ACACCCGCAAGAAATTTATCGGCCAAAGTCACTTACGGGGGCAAAAGACTTGNACTTAAAAATG | 3266 |
| 3987 | CTGAGGTGGTTTGGCGGGACAGGTGACAGTGCCTCCCTTTTGTATGACATCTCGTCTCGCGGG | 4046 |

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|------|----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| 3267 | Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------|----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|


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QY 7284 GCCGGGAGATTATGTGCTGCGCGGACGCTAGCGCAGACCCAGACCGAGCTGTGGA 7343
Db 6564 GAGAAAGAGATTATGACATTTTGGCAGGACGGTGGACACACCTTGACATAGAAATCTGGA 6623
QY 7344 AGCACCTTAGTAGCAGCAAGCTCATGCCCTTTTAAATCTCTATATGTGTTTCAAAAACAAC 7403
Db 6624 ---AAGAAATTGGGAAGGACCCAGCTCTCTTTAACTTGTTACATGTTTGGGAATAACAAC 6680
QY 7404 CCATCAGCACTCCAGGACATCAAGTCTTCTATGACAGATGTTTACAGCTGCTCTCA 7463
Db 6681 CTCGAAGAAAATCCATGACGTAAGAAATTACATACAGATGTTTACAGCTGCTGCTGA 6740
QY 7464 CTTTGGATTCCAGCTACACAAGCTGATCCCTGGTTATCCCAACAGACATGGATGCCA 7523
Db 6741 CATTTGGTTTCCATCTGCACATGCTATTCTCTGGATTCCCTGTTCCCAATTTGATTAA 6800
QY 7524 TGAACCCCTCTACAGAGCTCATCCACACAGATGAAAAGCGAGAGTGAGCAACAGCA 7583
Db 6801 CAGAACCTTCTTACGAACCTG-----TGAAGAGTCAAGAGTGGGATGATATAC 6848
QY 7584 AGTCTATCTCGGGGTACAGTGTGAAGTACAGAGCAGCTCAAGGCTTTGTACCTTAG 7643
Db 6849 CGCCCATCTTTCGGAGTCCAGCAGCAAGTGGCGCGGCGAGGCCAAGGCTTTCCTGTCGCTG 6908
QY 7644 AACGGTTTGACCAAGCTCTATGGCTCCACAATCACAGCTGCCAGCAGGCTCCAAAGACCA 7703
Db 6909 GGAAGATGGCGGAGGTGACGTGAGCGCGGCGCGGCGCGCGCGCTCTGCTGCT-- 6966
QY 7704 AGAAGTTTGATCCAGCGGCTCAGTCTTTTGGCAAGGGGTCAAGTTTGGCTTGAAGGATG 7763
Db 6967 -GTGGTTTCGCCACCGGTCAAGTCTGATCGCAAGGCGGTGATGCTGGCGGTGAGCCAGG 7025
QY 7764 GCGAGTGACACAGACATCATGATGTGCGCAATGAGGATGGCGGAGGGTTGCTGCCA 7823
Db 7026 GCCCGGTGCAGACCAACGTCTCAACATGCCCAACGAGGACTGCATCAAGGTGGCGGCGG 7085
QY 7824 TCTTTGAACCATGCCACTACTAGAGAACTGCACTTACCAATTTGATGGGGTGGATACCC 7883
Db 7086 TGCTCAACAACGCTTCTACTGTGAGAACCTGCACTTCAACATTCGAGGGCAAGACACGC 7145
QY 7884 ATTACTTTGTGAACCAAGGACCTTTCAGAGGTTGACCTTGGCCATCTTGGGCTCAGTGGGG 7943
Db 7146 ACTACTTTCATCAAGACCACCAAGCGCGGAGAGGACCTGGGACGCTGCGGTTCAGCAGCG 7205
QY 7944 GCGCGGCAACCTTGGAGAAATGGGGTCAAGCTACTGTGTCCAGATCAACACAGTACTTA 8003
Db 7206 GCGGCAAGGCGCTGGAGAACGGCATCAACGTGAGCGGTGTCGCACTCCACACCGTGGTGA 7265
QY 8004 ATGCGAGCTAGACGCTACACAGACATCCAGCTCCAGTACGGGGCACTGTGTTGAACA 8063
Db 7266 ACGGAGGACGCGCAGGTTTCGCGACCTGGAGATGCAAGTTTCGGCGCGCTGGCGTGCACG 7325
QY 8064 CAGGCTACGGGACAAACGTTGGATGAGGAGAGGCAAGGCTCCTGGAGCTTGGCCCGGCGA 8123
Db 7326 TGCGCTACGGCATGACCTTGGACGAGGAGAGGCGCGCATCTTGGAGCAGCGCGGCGAGC 7385
QY 8124 GAGCGGTGCGCAAGCGTGGGCTCCGAGCAGAGCAGACTGCGGGAAAGGGAGGAGAGGCC 8183
Db 7386 GCGCGCTCGCCCGGCGCTGGCGCGCGGAGCAGCAGCGCTGCGCGACGCGGAGAGGGCG 7445
QY 8184 TGCGGCGCTGACAGAGGGGAGAGCAGCAGGCTGCTGACACAGGCGGGTGCAGGCT 8243
Db 7446 CGCGCCTCTGACGAGAGGGGAGAGCGGAGCTGCTGAGCGCGCGGAGAGGTGCGAGGCT 7505
QY 8244 ACAGCGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAACTGTCTAGACAGCGCCAAACA 8303
Db 7506 ACGACGGGTACTAGTACTCTCGTGGGAGTACCCCGAGCTTGGCGCGGAGAGGTGCGAGGCT 7565
QY 8304 ACATCCACTTATGAGACAGAGCGAGATGGGCGGAGGTGACAG 8347
Db 7566 ACATCCAGTTCTCTCGCGCAGAGCGAGATCGCAGGAGGGGTAAG 7609
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RESULT 6
US-10-821-234-245/c
; Sequence 245, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 245
; LENGTH: 3626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-245

Query Match 18.7%; Score 1560.4; DB 6; Length 3626;
Best Local Similarity 68.0%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1036; Indels 21; Gaps 4;

QY 5049 TGATGACATACCATGCAATTCGGCGCTTCTGCGCAACCAAGCAATGAAACCGGATGGA 5108
Db 3621 TGTTTACTTACCATGCAATATGTGGCCCTTTTAGCCCACTAAAAGTGATGAAACTGGATGGA 3562
QY 5109 CAACATTTTATGATACGACAGAGCTTTGGCGCGCTGACAAATGTGACCTTCCCTACTGGCC 5168
Db 3561 CAACGTTTTTGTGATGATGACAGTGAAGTGGTCTGACAAATGTTTACGTTTCCAACTGGAG 3502
QY 5169 AGGTGAGCAGTGTCCGAAAGTGATACAGACAGTTTCACTGATGTCCAGGTGAGACCTCCA 5228
Db 3501 TGGTCAAAACCTGCAATGGGACATGGCAAGGCTATCACAGTGGACATTTGAGTCACTTA 3442
QY 5229 GC---NAGGATGATGTCAACCAACCAACCACTGCTGCCTCAGGCGCTTCTACACAC 5285
Db 3441 GCGGAGAAGAAGATGTGAGATCACTTCAAAATCTGCTCGATCGATTTCTTTCTACACCA 3382
QY 5286 TGCTGCAAGACCAAGTCCGGAACAGCTACTATACATCGGGGCGGATGGCTCTTGGCGGTGC 5345
Db 3381 TGGTTCAAGATCAGTTTAAAGAACAGCTACAGATTTGTTATGACGGCTCCTCAGAAATTA 3322
QY 5346 TGCTGGCCAAACGCGCATGGAGGTGGCGCTGACAGCTGAGGCCCACTTGTGGCTGGCAACG 5405
Db 3321 TCTACGCCAGTGGCTGGACTCACACTACCAACAGAGCGCACGTTCTGGCTGGCACCG 3262
QY 5406 TCNAACCCACCGTGGGCAAGAGGATGTCAAGTGGCCCATCGACACAGCGCTCAACCTGG 5465
Db 3261 CTAATCCGACGGTGGCAAAAGAAACATGACTTGGCTGGCGAGAACGGTCAAAACTTGG 3202
QY 5466 TGGAGTGGCGCCAGCCAAAGAGCAGGCTCGGGGCCAGAGTCACTGTCTTTGGGCGCGCGC 5525
Db 3201 TGGAAATGGAGATTCCGAAAGAGCAAGCCCAAGGAAAGTCAATGTCTTTGGCGCGCAAGC 3142
QY 5526 TGGCGGTGACACCAACGAAATCTCTATCTCTGGAATTTTGTATCGCGTTAAACGACACAGAGA 5585
Db 3141 TCAGGGTTAATGGCAGAAACCTCTTTTCACTTGTGATCGAATCGAACAACAAGACAGAAA 3082
QY 5586 AGATCTATGATGACCAACCGCAAGTTCACCTTCGGATTTCTGTACGACAGCGCGGGCGGC 5645
Db 3081 AGATCTATGACGACCAACCGTAAATTTCTACTGAGGATCGCCTACGACACGCTCTGGGGCACC 3022
QY 5646 CCAGCCTCTGGTCAACCCAGCAGCAGGCTGAATGGTGTCAACAGTGAATACTCTCCCTGGGG 5705
Db 3021 CGACTCTTGGCTGCCAAGCAGCAGCTGATGAGCGCTCATGTCACTTATTCATCCACAG 2962
QY 5706 GTTACATTTGCTGGCATCCAGAGGGGATCATGTGTGAAGAAATGGAATACGACACGCGG 5765
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Db 2961 GTCAAATTGCCAGATCCAGGAGGCCACCTAGCCGAAAGTAGATTATGACGGACAG 2902
Qy 5766 GCGCATCATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATCTTAGAGA 5825
Db 2901 GGAGGATCGGTCTCGGGTCTTTGCTGATGGTAAACATGGAGTTACATATTTAGAAA 2842
Qy 5826 AGTCCATGGTGTCTACTACACAGCCAGAGGCGATATATCTTTGATGTTGCAACGAATG 5885
Db 2841 AGTCCATGGTGTCTTCGCTTCATAGCAGCGGAGTACATCTTCGAATACGATATGTGG 2782
Qy 5886 ACCGCTCTCTTCTGTGAGATCCCAACGTGGCGGCGAGACACTAGAGACATCCGCT 5945
Db 2781 ACCGCTGTCTGCCATCACCATGCCAGTGGCTCGCCACACCATGCGACCATCCGAT 2722
Qy 5946 CAGTGGCTTACTACAGAAACATCTATCAGCCCTGAGGGCAATGCTCAGTCAACAGG 6005
Db 2721 CCATTGGCTACTACCGCAACATATACAACCCCGGAAAGCAACGCTCCATCATCAGG 2662
Qy 6006 ACTTCACTGAGGATGGGCACCTCTTACACCTTCTACCTGGGCACTGGCCGACGGTGA 6065
Db 2661 ACTACAACGAGGAAGGCTGCTTCTACAAACAGCTTCTTGGGTACAAGTCGAGGGTCT 2602
Qy 6066 TATCAAGTATGCAAACTGTCAAAGCTGGCAGAGCGCTCTATGACACCAACAAAGTCA 6125
Db 2601 TATTCAATACAGAGCGAGACTAGGCTCTCAGAAATTTATATATAGTACACAAGTCA 2542
Qy 6126 GTTTCACCTATGACGAGCGGAGCATGCTGAAGACCATCAACCTACAGATGAGGCT 6185
Db 2541 GTTTTACCTATGATGAACAGCAGGAGTCTTAAGACACAGTAACCTCCAGAGTGTGTT 2482
Qy 6186 TCACCTGCACCATCCGCTACAGTTGGGCCCTGATTGACCGACAGATCTTCGCT 6245
Db 2481 TTATTTGCCACCTATAGATACAGGCAATTTGGTCCCTGATTGACAGGCGAGTTTCGCT 2422
Qy 6246 TCAGTGAAGAGCATGGTCAACGCCGTTTTGACTACAACTATGACAAACAGCTTCGCG 6305
Db 2421 TTATGTAAGATGGATGGTAAATGCAAGATTTGACTATAGCTATGACAAACAGCTTCGAG 2362
Qy 6306 TGACAGCATGAGGCTGTGATCAACGAGACCCCACTGCCATTCATCTCTCGCTATG 6365
Db 2361 TGACAGCATGAGGCTGTGATCAATGAACCCCACTGCCTATTGATCTGATCAGTTTG 2302
Qy 6366 ATGATGTGTACGGCAAGACAGCAGTGTGGGAAGTTTGGTGTCAATTTACTATGACATTA 6425
Db 2301 ATGACATTTCTGGCAAGTTGAGCAGTTTGGAAAGTTTGGAGTTATATATATGATATTA 2242
Qy 6426 ACCAGATCATCACACAGCTGTGATGACCCACACCAAGCATTTTATGATCATGCGCAGGA 6485
Db 2241 ACCAGATCATTTCTACAGCTGTAATGACCTATACGAAGCACCTTTGATGCTCATGGCCGTA 2182
Qy 6486 TGAAGGAAGTGAGTATGAGATCTTCCGCTCGCTCATGTACTGGAATGACCGTCCAGTATG 6545
Db 2181 TCAAGGAGATTCAATATGAGATATTCAGTTCGCTCATGTACTGGAATTAACAATTCAGTATG 2122
Qy 6546 ATAAATATGGGGAGTGTGAAGAAGAGCTGAAGGTAGGACCCCTAGCCCAATACCACTC 6605
Db 2121 ATAAATATGGGTGGGTAAACCAAGAGAGAGATTTAAATAGGGCCCTTTTGGCCAAACCA 2062
Qy 6606 GCTACTCTCTATGATATGATGCTGACGCCAGCTGCGACACAGTCTCCATCAATGACAGC 6665
Db 2061 AATATGCTTATGAATATGATGTTGATGACAGCTCCAAACAGTTTTACCTCAATGAAAGA 2002
Qy 6666 CACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACTTACTGAGCCCTGGGAACA 6725
Db 2001 TAAATGGCGGTACAACCTACGATCTGAATGGAAACCTCCATTTACTGNAACCAAGTAAACA 1942
Qy 6726 GTGCAGGCTCACACCATACGTTATGACATCCGGGACCGCATCACTCGGCTGGGTGACG 6785
Db 1941 GTGCGCGTCTGACACCCCTTCGCTATGACCTGCGAGACAGAAATCACTCGACTGGGTGATG 1882
Qy 6786 TGCAATACAGATGATGAGTGGCTTCTCTGAGCAGCGGGCGGTGATATCTTTGAGT 6845
Db 1881 TTCAATATCGGTTGGATGAAGATGGTTCTTCTACGTCAAGGGGCAACCAAGTCTTTGAAAT 1822

Qy 6846 ACAACTCAGCTGGCTGCTCTCATCAAGGCCTACAAACCGGCTGGCAGCTGGAGTGTCAAGT 6905
Db 1821 ATAGCTCAAGGGGCTTCTAACTCGAGTTTACAGTAAAGGCAGTGGCTGGACAGTGATCT 1762
Qy 6906 ACCGCTACGATGGGCTGGGGGGCGCTGTCCAGCAAGAGCAGCACAGCCACACCTGC 6965
Db 1761 ACCGTTATGACGGCTCGGGAAGCGCTGTTTCTAGCAAAACCCAGTCTAGGACAGCACCTGC 1702
Qy 6966 AGTTCTTCTATGACAGCTGTACCAACCCCAAGGTCAACCACCTGTGACAAACCACTCCA 7025
Db 1701 AGTTTCTTATGCTGACTTAACCTTATCCCACTAGGATTAATCATGCTACAAACCTTCGA 1642
Qy 7026 GCTCTGAGATCACTCTCCCTCTACTACGACTTGAAGGACACCTCTTTGGCCATGAGCTGA 7085
Db 1641 GTTCAGAAATTAACCTCCCTGTATTAATGATCTCCAAGGACATCTTTTGGCCATGGAATCA 1582
Qy 7086 GCAGTGTGATGAGTTTACATAGCTTGTGACACATCGGGACCCCTCTTGTGCTCTTTA 7145
Db 1581 GCAGTGGGATGAATTTCTATTTGCACTCGGATTAACAGGGACACCACTGGCTGTGTCA 1522
Qy 7146 GTGAAACAGGTTTATGATCAAGCAATCTGTACACAGCTATGGGGAAGATCTACATGG 7205
Db 1521 GTAGCAATGGCTTATGCTGAACAGATTCACTGATACATGCGGAAATCTATTTTG 1462
Qy 7206 ATACCAACCCCACTTTTCAATCATATAGGCTACCATGCTGCTCTATGATCCACTCA 7265
Db 1461 ACTTAATATTTGACTTTTCACTGGTAAATGGAATTTATGCTGGCTGTATGACCACTCA 1402
Qy 7266 CCAAGCTGTCCACATGGGCGGCGAGATTTATGATGTGCGGAGCTGAGCTAGCC 7325
Db 1401 CCAATTAATCCACTTTGGGAAGAGATTAAGCAATTTTGGCAGGACGGTGGACAACAC 1342
Qy 7326 CAGACCAAGCTGTGGAAGCACCTTTAGTAGCAACACGTCATGCTCTTTAACTCTCTATA 7385
Db 1341 CTGACATAGAAATCTGGA---AAAGAAATGGGAAGGACCCAGCTCTTTTAACTTGTACA 1285
Qy 7386 TGTTCAAACACCAACCCCATCAGCAATCCAGGACATCAAGTCTCTATGACAGATG 7445
Db 1284 TGTTTAGGAATAACAACCCCTGCAAGCAAAATCCATGACGTGAAGATTAATCATCACAGATG 1225
Qy 7446 TTAACAGCTGGCTGCTCACCTTTGGATTCAGCTACACAACTGATCCCTGGTTATCCCA 7505
Db 1224 TTAACAGCTGGCTGGTGACATTTGGTTTCCATCTGCACAAATGCTATCTCTGGATTCCTCG 1165
Qy 7506 AACAGACATGATGCGCATGGAAACCCCTCTCAAGAGCTCATCCACACACAGATGAAACGC 7565
Db 1164 TTCCCAAAATTTGATTTTAAACAGAAACCTTCTTACGA-----ACTTGTGAAGAGTC 1117
Qy 7566 AGGAGTGGGACACACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTACAGAACAGCTCA 7625
Db 1116 AGCAGTGGGATGATATACCGCCCATCTTCGGAGTCCAGCAGCAAGTGGCGCGCAGGCCA 1057
Qy 7626 AGGCTTTTGTCACTTTAGAACGTTTGAACAGCTCTATGGCTCCCAAAATCAACAGCTGCC 7685
Db 1056 AGGCTTCTGTGCTGGGGAAGATGGCCGAGGTGAGTGAGCCGCGCCGCGCGC- 998
Qy 7686 AGCAGGCTCCAAAGACCAAGAAAGTTTGGATCCAGCGGCTCAGTCTTTTGGCAAGGGGTCA 7745
Db 997 --GGCGCGAGTCTCTGGCTGTGGTTCGCCACCGTCAAGTCTGATCGGCAAGGGCGTCA 940
Qy 7746 AGTTTTCCTTTGAAGGATGGCCGAGTGACCAAGACATCATAGTGTGGCCAATGAGGATG 7805
Db 939 TGCTGCGCTCAGCAGGCGCGGTGACACCAAGTGTCAACATCGCCAAACGAGGACT 880
Qy 7806 GCGAAGGTTGCTGCAATCTTTGAACCAATGCCCCATCTAGAGAACTTGCACTTTCAACA 7865
Db 879 GCATCAAGTGGCGCGGTCTCAACACGCTTCTACCTGGAACCTTGCACTTTCAACA 820
Qy 7866 TTGATGGGTTGATACCCATTAATTTGTAACACAGGACCTTCAGAGTGTGACCTGGCCA 7925
Db 819 TCAGGGCAAGGACAGCACTACTTCTATCAAGACCACCAACCGCCGAGAGCGACCTGGGCA 760

Db 1349 ATTGTGTGTCAGCCTGGATGGAGGAGCAGGCTGTGACGTAGCCATGGAGACTCTTT 1408
Qy 2547 GCGGTGACAGCAAGCAATGATGAGATGGCTGGTGAATGCAATGACACCTGACTGCT 2606
Db 1409 GCACAGATAGTAAGGACAAATGAAGGAGATGGACTCATTTGACTGCTATGCCGATTGCT 1468
Qy 2607 GCTCCAGCCCTGTGGCCATATCAACCGCTGTGCTGGCTCCCTAACCTCTGGACA 2666
Db 1469 GCTACAGAGTTCTGCCAGAATCAGCCCTATTGTGCGGGAATGCCGATCTCTCAGACA 1528
Qy 2667 TCATCCAGGAGACACAGTCCCTGTGTCCACAGCAGAACCTACACTCTCTTATGACCGCA 2726
Db 1529 TCATTAGCCAAAGCCTTCAATCGCCTTCTCAGCAAGCTGCCAAATCCTTTATGATGAA 1588
Qy 2727 TCAAGTTCTCTGGCAGGAGACAGACGCAATATCCCGGGGAGAACCCCTTTGATG 2786
Db 1589 TCAGTTTCTTTATAGGATCTGATACGCCATGTTATACCTGGGAAAGTCTCTTCAATA 1648
Qy 2787 GAGGCGATGCTGTGTTATTGCGGCCAAGTGATGACATCAGATGGAACCCCTGGTTG 2846
Db 1649 AGAGCTTGCATCTGTCTCAGAGGCCAAGTACTGACTGCTGATGGAATCCACTTATG 1708
Qy 2847 GTGTGAACATCAGTTTGTTCATTAACCCCTCTCTTTGGATATACATCAGCAGGCAAGATG 2906
Db 1709 GAGTAAATGCTCTCGTTTTTCCATTACCAGAAATATGGATATACTATTACC CGCAGGACG 1768
Qy 2907 GCAGCTTTGACTGTGTGCAAAATGGCGCATCTCCATCATCTGCGGTTGAGGGGAC 2966
Db 1769 GAATGTTTGAATGTGTGGCAATGTGGGGCTCTCTAACTTTGGTATTTGAACGATCCC 1828
Qy 2967 CTTTTCATCACACAGGACACCCCTGTGCTGCCATGGATCGCTTCTTTGTATGGAAA 3026
Db 1829 CATTCCTACTCAGTATCATACTGTGTGATTCATGGAATGTCTTTATGTGATGATA 1888
Qy 3027 CCATCATCATGAGACATGAGGAGAAATGAGATTCACAGCTGTCACTGAGCAATTTGCCC 3086
Db 1889 CCCTAGTCATGAAGAAAGAGAGAAATGACATTCACAGCTGTGATCTGAGTGGATTCGTGA 1948
Qy 3087 GCCCAACCCAGTCTCTCCATCCCACTGACGTCTCTCGCCAGCTCTCTGTCGAGAGA 3146
Db 1949 GCGCAATCCCAATCATGTGTCTATCACCTTTATCCACCTTTTTCAGATCTCTCTCTGAAG 2008
Qy 3147 AAGGCCCATTTGTGCGGAAATTCAGGCTTTGCGAGGAGAAATCTCTATCTCTGCTGCA 3206
Db 2009 ACAGTCCCATCATTCCTCCGAAACACAGTACTCCACGAGAAACTACAATTCAGGAACAG 2068
Qy 3207 AGATGAGGCTGAGTACTCTGAGCAGCCGACCCCTGGCTACAATCTGTCTGAGGATCA 3266
Db 2069 ATTTGAAACTCTCTACTTGAATTCAGAGCTGCAGGGTATAAGTTCAGTCTCTCAAGATCA 2128
Qy 3267 GCTCACCCACCGACCATCCCTTCAACCTCATGGAAGTGCACCTCATGGTAGCGGTG 3326
Db 2129 CCATGACCCAGTCTATTATTCATTAAATTAATGAAGGTTCATCTTATGTTAGCTGTAG 2188
Qy 3327 AGGCGCGCTCTTTCAGGAAGTGGTTGCTGCGAGCCCGCAGACCTGTCTATTATTTCATTT 3386
Db 2189 TAGGAAGACTCTTCCAAAGTGGTTCTCGCTCACCAAACTTGGCTATACTTTTCATAT 2248
Qy 3387 GGGACAAACAGACGTCTACAAACAGAAAGTGGTTTGGCTTTTCAAGACCTTTGTTCCG 3446
Db 2249 GGGATAAAACAGATGCATATAATCAGAAAGTCTATGGTCTATCTGAAAGCTGTTGTGTCAG 2308
Qy 3447 TGGGTTATGAATATGAATCCTGCCAGATCTAACTCTGTGGGAAAAAAGAACACAGTGC 3506
Db 2309 TTGGATATGATATGATGCTGTGTTGGACCTGACTCTGTGGGAAAGAGGACTGCCATTC 2368
Qy 3507 TGCAGGCTATGAATTCAGCCGCTCCAAAGCTTGGAGGATGGAGCTTAGACAAAACATCATG 3566
Db 2369 TGCAGGCTATGAATTTGATGCGTCCAACATGGGTGGCTGGACATTAGATAAACATCACG 2428
Qy 3567 CCCTCAACATTCNAAGTGGTATCTCTGCACAAAGGAATGGGGAAACAGTTTGTGCTC 3626
Db 2429 TGCTGGATGTACAGAACCGGTATATCTGTACAAGGGAAACGGGGAAAAACAGTTTCTCCC 2488

Qy 3627 AGCAGCCTCTGTGTCATTTGGGAGACATCATGGGCAA 3660
Db 2489 AGCAGCCTCAGTCTGATAGCTTCGAGGGTAA 2522

RESULT 8

US-11-096-051-5
; Sequence 5, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Keku, Rameesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Eitenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Curaseq!ist version 0.1
; SEQ ID NO 5
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(2473)
US-11-096-051-5

Query Match 13.8%; Score 1151.2; DB 9; Length 2482;
Best Local Similarity 67.8%; Pred. No. 1.2e-277; Indels 0; Gaps 0;
Matches 1609; Conservative 0; Mismatches 763

Qy 1287 AAGGAAAGCCAGTAGTTTCTTCCAGAGGACAGTTTCTATAGATTTCTGGAGAAATTGATG 1346
Db 111 ATGAAAAATTAGTGGATTTACGCAAGAAAATAACCATAGATTCGGGAACTTGATA 170
Qy 1347 TGGGAAGCGAGCCTCCGAGAATTCCTCTCGGACTTCTCGAGATCTCAAGTGTTC 1406
Db 171 TTGGCCGAGAGCAATTCAGAGATTCCTCCCGGATCTTCTGGAGATCACAGCTCTTCA 230
Qy 1407 TAGACCATCTGTGTCATCTGAAATTCAAATGTGTCTCTGGGAAAGGAGCCCTGTTGGCA 1466
Db 231 TTGATCAGCCACAGTTTCTTAAATTCATATCTCTTCGAAAGGATGCATTCGATGGAG 290
Qy 1467 TTTATGGCAGAAAGGCTCCCTCTTTCACATACACAGTTTGTGAGCTGTCTGG 1526
Db 291 TATATGGCGGAAAGGCTTACCGCTTCCCATACTCAGTATGACTTCGTGGAGCTCTGG 350
Qy 1527 ATGGCAGGAGCTCTTAACCCAGGAGCGGAGGAGCTAGAGGAGCCCGCCGAGTCTC 1586
Db 351 ATGGCAGCAGGCTGATTGCCAGAGAGCAGCGGAGCTGCTTGGAGCGGAGAGCCGGGC 410
Qy 1587 GGGGAACTGTGCCCCCTCCAGCCATGAGCAGGCTTTCATCCAGTATTTGGATTTCAGGAA 1646
Db 411 GGCAGGGAGATCCGTGAGCTTTCATGAGCGGCTTATCCAGTACTTGGATTCTGGAA 470
Qy 1647 TCTGGCATTGGCTTTTAAATGACGGAAGAGGATCAGAGTGGTTTCTTTCTCACCA 1706
Db 471 TCTGGCATTGGCTTTTAAATGATGGGAAATAATCAGAGCAGGCTGCTTTTAAATACCA 530
Qy 1707 CTGCCATTGAGTGGTGAATACTGCCCGCAGCAACTGCTATGCAATGGTGAATGCTCT 1766
Db 531 TTGTTATAGATCTGTGGTGGAAATGTCCTCCGAAATTCGCAATGGAAATGCGTTT 590

;
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuroSequelist version 0.1
; SEQ ID NO 13
; LENGTH: 1833
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1827)
US-11-096-051-13

Query Match 10.1%; Score 842.2; DB 9; Length 1833;
Best Local Similarity 66.7%; Pred. No. 1.7e-200;
Matches 1229; Conservative 0; Mismatches 593; Indels 21; Gaps 1;
QY 2469 TAGACCTGAATGGTTGGCACTGGCTCTGCCAGCTGGGCTGGAGAGGAGCTGGCTGTGACA 2528
DB 5 TTGACCAAAATGGCGACATTTGTGTGCCAGCTGGATGGAGAGGAGGCTGTGAGC 64
QY 2529 CTTCCATGAGAGCTGCTCGGTGACAGCAAAAGCAATGATGGAGATGGCCTGTGGACT 2588
DB 65 TAGCCATGGAGACTCTTTGCACAGATAGCAAGGACAAATGAAGGAGATGGACTCAATTGACT 124
QY 2589 GCATGGACCTGACTGCTGCCTCCAGCCCTGTGCCATATCAACCGCTGTGCTTGGCT 2648
DB 125 GCATGGATCCGATTTGCTGCCCTACAGAGTTCTGTGCCAATCAGCCCTATTGTTCGGGAC 184
QY 2649 CCCCTAAACCTCTGGACATCATCCAGGAGACACAGTCCCTGTGTACAGACAGAACCTTAC 2708
DB 185 TGCCGATCCTCAGGACATATTAGCCAAAGCTTCAATCGCTTCTCAGCAAGCTGCCA 244
QY 2709 ACTCCTTTATGACCGCATCAAGTTCTCTGTGGGAGGAGACAGCACATAATCCCGC 2768
DB 245 AATCCTTTTATGATGAATCAGTTCTCTTATAGGATCTGATAGCACCCATGTTATACCTG 304
QY 2769 GGGAGAACCCCTTGTATGAGGGGATGCTGTGTTATTCGTGGCCAAAGTGATGACATCAG 2828
DB 305 GAGAAAGTCTTTCAATAGAGCCTTGTGATCTGTATCAGAGGCGCAAGTACTGACTGCTG 364
QY 2829 ATGGAAACCCCTGTTGTGTGAACATCAGTTTGTCAATAACCCCTCTCTTTGGATATA 2888
DB 365 ATGGAACCTCACTTATTGGAGTAAATGTCTGCTTTTCCATTACCCAGAAATATGATATA 424
QY 2889 CAATCAGAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGATCTCCATCATCC 2948
DB 425 CTATTACCGCCAGGACGGAATGTTTGAATTTGGTGGCAAAATGGTGGGGCCTCTCTAACTT 484
QY 2949 TCGGTTTCGAGCGGCACCTTTTCATCACAGGAGCACACCTGTGGCTGCCATGGGATC 3008
DB 485 TGGTATTTGAACGATCCCATTTCTCATCTCAGTATCATCTGTGTGGATTCATGGGAATG 544
QY 3009 GCTCTTTGTATGAAACCAATCATCATGAGCATGAGGAGAATGAGATTTCCCAAGCTGTG 3068
DB 545 TCTTTTATGTGATGATACCCCTAGTCAATGAAGAAAGAGAAATGACATTTCCCAAGCTGTG 604
QY 3069 ACCTCAGCAATTTTGGCGCCGCCAACCCAGTGTCTCTCCATCCCACTGAGCTCTTCG 3128
DB 605 ATCTCAGTGGATTCGTGAGGGCCAAATCCCATTCATTTGTGTCTATCATCTTTATCCACCTTTT 664
QY 3129 CCAGCTCTCTGTGACAGAAAGGCCCAATTTGGCCGGAATTCAGGCTTTGACAGAGGAAA 3188
DB 665 TCAGATCTTCTCCTGAAGACAGTCCCATCATCTCCGAAACACAGGTACTCCACAGGAAA 724
QY 3189 TCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACTGTGAGCGCGGACCCCTCGGTACA 3248
DB 725 CTACAAATTCAGGAAACAGATTTGAACTCTCTACTTGTGAGTTCCAGAGCTGCAGGGTATA 784
QY 3249 AATCTGCTCTGAGGATCAGCTCCACCCACCGACCTCCCTTCAACCTCATGAGGTGC 3308
DB 785 AGTCAGTTCTCAAGATCACCATGACCCAGTCTATTATTTCCATTTAAATTTAATGAAGGTTT 844

QY 3309 ACCTCATGTGTAGCGGTGGAGGGCCGCTCTTTTCAGAAAGTGGTTCCGTGACGCCACAGACC 3368
DB 845 ATCTTATGGTAGCTGTAGTAGGAAGACTCTTCCAAAAGTGGTTTCTCGCTCCACAAACT 904
QY 3369 TGTCTATTATTTTCATTTGGGACAAGACAGACGCTCTACAAACCAAGAGGTGTTGGGGTTT 3428
DB 905 TGGCCTATATCTTTCATATGGGATAAACAGATGATATATATCAGAAAGTCTATGGTCTAT 964
QY 3429 CAGAAGCCTTTGTTTCCGTGGGTTATGAATATGAATCTCTGCCAGATCTAATCTCTGTGG 3488
DB 965 CTGAAGCTGTGTGTCTCAGTTGGATATGATGATGATGATGATGATGATGATGATGATG 1024
QY 3489 AAAAAAGAACAAAGTCTGCGAGGCTATGAATTTGACCGCTCAACGCTTGGAGGATGGA 3548
DB 1025 AAAAGAGGACTGCGCATTTCTCAGGGCTATGAATTTGGATGGCTCCAAACATGGTGGCTGA 1084
QY 3549 GCCTAGACAAACATCATGCGCTCAACATTCAAAAGTGGTATCTCTGCACAAAGGGAATCGG 3608
DB 1085 CATTAGATAAACATCATGCTGTGATGTACAGAACGGTATATCTGTACAGGGAAACCGGG 1144
QY 3609 AGAACCAAGTTTGTCTCAGCAGCCTCTCTGTCTATTGGGAGCATCATGGGCAATGGGCGCC 3668
DB 1145 AAAACCAAGTTTCATCTCCAGCAGCCTCCAGTCTGTGAGTAGCATCATGGGCAATGGGCGAA 1204
QY 3669 GGAGAACATCTCTGCGCCAGCTGCAACCGCTTGTCTGACGGCAACAGCTCTGCGCCC 3728
DB 1205 GGGCAGCATTTCTGCGCCAGTTGCAATGGTCAAGCTGATGGTAAACAGTTACTGCGCCC 1264
QY 3729 CAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCACATACATTA 3788
DB 1265 CAGTGGCGCTAGCTTGTGGGATCGATGGGAGTCTGTACGTAGGGGATTTCACTATGTGC 1324
QY 3789 GAAGGATCTTCCCTCTGGAAATGTCAACAACTCTTAGAGCTGAGGAAATAAAGATTCA 3848
DB 1325 GGGGATATTCTCTGGAAATGTAAACAGTCTCTAGAACTAAGCAGCAA----- 1376
QY 3849 GACATAGTCAGTCCAGCACACAAATACTACTCTGCGGCCACAGACCCCATGAGTGGGCGC 3908
DB 1377 -----CCAGCTCATAGATACTACTCTTGCACGGGATCCAGTCACGGGAGATC 1423
QY 3909 TCTTCTTTCTGACAGCAACAGCGCGGCTCTTTAAATTCAAAGTCCACTGTGTGTGTA 3968
DB 1424 TGTACGTTTCTGACACAAACACCCCGCAGAAATTTATCGCCCAAGTCACTTACGGGGGCAA 1483
QY 3969 AGACCTTGTCAAGAACTCTGAGGTGGTTCGGGGGACAGGTGACCAAGTGCCTCCCTTTG 4028
DB 1484 AAGACTTGACTTAAATAATGCAGAAAGTCTGCGCAGGACAGGGGAGCAATGCTTCCGTTG 1543
QY 4029 ATGACACTGCTCGCGGGATGGTGGGAAGGCCACAGAACCCACATCCCAATCCCGGG 4088
DB 1544 ACAGGGGAGATGTGGGGATGGAGGGAAGGCGGTGAAGCCACATCATGATGTCCTCAAG 1603
QY 4089 GTATTACAGTGGCAAGTTTGGGCTGATCTACTTCTGGATGGCACCATTGATCAGACGCA 4148
DB 1604 GAATGGCAGTTGATAAGAAATGGAATTAATCTACTTTGTGATGSAACCATGATTAGGAAAG 1663
QY 4149 TCATCAGAAATGGGATCATCTCCACCTGCTGGCTCTAATGATCTCATATGAGCCCGGC 4208
DB 1664 TTGACCAAAATGGAATCATATCAACTCTTCTGGGTTCTAACGATTTGACTTTCAGCCAGAC 1723
QY 4209 CACTCAGCTGTGATTTCTGTCTCATGATATTTTCCAGGTAAAGCTTGGAGTGGCCCCACAGACT 4268
DB 1724 CTTTAACCTTGTGACACACAGATGCACATCAGCCAGGTAGCTCTGGAAATGGCCCACTGACC 1783
QY 4269 TAGCCATCAACCAATGGCAAACTCACTTATATGTCTCCACAA 4311
DB 1784 TAGCCATTAACCCCTATGGATACTCCATTTATGTCTCTGGATAA 1826

RESULT 10
US-11-096-051-11
; Sequence 11, Application US/11096051

| | | | |
|----|------|---|------|
| Db | 1202 | GAAGATCACCATGACCCCAATCCACAGTGCCTTGAACCTCATCAAGTTTCATCTCATGGT | 1143 |
| Qy | 3319 | AGCGGTGGAGGGCGGCTCTTTCAGGAAGTGGTTGGCTGCAGGCCACAGACCTGTCCATTATTA | 3378 |
| Db | 1142 | TGCTGTAGAGGGGCACCTCTTCCAGAAGTCAATTCAGGCCCTCTCTAACTTGGCCTACAC | 1083 |
| Qy | 3379 | TTTTCATTTGGGACNAGACAGACGTCTACACACAGAGAGTGTTTTGGGCTTTTCAGNAGCCTT | 3438 |
| Db | 1082 | CTTTCATCTGGGACAAGACAGATGCTTACGGCCAAAGGTCTATGGACTCTCTGATGCTGT | 1023 |
| Qy | 3439 | TGTT | 3442 |
| Db | 1022 | TGTT | 1019 |

```

RESULT 14
US-10-750-185-39351
; Sequence 39351, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 39351
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Bovine 19866801410938
US-10-750-185-39351

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| | Query Match | 1.2% | Score 101.6; | DB 6; | Length 972; |
|----|-----------------------|--|--------------------|-----------|-------------|
| | Best Local Similarity | 76.2; | Pred. No. 1.2e-15; | | |
| | Matches 125; | Conservative 0; | Mismatches 39; | Indels 0; | Gaps 0; |
| Qy | 4088 | GGTATTACAGTGGCAAGTTTGGGCTCATCTACTTCGTGGATGGCAACCATGATCAGACGC | 4147 | | |
| Db | 272 | GGTATTGCAGTTGACAAGATGGGCTCATGTACTTGTGCAGCGCACCATGATCCGCAG | 331 | | |
| Qy | 4148 | ATCGATCAGAAATGGGATCATCTCCACCCCTGCTCGGGCTCTAATGATCTCAATCAGCCCGG | 4207 | | |
| Db | 332 | GTGCACCAAGATGGAATCATCTCACCTTGTCTGGGCTCCAAAGACCTCACCGCTGTCCGG | 391 | | |
| Qy | 4208 | CCACTCAGCTGTGATTCTGTCAATGGATATTTCCCAAGTAAAGCT | 4251 | | |
| Db | 392 | CCCTGAGCTGTGACTCCAGCATGGATGTGGCCCCAGGTGGGATT | 435 | | |

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RESULT 15
US-10-750-185-28736/c
; Sequence 28736, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2

```

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, CURRENT APPLICATION NUMBER: US10/750,185
,
, CURRENT FILING DATE: 2003-12-31
,
, PRIOR APPLICATION NUMBER: US 60/437,482
,
, PRIOR FILING DATE: 2002-12-31
,
, NUMBER OF SEQ ID NOS: 64922
,
, SOFTWARE: PatentIn version 3.1
,
, SEQ ID NO 28736
,
, LENGTH: 1835
,
, TYPE: DNA
,
, ORGANISM: Bovine
US-10-750-185-28736

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| | Query Match | 1.1%; | Score 92.6; | DB 6; | Length 1835; |
|----|------------------------------|---|----------------|-----------|--------------|
| | Best Local Similarity 62.1%; | Pred. No. 2.9e-13; | | | |
| | Matches 146; | Conservative 0; | Mismatches 89; | Indels 0; | Gaps 0; |
| Qy | 1816 | AGCTCTCTGCCCGTCTGTGTACGCGAAATGCCCAATACATCAAGAGGCAGATGCTTGTG | 1875 | | |
| Db | 273 | AGATTCTGTCCTTGTCTGTGTGGTATGAGATATATGAAAGGACACTGTGTCG | 214 | | |
| Qy | 1876 | CCACAGTGGCTGGAAGCGCCTGAGTGCATGTGCCCAACCAACAGTGTATCGATGTGGC | 1935 | | |
| Db | 213 | CCGAAATGGCTGGAAGGGCGCAGATGCCATGTTCCAGAGAGCAATGCATTGATCCAAC | 154 | | |
| Qy | 1936 | CTCAGCAACCATCGGCACCTGCATCAGGCGCACTGCATCTGCAACCTCGCTACAAAGG | 1995 | | |
| Db | 153 | GTGCTTTGGCCACGGCACCTTCATCATGGAGATTTCATCTGTGTGCCAGATACAAAGG | 94 | | |
| Qy | 1996 | CGAGAGCTGTGAGGAATGGACTGCATGTGACCCCAACATGTTTCAGCGCGGGTGTCT | 2050 | | |
| Db | 93 | AGAAATATCGAGGAAGCTCAGAGCCCTGTGTTAAATATATTTGCTTCAGGCTTTTC | 39 | | |

Search completed: December 10, 2005, 17:39:15
Job time : 641 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: December 9, 2005, 19:44:14 ; Search time 5039 Seconds
(without alignments)
11831.201 Million cell updates/sec

Title: US-10-029-020-13
Perfect score: 8354
Sequence: 1 gtttggatgtggaggac.....ccggaggtagacagaggac 8354

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 8354 | 100.0 | 8354 | 7 | US-10-383-201-43 |
| 2 | 8354 | 100.0 | 8354 | 7 | US-10-029-020-13 |
| 3 | 8225 | 98.5 | 8645 | 7 | US-10-467-535-22 |
| 4 | 7991.2 | 95.7 | 8355 | 7 | US-10-383-201-55 |
| 5 | 7779.2 | 93.1 | 8438 | 7 | US-10-042-865-1 |
| 6 | 3680.8 | 44.1 | 8624 | 8 | US-10-723-860-3169 |
| 7 | 3680.8 | 44.1 | 8624 | 9 | US-10-756-149-2959 |
| 8 | 3621.6 | 43.4 | 8774 | 8 | US-10-723-860-7176 |
| 9 | 3502.2 | 41.9 | 8645 | 7 | US-10-038-854-37 |
| 10 | 3473.8 | 41.6 | 8675 | 7 | US-10-038-854-35 |
| 11 | 3422 | 41.0 | 8473 | 7 | US-10-038-854-39 |
| 12 | 3398.8 | 40.7 | 8487 | 7 | US-10-038-854-41 |
| 13 | 3397.8 | 40.7 | 8689 | 3 | US-09-808-602-78 |
| 14 | 3397.8 | 40.7 | 8689 | 3 | US-09-800-198-66 |
| 15 | 3385 | 40.5 | 9826 | 3 | US-09-808-602-7 |
| 16 | 3385 | 40.5 | 9826 | 3 | US-09-800-198-7 |
| 17 | 3384.8 | 40.5 | 8797 | 3 | US-09-808-602-74 |
| 18 | 3384.8 | 40.5 | 8797 | 3 | US-09-808-602-77 |
| 19 | 3384.8 | 40.5 | 8797 | 3 | US-09-800-198-62 |
| 20 | 3384.8 | 40.5 | 8797 | 3 | US-09-800-198-65 |
| 21 | 3384.8 | 40.5 | 8797 | 9 | US-10-631-467-1171 |
| 22 | 3351.4 | 40.1 | 9729 | 3 | US-09-808-602-12 |
| 23 | 3351.4 | 40.1 | 9729 | 3 | US-09-800-198-12 |

| | | | | | | |
|----|--------|------|-------|---|--------------------|-------------------|
| 24 | 3258 | 39.0 | 8297 | 8 | US-10-723-860-4101 | Sequence 4101, Ap |
| 25 | 3258 | 39.0 | 12880 | 6 | US-10-295-027-927 | Sequence 927, App |
| 26 | 3165 | 37.9 | 9695 | 6 | US-10-144-194A-81 | Sequence 81, Appl |
| 27 | 3165 | 37.9 | 9695 | 8 | US-10-491-566-81 | Sequence 81, Appl |
| 28 | 3158.4 | 37.8 | 8575 | 7 | US-10-072-012-143 | Sequence 143, App |
| 29 | 3137.4 | 37.6 | 7781 | 8 | US-10-723-860-2302 | Sequence 2302, Ap |
| 30 | 3070.8 | 36.8 | 8409 | 3 | US-09-808-602-79 | Sequence 79, Appl |
| 31 | 3070.8 | 36.8 | 8409 | 3 | US-09-800-198-67 | Sequence 67, Appl |
| 32 | 3068.6 | 36.7 | 9058 | 6 | US-10-144-194A-79 | Sequence 79, Appl |
| 33 | 3068.6 | 36.7 | 9058 | 8 | US-10-491-566-79 | Sequence 79, Appl |
| 34 | 2845.4 | 31.7 | 6810 | 8 | US-10-723-860-8301 | Sequence 8301, Ap |
| 35 | 2587.2 | 31.0 | 6771 | 8 | US-10-723-860-6509 | Sequence 6509, Ap |
| 36 | 2533 | 30.3 | 6560 | 3 | US-09-808-602-76 | Sequence 76, Appl |
| 37 | 2533 | 30.3 | 6560 | 3 | US-09-800-198-64 | Sequence 64, Appl |
| 38 | 2463 | 29.5 | 5309 | 8 | US-10-723-860-4493 | Sequence 4493, Ap |
| 39 | 1708.8 | 20.5 | 3111 | 3 | US-09-773-517-12 | Sequence 12, Appl |
| 40 | 1708.8 | 20.5 | 3111 | 3 | US-09-792-025-12 | Sequence 12, Appl |
| 41 | 1708.8 | 20.5 | 3111 | 3 | US-09-849-868-12 | Sequence 12, Appl |
| 42 | 1708.8 | 20.5 | 3111 | 5 | US-10-290-578-1 | Sequence 1, Appl |
| 43 | 1708.8 | 20.5 | 3111 | 6 | US-10-453-183-12 | Sequence 12, Appl |
| 44 | 1673.6 | 20.0 | 1680 | 5 | US-10-290-578-3 | Sequence 3, Appl |
| 45 | 1562.6 | 18.7 | 4245 | 9 | US-10-494-940-38 | Sequence 38, Appl |

ALIGNMENTS

RESULT 1

US-10-383-201-43
; Sequence 43, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2003-03-06
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Curaseq version 0.1
; SEQ ID NO 43
; LENGTH: 8354
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (35)..(8341)
US-10-383-201-43
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 8354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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61 CCGCTCGCTGACCCGCGCGCGAGCGCGGCGCTACACAGCTCGTCCGCGGAG 120
Db
61 CCGCTCGCTGACCCGCGCGCGAGCGCGGCGCTACACAGCTCGTCCGCGGAG 120
QY
121 CGAGGAGGCAAGCCCGCAGAAATCGTACAGCTCCAGCGAGACCTGGAAGGCTTACGA 180
Db
121 CGAGGAGGCAAGCCCGCAGAAATCGTACAGCTCCAGCGAGACCTGGAAGGCTTACGA 180
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Db
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1081 CTCAGCCACTGTGGTCTATCTGCTGGCATACTTTGTGGCCATGCACTGTTTGGCCTAAA 1140
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Db
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Db
2101 CGAGACCCCGGAGGCGACATGCTTTAGACCAAGTGTTCAGGCGCAGGAACTTCTCTCCCGGA 2160
QY
2161 CACCGGGCTTTGAGCTGTGACCCCAAGCTGGACTGACACGACTGTTCTATCGAGATCTG 2220
Db
2161 CACCGGGCTTTGAGCTGTGACCCCAAGCTGGACTGACACGACTGTTCTATCGAGATCTG 2220

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|----|------|---|------|----|------|--|------|
| QY | 2221 | TGCTGCCGACTGTGTGGCCATCGCGTGTGCGTAGGGGACCTGCGCGTGCAGGATGG | 2280 | QY | 3301 | GAAGGTGCACCTCATGTGTAGCGTGGAGGGCGCGCTCTTTCAGGAAGTGTGCTTCGCAGC | 3360 |
| DB | 2221 | TGCTGCCGACTGTGTGGCCATCGCGTGTGCGTAGGGGACCTGCGCGTGCAGGATGG | 2280 | DB | 3301 | GAAGGTGCACCTCATGTGTAGCGTGGAGGGCGCGCTCTTTCAGGAAGTGTGCTTCGCAGC | 3360 |
| QY | 2281 | CTGGATGGGGCAGCCTGCGAACAGCGGGCTGCCACCGCGCTGTGCCGAGCATGGAC | 2340 | QY | 3361 | CCGAGCCTGTCTTATTTTTCATTTGGGACAGACAGCGTCTACAAACGAGGTGT | 3420 |
| DB | 2281 | CTGGATGGGGCAGCCTGCGAACAGCGGGCTGCCACCGCGCTGTGCCGAGCATGGAC | 2340 | DB | 3361 | CCGAGCCTGTCTTATTTTTCATTTGGGACAGACAGCGTCTACAAACGAGGTGT | 3420 |
| QY | 2341 | CTGCCGGACGGCAAGTGGAGTGCAGCCCTGCTCGAATGGGACATGCAACCATCG | 2400 | QY | 3421 | TGGGCTTTTCAGAAAGCCTTGTTCCTGCTGGTGTATGAATATGAATCTCTGCCAGATCTAAT | 3480 |
| DB | 2341 | CTGCCGGACGGCAAGTGGAGTGCAGCCCTGCTCGAATGGGACATGCAACCATCG | 2400 | DB | 3421 | TGGGCTTTTCAGAAAGCCTTGTTCCTGCTGGTGTATGAATATGAATCTCTGCCAGATCTAAT | 3480 |
| QY | 2401 | TCACTATCTGGATAGGAGTAAAGAGGTTGCCCTGGTGTGCAATGGCAACGGCAG | 2460 | QY | 3481 | CCTGTGGGAAAAAGAACAAAGTGTGAGGGCTATGAATTTGAGCGCTTCCAAGCTTG | 3540 |
| DB | 2401 | TCACTATCTGGATAGGAGTAAAGAGGTTGCCCTGGTGTGCAATGGCAACGGCAG | 2460 | DB | 3481 | CCTGTGGGAAAAAGAACAAAGTGTGAGGGCTATGAATTTGAGCGCTTCCAAGCTTG | 3540 |
| QY | 2461 | ATGTACTTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGTGGAGAGAGCTGG | 2520 | QY | 3541 | AGGATGGAGCCTTAGACAAACATCATGCGCTCAACATTTCAAGTGGTATCTTGACAAAGG | 3600 |
| DB | 2461 | ATGTACTTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGTGGAGAGAGCTGG | 2520 | DB | 3541 | AGGATGGAGCCTTAGACAAACATCATGCGCTCAACATTTCAAGTGGTATCTTGACAAAGG | 3600 |
| QY | 2521 | CTGTGACATCTCATGAGAGCTGCTGCGGTGACAGAAAGACAAATGATGGAGATGGCT | 2580 | QY | 3601 | GAATGGGAGAACCAAGTTTGTCTCAGCAGCTCTCTGTCTATTGGGAGCATCATGGGCAA | 3660 |
| DB | 2521 | CTGTGACATCTCATGAGAGCTGCTGCGGTGACAGAAAGACAAATGATGGAGATGGCT | 2580 | DB | 3601 | GAATGGGAGAACCAAGTTTGTCTCAGCAGCTCTCTGTCTATTGGGAGCATCATGGGCAA | 3660 |
| QY | 2581 | GGTGGACTGACATGCACTGCTGCTGCCCTCCAGCCCTGTGTCATATCAACCCGCTGTG | 2640 | QY | 3661 | TGGGCGCGGAGAGCATCTCTGCCAGCTGCAACCGCTTGTCTGACGGCAACAGCT | 3720 |
| DB | 2581 | GGTGGACTGACATGCACTGCTGCTGCCCTCCAGCCCTGTGTCATATCAACCCGCTGTG | 2640 | DB | 3661 | TGGGCGCGGAGAGCATCTCTGCCAGCTGCAACCGCTTGTCTGACGGCAACAGCT | 3720 |
| QY | 2641 | CCTTGGCTCCCCCTAAACCTCTGGACATCATCCAGGAGACACAGGTCCCTGTGTACAGCA | 2700 | QY | 3721 | CCTGGGCGCAGTGGGCTCACCCTGTGCTGACGGGAGCCTCTATGTGGTGTATTCAA | 3780 |
| DB | 2641 | CCTTGGCTCCCCCTAAACCTCTGGACATCATCCAGGAGACACAGGTCCCTGTGTACAGCA | 2700 | DB | 3721 | CCTGGGCGCAGTGGGCTCACCCTGTGCTGACGGGAGCCTCTATGTGGTGTATTCAA | 3780 |
| QY | 2701 | GAACCTACATCTCTATGACCGCATCAAGTTCTCTGTGGGAGGACAGCAGCAGCAT | 2760 | QY | 3781 | CTACATTAGAAGATCTTCCCTCTGCAAAATGTCTACAAACATCTTAGAGCTGAGGAATAA | 3840 |
| DB | 2701 | GAACCTACATCTCTATGACCGCATCAAGTTCTCTGTGGGAGGACAGCAGCAGCAT | 2760 | DB | 3781 | CTACATTAGAAGATCTTCCCTCTGCAAAATGTCTACAAACATCTTAGAGCTGAGGAATAA | 3840 |
| QY | 2761 | AATCCCGGGAGAACCCCTTTCATATGGAGGACATGTTGTGTTATTCGTGGCCAAAGTAT | 2820 | QY | 3841 | AGATTTTCAGACATAGTTCACAGTCCAGCACACAAATACTACTTGGGCGCACAGACCCCATGAG | 3900 |
| DB | 2761 | AATCCCGGGAGAACCCCTTTCATATGGAGGACATGTTGTGTTATTCGTGGCCAAAGTAT | 2820 | DB | 3841 | AGATTTTCAGACATAGTTCACAGTCCAGCACACAAATACTACTTGGGCGCACAGACCCCATGAG | 3900 |
| QY | 2821 | GACATCAGATGGAAACCCCTCTGTGTGTGAACATCAGTTTGTCAATAACCCCTCTCTT | 2880 | QY | 3901 | TGGGCGCGTCTTCTTTCAGACAAACAGCCGGCGGGTCTTTAAATCAAGTCCCATGT | 3960 |
| DB | 2821 | GACATCAGATGGAAACCCCTCTGTGTGTGAACATCAGTTTGTCAATAACCCCTCTCTT | 2880 | DB | 3901 | TGGGCGCGTCTTCTTTCAGACAAACAGCCGGCGGGTCTTTAAATCAAGTCCCATGT | 3960 |
| QY | 2881 | TGGATATACAAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC | 2940 | QY | 3961 | GGTGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGACAGGTGACCAAGTGCCT | 4020 |
| DB | 2881 | TGGATATACAAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC | 2940 | DB | 3961 | GGTGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGACAGGTGACCAAGTGCCT | 4020 |
| QY | 2941 | CATCATCTCTGGGTTGAGCGGCACCTTTCATCACACAGGAGCACACCTGTGGCTGCC | 3000 | QY | 4021 | CCCCCTTTGATGACATCTCGCTGCGGGGATGGTGGGAAAGGCCACAGAAAGCCACTCACAA | 4080 |
| DB | 2941 | CATCATCTCTGGGTTGAGCGGCACCTTTCATCACACAGGAGCACACCTGTGGCTGCC | 3000 | DB | 4021 | CCCCCTTTGATGACATCTCGCTGCGGGGATGGTGGGAAAGGCCACAGAAAGCCACTCACAA | 4080 |
| QY | 3001 | ATGGGATCGCTTCTTGTGATGAAACCATCATCATGAGACATGAGAGATGAGATTCC | 3060 | QY | 4081 | TCCAGGGGTATTAAGTGGGACAGTTTGGGCTGATCTACTTCTGTTGGATGGGACCATGAT | 4140 |
| DB | 3001 | ATGGGATCGCTTCTTGTGATGAAACCATCATCATGAGACATGAGAGATGAGATTCC | 3060 | DB | 4081 | TCCAGGGGTATTAAGTGGGACAGTTTGGGCTGATCTACTTCTGTTGGATGGGACCATGAT | 4140 |
| QY | 3061 | CAGCTGTGACCTGAGCAATTTTGGCGCCCAACCCAGTCTCTCTCATCCCGCATGAC | 3120 | QY | 4141 | CAGAGCATCTGATCAAGATGGGATCATCTCCACCTCTCGGCTCTAAATGATCTCACATC | 4200 |
| DB | 3061 | CAGCTGTGACCTGAGCAATTTTGGCGCCCAACCCAGTCTCTCTCATCCCGCATGAC | 3120 | DB | 4141 | CAGAGCATCTGATCAAGATGGGATCATCTCCACCTCTCGGCTCTAAATGATCTCACATC | 4200 |
| QY | 3121 | GTCCCTTCGCGACTCTGTGAGAGAGGCGCCATTTGCGCGGAATTCAGGCTTTGCA | 3180 | QY | 4201 | AGCCCGGCGCACTCAGCTGTGATTTCTGTCATGGATAATTTCCAGGTAAGACTGGAGTGGCC | 4260 |
| DB | 3121 | GTCCCTTCGCGACTCTGTGAGAGAGGCGCCATTTGCGCGGAATTCAGGCTTTGCA | 3180 | DB | 4201 | AGCCCGGCGCACTCAGCTGTGATTTCTGTCATGGATAATTTCCAGGTAAGACTGGAGTGGCC | 4260 |
| QY | 3181 | GGAGGAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACTCTGAGCAGCGGACCCC | 3240 | QY | 4261 | CACAGATTTAGCCATCAACCCCAATGGAACAACTCACTTTATGCTCTCGAACCAATGTGT | 4320 |
| DB | 3181 | GGAGGAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACTCTGAGCAGCGGACCCC | 3240 | DB | 4261 | CACAGATTTAGCCATCAACCCCAATGGAACAACTCACTTTATGCTCTCGAACCAATGTGT | 4320 |
| QY | 3241 | TGGCTACAAATCTGTCTGAGGATFAGCTCTCACCCACCGACCATCCCTTCAACCTCAT | 3300 | QY | 4321 | CCTGCAAAATCTCTGAAAACCAACAGGTGCGCATTTGTGCGGGAGGCCCATGACCTGCCA | 4380 |
| DB | 3241 | TGGCTACAAATCTGTCTGAGGATFAGCTCTCACCCACCGACCATCCCTTCAACCTCAT | 3300 | DB | 4321 | CCTGCAAAATCTCTGAAAACCAACAGGTGCGCATTTGTGCGGGAGGCCCATGACCTGCCA | 4380 |
| | | | | QY | 4381 | GGTCCCTGGCATTTGACCACTTCTCTGCTAAGCAAGGTGGCCATCCACGCAACCCCTGGAGTC | 4440 |

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Db 6301 CCGGGTGACAGCATGACGCTGTGATCAACGAGAGCCCACTGCCCATTTGATCTCTATCG 6360
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RESULT 2

US-10-029-020-13
; Sequence 13, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14

same like as file 1

| | | | | | | | | | |
|---|-----|--|-----|--|--|--|--|--|--|
| ; PRIOR APPLICATION NUMBER: 60/294,075 | | | | | | | | | |
| ; PRIOR FILING DATE: 2001-05-29 | | | | | | | | | |
| ; BEST APPLICATION NUMBER: 60/288,153 | | | | | | | | | |
| ; PRIOR FILING DATE: 2001-05-02 | | | | | | | | | |
| ; NUMBER OF SEQ ID NOS: 190 | | | | | | | | | |
| ; SOFTWARE: PatentIn Ver. 2.1 | | | | | | | | | |
| ; SEQ ID NO 13 | | | | | | | | | |
| ; LENGTH: 8354 | | | | | | | | | |
| ; TYPE: DNA | | | | | | | | | |
| ; ORGANISM: Homo sapiens | | | | | | | | | |
| US-10-029-020-13 | | | | | | | | | |
| Query Match 100.0%; Score 8354; DB 7; Length 8354; | | | | | | | | | |
| Best Local Similarity 100.0%; Pred. No. 0; | | | | | | | | | |
| Matches 8354; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| QY | 1 | GTTTGTGGATGTGGAGAGCGGGCCGGAGGCCATGGACGTGAAGGAGGAGGAACCTTTA | 60 | | | | | | |
| DB | 1 | GTTTGTGGATGTGGAGAGCGGGCCGGAGGCCATGGACGTGAAGGAGGAGGAACGCTTA | 60 | | | | | | |
| QY | 61 | CGCTCGCTGACCCGCGCGCGAGCCGAGCGCGCTACACAGCTGTCGCGGAGAG | 120 | | | | | | |
| DB | 61 | CGCTCGCTGACCCGCGCGCGAGCCGAGCGCGCTACACAGCTGTCGCGGAGAG | 120 | | | | | | |
| QY | 121 | CGAGGAGGCAAGCCCGCAGAAATCGTACAGCTCCAGCGAGACCCCTGAAGGCTACGA | 180 | | | | | | |
| DB | 121 | CGAGGAGGCAAGCCCGCAGAAATCGTACAGCTCCAGCGAGACCCCTGAAGGCTACGA | 180 | | | | | | |
| QY | 181 | CGAGGAGCCCGCTAGCTATGGCAGCGCGCTCAAGGACATTTGTGCCGAGGAGCCGA | 240 | | | | | | |
| DB | 181 | CGAGGAGCCCGCTAGCTATGGCAGCGCGCTCAAGGACATTTGTGCCGAGGAGCCGA | 240 | | | | | | |
| QY | 241 | GGAAATTCGCCGACAGGTGCCAACTTACCTCTGGGAGCTGGGGCTGGGAAGATTAAC | 300 | | | | | | |
| DB | 241 | GGAAATTCGCCGACAGGTGCCAACTTACCTCTGGGAGCTGGGGCTGGGAAGATTAAC | 300 | | | | | | |
| QY | 301 | GGCCCTCAACGGGACCTGTACCGGACAGACATTTGGCTGCCCAATGGCGCTACTCCAT | 360 | | | | | | |
| DB | 301 | GGCCCTCAACGGGACCTGTACCGGACAGACATTTGGCTGCCCAATGGCGCTACTCCAT | 360 | | | | | | |
| QY | 361 | GGGGCTGCTCTGATGCCGACATGGAGGCTGACACGCTGTCCTCCCTGAGCACCCCGT | 420 | | | | | | |
| DB | 361 | GGGGCTGCTCTGATGCCGACATGGAGGCTGACACGCTGTCCTCCCTGAGCACCCCGT | 420 | | | | | | |
| QY | 421 | GGCTCTGTGGGCGCGGAGCACACGCTCAGGGCGAGCTCCTGCTGTCCAGCGGCGCA | 480 | | | | | | |
| DB | 421 | GGCTCTGTGGGCGCGGAGCACACGCTCAGGGCGAGCTCCTGCTGTCCAGCGGCGCA | 480 | | | | | | |
| QY | 481 | TTCCAATCTCACTCACCGACACCGAGCATGAAACACTGAGACTGATCATCCGGGCGG | 540 | | | | | | |
| DB | 481 | TTCCAATCTCACTCACCGACACCGAGCATGAAACACTGAGACTGATCATCCGGGCGG | 540 | | | | | | |
| QY | 541 | CTGACAGAACACGGCGGCTCCGACGCGCGCGCGCGCTCTGCGACGCCACACCCC | 600 | | | | | | |
| DB | 541 | CTGACAGAACACCGCGGCTCCGACGCGCGCGCGCGCTCTGCGACGCCACACCCC | 600 | | | | | | |
| QY | 601 | CAACACAGACACCGCGCTCCATTAACCTCCTGAAACCGGGGCACTTACGCGGAGAG | 660 | | | | | | |
| DB | 601 | CAACACAGACACCGCGCTCCATTAACCTCCTGAAACCGGGGCACTTACGCGGAGAG | 660 | | | | | | |
| QY | 661 | CAACCCAGCGCGCGCGCGCGACCACTCGCTCTCCGGAGAGCGCCCTGCGCGCGCGC | 720 | | | | | | |
| DB | 661 | CAACCCAGCGCGCGCGCGCGACCACTCGCTCTCCGGAGAGCGCCCTGCGCGCGCGC | 720 | | | | | | |
| QY | 721 | CCAGAGCTGCCCACGCGCGAGGAACTGCTGCTCAAGAGCAACATCCCCCTGGAGAC | 780 | | | | | | |
| DB | 721 | CCAGAGCTGCCCACGCGCGAGGAACTGCTGCTCAAGAGCAACATCCCCCTGGAGAC | 780 | | | | | | |
| QY | 781 | CAGGAACCTTAGCAAGACCAATTCCTAGGACATTGAGGACCACTCATTTAGATGGA | 840 | | | | | | |
| DB | 781 | CAGGAACCTTAGCAAGACCAATTCCTAGGAGCAATTGAGGACCACTCATTTAGATGGA | 840 | | | | | | |
| QY | 841 | CATTCTCGGCGCTCCGCCCATGATGGGGCTTACAGTGAACGGGCACTTCTCTCAAGCC | 900 | | | | | | |

| | | | | | | | | | |
|----|------|--|------|--|--|--|--|--|--|
| DB | 841 | CATTCTCGGCGCTCCGCCCATGATGGGGCTTACAGTGAACGGGCACTTCTCTCAAGCC | 900 | | | | | | |
| QY | 901 | TGGAGGACCTCCCGCTCTTCTGCACACATACACAGGGTACCACCTGAGCTCCAGCAC | 960 | | | | | | |
| DB | 901 | TGGAGGACCTCCCGCTCTTCTGCACACATACACAGGGTACCACCTGAGCTCCAGCAC | 960 | | | | | | |
| QY | 961 | AGTGTACTCTCTCCGCGCGAGACCCCTGCGCGCGAGCACTTTCGCCCGCGGCTTTAA | 1020 | | | | | | |
| DB | 961 | AGTGTACTCTCTCCGCGCGAGACCCCTGCGCGCGAGCACTTTCGCCCGCGGCTTTAA | 1020 | | | | | | |
| QY | 1021 | CCTCAAGAAGCCCTCAAGTACTGTAACCTGGAAGTGCAGCCCTGAGCGCCATCTCAT | 1080 | | | | | | |
| DB | 1021 | CCTCAAGAAGCCCTCAAGTACTGTAACCTGGAAGTGCAGCCCTGAGCGCCATCTGTCAT | 1080 | | | | | | |
| QY | 1081 | CTCAGCCACTCTGCTCATCTCTGCTGGCATCTTTGTGGCCATGACCTGTTTGGCCCTAAA | 1140 | | | | | | |
| DB | 1081 | CTCAGCCACTCTGCTCATCTCTGCTGGCATCTTTGTGGCCATGACCTGTTTGGCCCTAAA | 1140 | | | | | | |
| QY | 1141 | CTGSCACTCTGAGCCGATGAGGGGAGATGTATAGATCACGGAGGACACAGCCAGCAG | 1200 | | | | | | |
| DB | 1141 | CTGSCACTCTGAGCCGATGAGGGGAGATGTATAGATCACGGAGGACACAGCCAGCAG | 1200 | | | | | | |
| QY | 1201 | TTGSCCTGTGCCAACCGACGCTCTCCCTATACCCCTCAGGGGGCACTGCTTAGAGACCCC | 1260 | | | | | | |
| DB | 1201 | TTGSCCTGTGCCAACCGACGCTCTCCCTATACCCCTCAGGGGGCACTGCTTAGAGACCCC | 1260 | | | | | | |
| QY | 1261 | TGACAGAAAGGCAAGAAACCAAGAAAGAAAGCCAGTAGTTTCTTCCAGAGGACAG | 1320 | | | | | | |
| DB | 1261 | TGACAGAAAGGCAAGAAACCAAGAAAGAAAGCCAGTAGTTTCTTCCAGAGGACAG | 1320 | | | | | | |
| QY | 1321 | TTTTCATAGATCTGGAGAAATTCATGTTGGGAAAGGCGAGCCCTCCAGAGAAATTCCTCTGG | 1380 | | | | | | |
| DB | 1321 | TTTTCATAGATCTGGAGAAATTCATGTTGGGAAAGGCGAGCCCTCCAGAGAAATTCCTCTGG | 1380 | | | | | | |
| QY | 1381 | CACCTTCTGAGATCTCAAGTGTTCATAGACACCTCTGTGCATCTGAAATTCATGTGTC | 1440 | | | | | | |
| DB | 1381 | CACCTTCTGAGATCTCAAGTGTTCATAGACACCTCTGTGCATCTGAAATTCATGTGTC | 1440 | | | | | | |
| QY | 1441 | TTTGGGAAAGGCGAGCCCTGTTGGCAATTTATGCGAGAAAGGCTCCCTCTTACATAC | 1500 | | | | | | |
| DB | 1441 | TTTGGGAAAGGCGAGCCCTGTTGGCAATTTATGCGAGAAAGGCTCCCTCTTACATAC | 1500 | | | | | | |
| QY | 1501 | ACAGTTTGACTTGTGGAGCTGCTGATGGCAGAGGCTCCTAACCCAGAGAGCGGAG | 1560 | | | | | | |
| DB | 1501 | ACAGTTTGACTTGTGGAGCTGCTGATGGCAGAGGCTCCTAACCCAGAGAGCGGAG | 1560 | | | | | | |
| QY | 1561 | CCTAGAGGGGACCCCGCGCAGTCTCGGGGAACTGTGCCCCCTCCAGCCATGAGACAGG | 1620 | | | | | | |
| DB | 1561 | CCTAGAGGGGACCCCGCGCAGTCTCGGGGAACTGTGTGCCCTCCAGCCATGAGACAGG | 1620 | | | | | | |
| QY | 1621 | CTTTCATCCAGTATTTGGAATTCAGGAATCTGGCACTTTGGCTTTTAAATGACGGAAGGA | 1680 | | | | | | |
| DB | 1621 | CTTTCATCCAGTATTTGGAATTCAGGAATCTGGCACTTTGGCTTTTAAATGACGGAAGGA | 1680 | | | | | | |
| QY | 1681 | GTGAGAGTGTGTTTCTTCTCACACTGCTTGTGAGTGGTGGATTAATGCTCCCGACAA | 1740 | | | | | | |
| DB | 1681 | GTGAGAGTGTGTTTCTTCTCACACTGCTTGTGAGTGGTGGATTAATGCTCCCGACAA | 1740 | | | | | | |
| QY | 1741 | CTGCTATGGCAATGCTGACTGCTCTGGGACCTGCCACTGCTTCTGCTGCTTCTCTGGG | 1800 | | | | | | |
| DB | 1741 | CTGCTATGGCAATGCTGACTGCTCTGGGACCTGCCACTGCTTCTGCTGCTTCTCTGGG | 1800 | | | | | | |
| QY | 1801 | CCCCGACTGTGGAGAGCCCTCTGCCCCGTGCTGTAGCGGAAATGGCCCAATACATGAA | 1860 | | | | | | |
| DB | 1801 | CCCCGACTGTGGAGAGCCCTCTGCCCCGTGCTGTAGCGGAAATGGCCCAATACATGAA | 1860 | | | | | | |
| QY | 1861 | AGGCAGATGCTGTGCCACAGTGGCTGGAAGAGCGCTGAGTGCATGTGCCCAACCA | 1920 | | | | | | |
| DB | 1861 | AGGCAGATGCTGTGCCACAGTGGCTGGAAGAGCGCTGAGTGCATGTGCCCAACCA | 1920 | | | | | | |
| QY | 1921 | GTGTATCGATGTGGCTGTGAGCAACCATGGCACCTGTCATCAGGGGCACTGTCATCTG | 1980 | | | | | | |

QY 4141 CAGACGATCGATCAGATGGGATCATCTCCACCCCTGCTCGGCTTAATGATCTCACATC 4200
DB |||||
QY 4141 CAGACGATCGATCAGATGGGATCATCTCCACCCCTGCTCGGCTTAATGATCTCACATC 4200
DB |||||
QY 4201 AGCCCGGCCACTCAGCTGTGATTTCTGTATGGATATTTCCCAAGGTAAGACTGGAGTGGCC 4260
DB |||||
QY 4201 AGCCCGGCCACTCAGCTGTGATTTCTGTATGGATATTTCCCAAGGTAAGACTGGAGTGGCC 4260
DB |||||
QY 4261 CACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGCTCTCGACAAATGTGGT 4320
DB |||||
QY 4261 CACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGCTCTCGACAAATGTGGT 4320
DB |||||
QY 4321 CCTGCAAAATCTCTGAAAAACACCAAGGTGCGCATTTGTCGCCGGAGGCCCATGCACTGCCA 4380
DB |||||
QY 4321 CCTGCAAAATCTCTGAAAAACACCAAGGTGCGCATTTGTCGCCGGAGGCCCATGCACTGCCA 4380
DB |||||
QY 4381 GGTCTCTGGCATTTGACCACTTCTGCTAAAGCAAGGTGGCCATCCACGCAACCCCTGGAGTC 4440
DB |||||
QY 4381 GGTCTCTGGCATTTGACCACTTCTGCTAAAGCAAGGTGGCCATCCACGCAACCCCTGGAGTC 4440
DB |||||
QY 4441 AGCCACGGCTTTGGCTGTTTACAAATGGGGTCTGTATATTTCTGTAGACTGTAGAGAA 4500
DB |||||
QY 4441 AGCCACGGCTTTGGCTGTTTACAAATGGGGTCTGTATATTTCTGTAGACTGTAGAGAA 4500
DB |||||
QY 4501 AAAGATCAACCGCATCAGCAGGTCACTAGTGGAGAGATCTCACTCGTTTCTGGGCG 4560
DB |||||
QY 4501 AAAGATCAACCGCATCAGCAGGTCACTAGTGGAGAGATCTCACTCGTTTCTGGGCG 4560
DB |||||
QY 4561 CCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTTTCTGGAGACGATGG 4620
DB |||||
QY 4561 CCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTTTCTGGAGACGATGG 4620
DB |||||
QY 4621 TTATGCCAAGGATGCAAGGTTAAATACCCCATCTTCTTGGCTGTGTGTGATGGGGA 4680
DB |||||
QY 4621 TTATGCCAAGGATGCAAGGTTAAATACCCCATCTTCTTGGCTGTGTGTGATGGGGA 4680
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QY 4681 GCTCTACGTGGCGACCTTTGGGAAACATCGGAATTCGGTTTATCCGGAAAGAACAGCCCTTT 4740
DB |||||
QY 4681 GCTCTACGTGGCGACCTTTGGGAAACATCGGAATTCGGTTTATCCGGAAAGAACAGCCCTTT 4740
DB |||||
QY 4741 CTTCAACACCCAGAACATGTATGAGCTGTCTTACCAATTTGACAGGAGCTCTATCTGTT 4800
DB |||||
QY 4741 CTTCAACACCCAGAACATGTATGAGCTGTCTTACCAATTTGACAGGAGCTCTATCTGTT 4800
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QY 4801 TGATACCCCGGCAAGCCTGTACACCAAGGCTGCCACAGGAGCTACTGTGACAA 4860
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QY 4801 TGATACCCCGGCAAGCCTGTACACCAAGGCTGCCACAGGAGCTACTGTGACAA 4860
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QY 4861 CTTTACCTACACTGGGGACGGGACATCACACTCATCAGACAAATGGCAACATGGT 4920
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QY 4921 AAATGTCCGCCAGACTCTACTGGGATGCCCTCTGGCTGTGTGTGTCAGATGGCCAGGT 4980
DB |||||
QY 4921 AAATGTCCGCCAGACTCTACTGGGATGCCCTCTGGCTGTGTGTGTCAGATGGCCAGGT 4980
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QY 4981 GTACTGGGTGACCATGGGACCAACAGTGCATCAAGAGTGTGACCAACAGGACACGA 5040
DB |||||
QY 4981 GTACTGGGTGACCATGGGACCAACAGTGCATCAAGAGTGTGACCAACAGGACACGA 5040
DB |||||
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DB |||||
QY 5041 GTTGGCCATGATGACATACCATGGCAATTCGGCCCTTCTGGCAACCAAAAGCAATGAAA 5100
DB |||||
QY 5101 CGGATGGACAACTTTATGAGTACGACAGCTTTGGCCGCTGTACAAATGTGACTTCCC 5160
DB |||||
QY 5101 CGGATGGACAACTTTATGAGTACGACAGCTTTGGCCGCTGTACAAATGTGACTTCCC 5160
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QY 5161 TACTGGCCAGGTGACAGTTTCCGAAGTGTATACAGACAGTTTCAGTGCATGTCCAGGTAGA 5220
DB |||||
QY 5161 TACTGGCCAGGTGACAGTTTCCGAAGTGTATACAGACAGTTTCAGTGCATGTCCAGGTAGA 5220
DB |||||
QY 5221 GACCTCCAGCAAGGATGATGTCAACATTAACCAACCAACCTGTCTGCTCAGGCGCCTTCTA 5280

DB 5221 GACCTCCAGCAAGGATGATGTCAACATAAACCAACCAACCTGTCTGCTCAGGCGCCTTCTA 5280
QY |||||
QY 5281 CACACTGCTGCAAGCAAAAGTCCGGAACAGACTACTACATCGGGCCGATGCTCTTTGCG 5340
DB |||||
QY 5281 CACACTGCTGCAAGCAAAAGTCCGGAACAGACTACTACATCGGGCCGATGCTCTTTGCG 5340
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QY 5341 GCTGCTGTGGCCAAACGGCATGGAGGTGGGCTCGAGACTGAGGCCCACTTTGCTGGCTGG 5400
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QY 5701 TGGGGGTTACATTTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCA 5760
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QY 5821 AGAAGTCTCATGGTGTCTACTACACGCCAGAGCAGTATATCTTTGAGTTTCGACAA 5880
DB |||||
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QY 5881 GATGACCGGCTCTCTTCTGTGACGATGCCAAAGTGGCGGCGGAGACACTAGAGACCAT 5940
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QY 5881 GATGACCGGCTCTCTTCTGTGACGATGCCAAAGTGGCGGCGGAGACACTAGAGACCAT 5940
DB |||||
QY 5941 CCGCTCAGTGGGCTTACTACAGAAACATCTATCAGCCCCCTTGAGGGCAATGCCTCAGTCTAT 6000
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QY 5941 CCGCTCAGTGGGCTTACTACAGAAACATCTATCAGCCCCCTTGAGGGCAATGCCTCAGTCTAT 6000
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QY 6001 ACAGGACTTCACTGAGGATGGGCACTCTCTTCAACCTTCTACCTGGGCACTGGCCGCGAG 6060
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QY 6061 GGTGATATACAACTATGGCAAACTGTCAAAGCTGGCAGAGACCTCTATGACACCAACCA 6120
DB |||||
QY 6121 GGTGATATACAACTATGACAGAGCGCAGGATGTCTGAAAGCCTCAACCTACAGAAATGA 6180
DB |||||
QY 6121 GGTGATATACAACTATGACAGAGCGCAGGATGTCTGAAAGCCTCAACCTACAGAAATGA 6180
DB |||||
QY 6181 GGGCTTCACTGCAACATCCGCTACCGTTCAGATTTGGGCCCTCTGATTCGACGACAGTCTTT 6240
DB |||||
QY 6181 GGGCTTCACTGCAACATCCGCTACCGTTCAGATTTGGGCCCTCTGATTCGACGACAGTCTTT 6240
DB |||||
QY 6241 CCGCTTCACTGAGAAAGGATGTCACCGCGGTTTTGACTACAACTATGACAAACAGCTTT 6300
DB |||||
QY 6241 CCGCTTCACTGAGAAAGGATGTCACCGCGGTTTTGACTACAACTATGACAAACAGCTTT 6300
DB |||||
QY 6301 CCGGGTGAACGAGCATGAGGCTGTGATCAACGAGACCCCACTGCCCACTGATCTCTATCG 6360

| | | | | | | | |
|--|-----|---|-----|------|---|--|------|
| / APPLICANT: WARREN, Bridget A.; ELLIOTT, Vicki S. | | | | QY | 481 | TTTCCAATCTCACACTCACCGGACACCGAGCATGAAAAACACTGAGACTGATCATCTCGGGCGG | 540 |
| / APPLICANT: BAUGHN, Mariah R.; DING, Li | | | | Db | 563 | | |
| / APPLICANT: XU, Yuming; GIETZEN, Kimberly J. | | | | Db | 563 | TTTCCAATCTCACACTCACCGGACACCGAGCATGAAAAACACTGAGAC-----TCCGGGCGG | 616 |
| / APPLICANT: TANG, Tom Y.; LAL, Preeti G. | | | | QY | 541 | | |
| / APPLICANT: DUGGAN, Brendan M.; BURFORD, Neil | | | | Db | 541 | CCTGCAGAAACACACGCGGGCTCCGGAGCGCGCCCGCGCTCTCGCACGCCACACACCCC | 600 |
| / APPLICANT: LU, Dying Aina M.; RICHARDSON, Thomas W. | | | | Db | 617 | | |
| / APPLICANT: TRAN, Uyen K.; KHARE, Reena | | | | QY | 617 | CCTGCAGAAACACACGCGGGCTCCGGAGCGCGCCCGCGCTCTCGCACGCCACACACCCC | 676 |
| / APPLICANT: CHAWLA, Narinder K. | | | | QY | 601 | | |
| / TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH | | | | Db | 601 | CAACACAGACACACGCGGCTCCATTAACTCTCTGAAACCGGGGCAACTTCACGCGGAGGAG | 660 |
| / FILE REFERENCE: PF-0903 USN | | | | Db | 677 | | |
| / CURRENT APPLICATION NUMBER: US/10/467,535 | | | | QY | 677 | CAACACAGACACACGCGGCTCCATTAACTCTCTGAAACCGGGGCAACTTCACGCGGAGGAG | 736 |
| / CURRENT FILING DATE: 2003-08-08 | | | | QY | 661 | | |
| / PRIOR APPLICATION NUMBER: PCT/US02/03715 | | | | Db | 661 | CAACCCAGCCGGGCGCCCGCCAGGACCACTCGCTCTCCGAGAGAGCCCTCTCGCGGCGGCGC | 720 |
| / PRIOR FILING DATE: 2002-08-02 | | | | Db | 737 | | |
| / PRIOR APPLICATION NUMBER: US 60/268,111 | | | | QY | 737 | CAACCCAGCCGGGCGCCCGCCAGGACCACTCGCTCTCCGAGAGAGCCCTCTCGCGGCGGCGC | 796 |
| / PRIOR FILING DATE: 2001-02-09 | | | | QY | 721 | | |
| / PRIOR APPLICATION NUMBER: US 60/271,175 | | | | Db | 721 | CCAGGAGCCTGCCACGCCCCAGGAGAACTGGCTCTCAACAGCAACATCCCCCTTGGAGAC | 780 |
| / PRIOR FILING DATE: 2001-02-23 | | | | Db | 797 | | |
| / PRIOR APPLICATION NUMBER: US 60/274,503 | | | | QY | 797 | CCAGGAGCCTGCCACGCCCCAGGAGAACTGGCTCTCAACAGCAACATCCCCCTTGGAGAC | 856 |
| / PRIOR FILING DATE: 2001-03-08 | | | | QY | 781 | | |
| / PRIOR APPLICATION NUMBER: US 60/274,552 | | | | Db | 781 | CAGGAACCTAGGCAAGCAGGCCATTCCTTAGGACATTCAGGAGACAACTCATTTAGATGGA | 840 |
| / PRIOR FILING DATE: 2001-03-09 | | | | Db | 857 | | |
| / NUMBER OF SEQ ID NOS: 24 | | | | QY | 857 | CAGAAACCTAGGCAAGCAGGCCATTCCTTAGGACATTCCTAGGAGCAACCTCATTTAGATGGA | 916 |
| / SOFTWARE: PERL Program | | | | QY | 841 | | |
| / SEQ ID NO 22 | | | | Db | 841 | CATTCTCGGCGCTCCCGCCCATGATGGGCTTACAGTGACGGGCACTTCCTCTTCAAGCC | 900 |
| / LENGTH: 8645 | | | | Db | 917 | | |
| / TYPE: DNA | | | | QY | 917 | CATTCTCGGCGCTCCCGCCCATGATGGGCTTACAGTGACGGGCACTTCCTCTTCAAGCC | 976 |
| / ORGANISM: Homo sapiens | | | | QY | 901 | | |
| / FEATURE: | | | | Db | 901 | TGGAGGCACCTCCCGCGCTCTTCTGACACCATCACAGGGGTACCCACTGAGCTCCAGCAC | 960 |
| / NAME/KEY: misc feature | | | | Db | 977 | | |
| / OTHER INFORMATION: Incyte ID No: 7488573CB1 | | | | QY | 977 | TGGAGGCACCTCCCGCGCTCTTCTGACACCATCACAGGGGTACCCACTGAGCTCCAGCAC | 1036 |
| / FEATURE: | | | | QY | 961 | | |
| / NAME/KEY: unsure | | | | Db | 961 | AGTGACTCTCTCCGCGCCGACCCCTGCGCCGAGACACCTTCGCGCGGCGGCTTTAA | 1020 |
| / LOCATION: 93 | | | | Db | 1037 | | |
| / OTHER INFORMATION: a, t, c, g, or other | | | | QY | 1037 | AGTGACTCTCTCCGCGCCGACCCCTGCGCCGAGACACCTTCGCGCGGCGGCTTTAA | 1096 |
| US-10-467-535-22 | | | | QY | 1021 | | |
| Query Match | | 98.5%; Score 8225; DB 7; Length 8645; | | Db | 1097 | | |
| Best Local Similarity | | 99.4%; Pred. No. 0; | | QY | 1097 | CCTCAAGAAAGCCCTCCAAAGTACTGTAACTGGAAGTGGCGAGCCCTGAGCGGCATCTGTCAT | 1156 |
| Matches 8300; Conservative | | 0; Mismatches 21; Indels 33; Gaps 3; | | QY | 1081 | | |
| QY | 1 | GTTTGTGATGTGGAGGAGCGCGCGCGGAGCCATGGACGTGGAAGGAGAGAGCCCTTA | 60 | 1157 | | | |
| Db | | | | 83 | GTTTGTGATGTTGGAGGAGCGCGCGCGGAGCCATGGACGTGGAAGGAGAGAGCCCTTA | 142 | |
| QY | 61 | CGCTCGCTGACCCCGCGCGGAGCGCGAGCGCGCTACACCAGCTCGTCGCGGGACAG | 120 | 1141 | | | |
| Db | | | | 143 | CGCTCGCTGACCCCGCGCGGAGCGCGAGCGCGCTACACCAGCTCGTCGCGGGACAG | 202 | |
| QY | 121 | CGAGGAGGCAAGCCCGCGAGAAATCGTACAGCTCCAGCGAGACCCCTGAAGGCTACGA | 180 | 1201 | | | |
| Db | | | | 203 | CGAGGAGGCAAGCCCGCGAGAAATCGTACAGCTCCAGCGAGACCCCTGAAGGCTACGA | 262 | |
| QY | 181 | CCAGGAGCGCCGCTAGCTATGGAGCGCGGTCAAGACATTTGCGCGAGGAGGCGGA | 240 | 1261 | | | |
| Db | | | | 263 | CNAGGAGCCCGCTAGCCTATGGAGCGCGGTCAAGACATTTGCGCGAGGAGGCGGA | 322 | |
| QY | 241 | GGAATTCGCCGACAGGTGCCAATCTTACCCCTGCGGAGCTGGGGCTGGAAGAAGTAAC | 300 | 1321 | | | |
| Db | | | | 323 | GGAATTCGCCGACAGGTGCCAATCTTACCCCTGCGGAGCTGGGGCTGGAAGAAGTAAC | 382 | |
| QY | 301 | GCCCCCTCAGGGAGCCTGTATCCGACAGACATTTGGGCTGCCCAATGGCGCTACTCCAT | 360 | 1381 | | | |
| Db | | | | 383 | GCCCCCTCAGGGAGCCTGTATCCGACAGACATTTGGGCTGCCCACTGCGGCTACTCCAT | 442 | |
| QY | 361 | GGGGGCTGGCTCTGATGCGGACATGGAGGCTGACACGTGTGTCTCCCTGAGCACCCCGT | 420 | 1441 | | | |
| Db | | | | 443 | GGGGGCTGGCTCTGATGCGGACATGGAGGCTGACACGTGTGTCTCCCTGAGCACCCCGT | 502 | |
| QY | 421 | GGCTCTGTGGGCGGAGGACACAGCTCAGGGGAGAGCTCTCTGCTGTCCAGCGGCGCAA | 480 | 1501 | | | |
| Db | | | | 503 | GGCTCTGTGGGCGGAGGACACAGCTCAGGGGAGAGCTCTCTGCTGTCCAGCGGCGCAA | 562 | |

1631 CCTAGAGGGACCCCGCCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAGACAGG 1690
1621 CTTTCATCCAGTATTGGATTTCAGGAATCTGGCACTTGGCTTTTACATGACGGAAAGGA 1680
1691 CTTTCATCCAGTATTGGATTTCAGGAATCTGGCACTTGGCTTTTACAAATGACGGAAAGGA 1750
1681 GTGAGAAAGTGGTTTCTTTCTCACCAGTCGATTTAGTTCGGTGGATTAATGCCCCCAGCAA 1740
1751 GTGAAAGTGGTTTCTTTCTCACCAGTCGATTTAGTTCGGTGGATTAATGCCCCCAGCAA 1810
1741 CTGCTATGGCAATGGTGAATCTCTGGGACCTGCACTGCTTCTGGGTTTCTGGG 1800
1811 CTGCTATGGCAATGGTGAATCTCTGGGACCTGCACTGCTTCTGGGTTTCTGGG 1870
1801 CCGGACTGTGGCAGAGCCTCTGCCCCGCTCTGTAGCGGAATGGCCAAATACATGAA 1860
1871 CCGGACTGTGGCAGAGCCTCTGCCCCGCTCTGTAGCGGAATGGCCAAATACATGAA 1930
1861 AGCAGATGCTGTGCCACAGTGGCTGGAAGGCTGAGTGGATGTGCCACCAACCA 1920
1931 AGGAGATGCTGTGCCACAGTGGCTGGAAGGCTGAGTGGATGTGCCACCAACCA 1990
1921 GTGTATCGATGTGGCTCTGACGCAACCATGGCACCCTGCATCAGGGCACCTGCATCTGCAA 2050
1991 GTGTATCGATGTGGCTCTGACGCAACCATGGCACCCTGCATCAGGGCACCTGCATCTGCAA 2050
1981 CCTTGGCTCAAGGGCGAGAGCTGTGAGGAAGTGGATGGATGGACCCCACTGTTTCAGG 2040
2051 CCTTGGCTCAAGGGCGAGAGCTGTGAGGAAGTGGATGGATGGACCCCACTGTTTCAGG 2110
2041 CCGGGTGTCTGCGTAGAGCGGAATGCCATTGCTTTGGATGGGGAGGCAACCACTG 2100
2111 CCGGGTGTCTGCGTAGAGCGGAATGCCATTGCTTTGGATGGGGAGGCAACCACTG 2170
2101 CGAGACCCCGAGGGCCACATGCTTAGACCACTGTTTCAGGGCCAGGAACTTCTCCCGGA 2160
2171 CGAGACCCCGAGGGCCACATGCTTAGACCACTGTTTCAGGGCCAGGAACTTCTCCCGGA 2230
2161 CACGGGCTTTGAGCTGTGACCCAGCTGGAAGTGGACAGCACTGTTCTATCGAGATCTG 2220
2231 CACGGGCTTTGAGCTGTGACCCAGCTGGAAGTGGACAGCACTGTTCTATCGAGATCTG 2290
2221 TGCTGCCGACTGTGGTGGCAATGGCGTGTGGTAGGGGGGACCTTGGCCCTGCGAGATGG 2280
2291 TGCTGCCGACTGTGGTGGCAATGGCGTGTGGTAGGGGGGACCTTGGCCCTGCGAGATGG 2350
2281 CTGGATGGGGGACGCTGCGACCAAGCGGGCTGCGCACCCGCGCTGTGCCGAGCATGGGAC 2340
2351 CTGGATGGGGGACGCTGCGACCAAGCGGGCTGCGCACCCGCGCTGTGCCGAGCATGGGAC 2410
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2411 CTGCCGCGAGCGGAAGTGCAGTGCAGCCCTGTGGCTGGAAATGGCGAAACATGCAACCATCGC 2470
2401 TCACATCTCGATAGGCTAGTTAAAGAGGCTTGCCTGGTTGGCAATGGCAACGCGAG 2460
2471 TCACATCTCGATAGGCTAGTTAAAGAGGCTTGCCTGGTTGGCAATGGCAACGCGAG 2530
2461 ATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGGCTGGAGAGGAGCTGG 2520
2531 ATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGGCTGGAGAGGAGCTGG 2590
2521 CTGTGACATTTCCATGGAGACTGCTCGGGTGAAGCAAGAGCAATGATGGAGATGGCCT 2580
2591 CTGTGACATTTCCATGGAGACTGCTCGGGTGAAGCAAGAGCAATGATGGAGATGGCCT 2650
2581 GGTGACTGATGACCCCTGACTGCTGCTCCAGCCCTGTCCTATACCCGCTGTG 2640
2651 GGTGACTGATGACCCCTGACTGCTGCTCCAGCCCTGTCCTATATCAACCCGCTGTG 2710
2641 CTTTGGCTCCCTAACTCTGAGACATATCCAGGAGACAGAGTCCCTGTGTACAGCA 2700

2711 CCTTGGCTCCCTAACTCTGAGACATATCAGGAGACACAGGTCCCTGTGTGTCAGCA 2770
2701 GAACCTTACACTCTCTTATGACCGCATCAAGTTCCTCGTGGGAGGAGCAGCAGCAGCAT 2760
2771 GAACCTTACACTCTCTTATGACCGCATCAAGTTCCTCGTGGGAGGAGCAGCAGCAGCAT 2830
2761 AATCCCGGGGAGAACCCCTTTGATGAGGGGATGCTTGTGTTATTTCTGTGGCCAAAGTGT 2820
2831 AATCCCGGGGAGAACCCCTTTGATGAGGGGATGCTTGTGTTATTTCTGTGGCCAAAGTGT 2890
2821 GACATCAGATGGAAACCCCTCTGGTGTGAAACATCACTTTGTCAATAACCCCTCTCTT 2880
2891 GACATCAGATGGAAACCCCTCTGGTGTGAAACATCACTTTGTCAATAACCCCTCTCTT 2950
2881 TGGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTTGGTGAACAAATGGCGGCATCTC 2940
2951 TGGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTTGGTGAACAAATGGCGGCATCTC 3010
2941 CATCATCTCTGGGTTTCGAGCGGCACCTTTTCATCACAGGAGCAACCCCTGTGGGTGCC 3000
3011 CATCATCTCTGGGTTTCGAGCGGCACCTTTTCATCACAGGAGCAACCCCTGTGGGTGCC 3070
3001 ATGGGATCGCTTCTTTGTCTATGGAACCATCATCATGAGACATGAGAGAAATGAGATTCC 3060
3071 ATGGGATCGCTTCTTTGTCTATGGAACCATCATCATGAGACATGAGAGAAATGAGATTCC 3130
3061 CAGCTGTGACCTGAGCAATTTTGGCCGCCCAACCCAGTCTCTCCATCCCACTGAC 3120
3131 CAGCTGTGACCTGAGCAATTTTGGCCGCCCAACCCAGTCTCTCTCCATCCCACTGAC 3190
3121 GTCCTTTCGCGAGCTCTGTGTCAGAGAAAGCCCATTTGTCCGGAAATTCAGGCTTTGCA 3180
3191 GTCCTTTCGCGAGCTCTGTGTCAGAGAAAGCCCATTTGTCCGGAAATTCAGGCTTTGCA 3250
3181 GAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACTGAGCAGCGGACCCC 3240
3251 GAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACTGAGCAGCGGACCCC 3310
3241 TGCTCAAAATCTCTCTGAGGATCAGCTTCAACCCAGCATCCCTTTCAACCTCAT 3300
3311 TGCTCAAAATCTCTCTGAGGATCAGCTTCAACCCAGCATCCCTTTCAACCTCAT 3370
3301 GAGGTCACCTCATGCTAGCGTGGAGGCGCCCTTTTCAGAAATGCTGCTGCGTGAGC 3360
3371 GAGGTCACCTCATGCTAGCGTGGAGGCGCCCTTTTCAGAAATGCTGCTGCGTGAGC 3430
3361 CCAGACCTGTCTCTATTTTCATTTTGGGCAAGACAGCTCTACAAACAGAGGTTT 3420
3431 CCAGACCTGTCTCTATTTTCATTTTGGGCAAGACAGCTCTACAAACAGAGGTTT 3490
3421 TGGGCTTTCAGAGACCTTTGTTTCCGTGGGTTATGAATATGAATCTCTGCCAGATCTAAT 3480
3491 TGGGCTTTCAGAGACCTTTGTTTCCGTGGGTTATGAATATGAATCTCTGCCAGATCTAAT 3550
3481 CTTGTGGGAAAAAAGAACCAACAGTGTGCAAGGCTATGAAATTTGACGCGTCTCAAGCTTGG 3540
3551 CTTGTGGGAAAAAAGAACCAACAGTGTGCAAGGCTATGAAATTTGACGCGTCTCAAGCTTGG 3610
3541 AGGATGGAGCTTAGACAAACATCATGCTTCAACATTTCAAAGTGGTATCTCTGCACAAAGG 3600
3611 AGGATGGAGCTTAGACAAACATCATGCTTCAACATTTCAAAGTGGTATCTCTGCACAAAGG 3670
3601 GAATGGGAGAACCAAGTTTGTGTCTCAGCAGCCTCTGTCTATTTGGGAGCATCATGGGCAA 3660
3671 GAATGGGAGAACCAAGTTTGTGTCTCAGCAGCCTCTGTCTATTTGGGAGCATCATGGGCAA 3730
3661 TGCGCGCCGAGAGGATCTCTCTGCCCCAGCTGCAACGGCTTGTCTGACGGCAACAGCT 3720
3731 TGCGCGCCGAGAGGATCTCTCTGCCCCAGCTGCAACGGCTTGTCTGACGGCAACAGCT 3790
3721 CTTGGCCCCAGTGGCCCTCACTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAA 3780
3791 CTTGGCCCCAGTGGCCCTCACTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAA 3850

QY 3781 CTACATTAGAGGATCTTCCCTCTCGAAATGTCAACAACTCCTAGAGCTAGGNAATA 3840
DB |||||
DB 3851 CTACATTAGAGGATCTTCCCTCTCGAAATGTCAACAACTCCTAGAGCTG----- 3902
QY 3841 AGATTTTCAGACATAGTCAGAGTCAGACACACAAATACTACTCGGCCACAGAGCCCATGAG 3900
DB |||||
DB 3903 -----AGTCAGATCCAGACACACAAATACTACTCGGCCACAGAGCCCATGAG 3949
QY 3901 TGGGGCGCTTCTCTCTTCGACAGCAACAGCGCGGGTCTTTAAATCAAGTCCACTGT 3960
DB |||||
DB 3950 TGGGGCGCTTCTCTCTTCGACAGCAACAGCGCGGGTCTTTAAATCAAGTCCACTGT 4009
QY 3961 GGTGTGTAAAGGACCTTGTCAAGAACTCTGAGGTGTTCGGGGACAGGTGACAGTGCT 4020
DB |||||
DB 4010 GGTGTGTAAAGGACCTTGTCAAGAACTCTGAGGTGTTCGGGGACAGGTGACAGTGCT 4069
QY 4021 CCCCTTTGATGACATCGCTCGGGGATGTTGGGAAGGCCACAGAAAGCCACACTCACCAA 4080
DB |||||
DB 4070 CCCCTTTGATGACATCGCTCGGGGATGTTGGGAAGGCCACAGAAAGCCACACTCACCAA 4129
QY 4081 TCCAGGGGTATTACAGTGGACAAGTTTGGGCTGATCTACTTCTGTGGATGGACCAATGAT 4140
DB |||||
DB 4130 TCCAGGGGCAATTACAGTGGACAAGTTTGGGCTGATCTACTTCTGTGGATGGACCAATGAT 4189
QY 4141 CAGACGCATCGATCAGAAATGGGATCATCTCCACCTGCTCGGCTCTTAATGATCTCACATC 4200
DB |||||
DB 4190 CAGACGCATCGATCAGAAATGGGATCATCTCCACCTGCTCGGCTCTTAATGATCTCACATC 4249
QY 4201 AGCCGGCCACTCAGCTGTGATTTCTGTCATGGATATTTCCAGGTAAAGACTGGAGTGCC 4260
DB |||||
DB 4250 AGCCGGCCACTCAGCTGTGATTTCTGTCATGGATATTTCCAGGTTCACCTGGAGTGCC 4309
QY 4261 CACAGACTTAGCCATCAACCCCAATGGACAACCTCACTTTATGTCTCGACAACAAATGTGT 4320
DB |||||
DB 4310 CACAGACTTAGCCATCAACCCCAATGGACAACCTCACTTTATGTCTCGACAACAAATGTGT 4369
QY 4321 CTGCAAAATCTCTGAAAACACACAGGTGGGCAATGTCGCCGGAGGCCCATGCACTGCCA 4380
DB |||||
DB 4370 CTGCAAAATCTCTGAAAACACACAGGTGGGCAATGTCGCCGGAGGCCCATGCACTGCCA 4429
QY 4381 GGTCTCTGCAATGACCACTTCTCTAAAGCAAGGTGGCCATCCACGCAACCTCGAGTC 4440
DB |||||
DB 4430 GGTCTCTGCAATGACCACTTCTCTAAAGCAAGGTGGCCATCCACGCAACCTCGAGTC 4489
QY 4441 AGCCACCGCTTGGCTGTTTACAAATGGGGTCTGTATATGCTGAGACTGATGAGAA 4500
DB |||||
DB 4490 AGCCACCGCTTGGCTGTTTACAAATGGGGTCTGTATATGCTGAGACTGATGAGAA 4549
QY 4501 AAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGGAGAGATCTCACTCGTTGCTGGGC 4560
DB |||||
DB 4550 AAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGGAGAGATCTCACTCGTTGCTGGGC 4609
QY 4561 CCCAGTGGCTGTGACTGTAAATAATGATGCCAACTGTGATGTTTTCGAGAGCATGG 4620
DB |||||
DB 4610 CCCAGTGGCTGTGACTGTAAATAATGATGCCAACTGTGATGTTTTCGAGAGCATGG 4669
QY 4621 TTATGCCAAGGATGCAAGTTAAATACCCCACTTCTTGGCTGTGTGCTGATGGGA 4680
DB |||||
DB 4670 TTATGCCAAGGATGCAAGTTAAATACCCCACTTCTTGGCTGTGTGCTGATGGGA 4729
QY 4681 GCTCTACGTGGCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAGCCCTTT 4740
DB |||||
DB 4730 GCTCTACGTGGCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAGCCCTTT 4789
QY 4741 CCTCAACCCAGAACATGATGAGCTGTCTTCAACAAATGACCAAGAGCTCTATCTGT 4800
DB |||||
DB 4790 CCTCAACCCAGAACATGATGAGCTGTCTTCAACAAATGACCAAGAGCTCTATCTGT 4849
QY 4801 TGATACCAACCGCAAGCACTGTACACCAAGCCCTGCCACAGGAGACTACCTGTACAA 4860
DB |||||
DB 4850 TGATACCAACCGCAAGCACTGTACACCAAGCCCTGCCACAGGAGACTACCTGTACAA 4909

QY 4861 CTTCCACTTACACTGGGACCGGCACATCACACTCATCACAGACAACTATGSCAACATGGT 4920
DB |||||
DB 4910 CTTCCACTTACACTGGGACCGGCACATCACACTCATCACAGACAACTATGSCAACATGGT 4969
QY 4921 AAATGTTCGGCGAGACTCTACTGGGATGCCCTCTGGCTGTGTGCCAGATGCCAGGT 4980
DB |||||
DB 4970 AAATGTTCGGCGAGACTCTACTGGGATGCCCTCTGGCTGTGTGCCAGATGCCAGGT 5029
QY 4981 GTACTGGGTGACCAATGGGCACCAACAGTGACCTCAAGAGTGTGACCAACAAAGACACGA 5040
DB |||||
DB 5030 GTACTGGGTGACCAATGGGCACCAACAGTGACCTCAAGAGTGTGACCAACAAAGACACGA 5089
QY 5041 GTTCGCCATGATGACATACCATGCAATTCGGGCTTCTGSCAACCAAAAGCAATGAAA 5100
DB |||||
DB 5090 GTTCGCCATGATGACATACCATGCAATTCGGGCTTCTGSCAACCAAAAGCAATGAAA 5149
QY 5101 CGGATGGACAACTATTTATGATGACGACAGCTTTGGCGGCTCTGACAAATGTGACTTTCCC 5160
DB |||||
DB 5150 CGGATGGACAACTATTTATGATGACGACAGCTTTGGCGGCTCTGACAAATGTGACTTTCCC 5209
QY 5161 TACTGGCCAGGTGAGCAGTTTCGAAAGTGATACAGACAGTTTCAGTGATGTCAGGTAGA 5220
DB |||||
DB 5210 TACTGGCCAGGTGAGCAGTTTCGAAAGTGATACAGACAGTTTCAGTGATGTCAGGTAGA 5269
QY 5221 GACCTCCAGCAAGGATGATGTCAACATAACCAACCTGTCTGCTCAGCGGCTTCTA 5280
DB |||||
DB 5270 GACCTCCAGCAAGGATGATGTCAACATAACCAACCTGTCTGCTCAGCGGCTTCTA 5329
QY 5281 CACACTCTCTCAAGACCAAGTCCGGAACTACTACTATCATCCGGGCGGATGGCTCTTTGCG 5340
DB |||||
DB 5330 CACACTCTCTCAAGACCAAGTCCGGAACTACTACTATCATCCGGGCGGATGGCTCTTTGCG 5389
QY 5341 GCTGCTCTGGCCAAACCGCATGAGGTGGCGCTGCAGACTGAGCCCACTTGTGGCTGG 5400
DB |||||
DB 5390 GCTGCTCTGGCCAAACCGCATGAGGTGGCGCTGCAGACTGAGCCCACTTGTGGCTGG 5449
QY 5401 CACCGTCAACCCCAACCGTGGGCAAGAGAAATGTCACTGCTCCCATCGACAAACCGCTCAA 5460
DB |||||
DB 5450 CACCGTCAACCCCAACCGTGGGCAAGAGAAATGTCACTGCTGCCCATCGACAAACCGCTCAA 5509
QY 5461 CTTGTTGGATGGCGCCAGCGCAAGAGAGGTTCGGGGCCAGGTCACTGTCTTTGGGCG 5520
DB |||||
DB 5510 CTTGTTGGATGGCGCCAGCGCAAGAGAGGTTCGGGGCCAGGTCACTGTCTTTGGGCG 5569
QY 5521 CCGCTCTGGGTGCACAAACCGAAATCTCTCTATCTCTGGAATTTGATGCGGTACACGCAC 5580
DB |||||
DB 5570 CCGCTCTGGGTGCACAAACCGAAATCTCTCTATCTCTGGAATTTGATGCGGTACACGCAC 5629
QY 5581 AGAGAAGATCTATGATGACCAACCGCAAGTTTCACTTTCGGATTTCTGTACCAACGAGCGGG 5640
DB |||||
DB 5630 AGAGAAGATCTATGATGACCAACCGCAAGTTTCACTTTCGGATTTCTGTACCAACGAGCGGG 5689
QY 5641 GCGGCCAGGCTCTGTGTCACCAAGCAGAGGTGAAATGGTGTCAACGTGACATCTCTCCC 5700
DB |||||
DB 5690 GCGGCCAGGCTCTGTGTCACCAAGCAGAGGTGAAATGGTGTCAACGTGACATCTCTCCC 5749
QY 5701 TGGGGGTTCATTTGCTGGCATCCAGAGGGGCATCATGCTCTGAAAGAAATGGAATACGACCA 5760
DB |||||
DB 5750 TGGGGGTTCATTTGCTGGCATCCAGAGGGGCATCATGCTCTGAAAGAAATGGAATACGACCA 5809
QY 5761 GCGGGGCGCATCACATCCAGGATCTTTCGCTGATGGGAAGACATGGAGCTTACATACTTT 5820
DB |||||
DB 5810 GCGGGGCGCATCACATCCAGGATCTTTCGCTGATGGGAAGACATGGAGCTTACATACTTT 5869
QY 5821 AGAGAAGTTCATGGTGTGCTACTACAGCCAGAGCGAGTATATCTTTGAGTTTCAGCAA 5880
DB |||||
DB 5870 AGAGAAGTTCATGGTGTGCTACTACAGCCAGAGCGAGTATATCTTTGAGTTTCAGCAA 5929
QY 5881 GAATGACCGCTCTCTTCTGTGACGATGCCAAAGTGGCGGCGACACACTAGAGACCAT 5940
DB |||||
DB 5930 GAATGACCGCTCTCTTCTGTGACGATGCCAAAGTGGCGGCGACACACTAGAGACCAT 5989
QY 5941 CCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCTCTCAGTCAT 6000

| | | | |
|----|------|--|------|
| Db | 5990 | CGGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCGCTCAGTCAAT | 6049 |
| Qy | 6001 | ACAGGACTTCACCTGAGGATGGGCACCTCTTCACACCTTTCTACCTGGGCACCTGGCCGCAG | 6060 |
| Db | 6050 | ACAGGACTTCACCTGAGGATGGGCACCTCTTCACACCTTTCTACCTGGGCACCTGGCCGCAG | 6109 |
| Qy | 6061 | GGTGATATACAAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACAA | 6120 |
| Db | 6110 | GGTGATATACAAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACAA | 6169 |
| Qy | 6121 | GGTCAGTTTCACTATGACGAGACGGCAGGCATGCTGTAAGACCATCAACCTACAGAAATGA | 6180 |
| Db | 6170 | GGTCAGTTTCACTATGACGAGACGGCAGGCATGCTGTAAGACCATCAACCTACAGAAATGA | 6229 |
| Qy | 6181 | GGGCTTCACCTGCACCATCCGCTACCGTTCAGATTGGGCCCTCGATTGACGACAGATCTT | 6240 |
| Db | 6230 | GGGCTTCACCTGCACCATCCGCTACCGTTCAGATTGGGCCCTCGATTGACGACAGATCTT | 6289 |
| Qy | 6241 | CGGCTTCACCTGAGGAAGGATGGTCAACGGCCCGTTTGACTACAACTATGACAAACAGCTT | 6300 |
| Db | 6290 | CGGCTTCACCTGAGGAAGGATGGTCAACGGCCCGTTTGACTACAACTATGACAAACAGCTT | 6349 |
| Qy | 6301 | CGGGTGACAGCATGACGGCTGTGATCAACGAGACCCCATCTGCCCATTTGATCTCTATCG | 6360 |
| Db | 6350 | CGGGTGACAGCATGACGGCTGTGATCAACGAGACCCCATCTGCCCATTTGATCTCTATCG | 6409 |
| Qy | 6361 | CTATGATGATGTGTGAGGCAAGCAGACGAGTTTGGGAAGTTTGGTGCTATTTACTATGA | 6420 |
| Db | 6410 | CTATGATGATGTGTGAGGCAAGCAGACGAGTTTGGGAAGTTTGGTGCTATTTACTATGA | 6469 |
| Qy | 6421 | CATTAAACAGATCATCACACAGCTGTCTATGACCCACACCAAGCAATTTTGATGATATGG | 6480 |
| Db | 6470 | CATTAAACAGATCATCACACAGCTGTCTATGACCCACACCAAGCAATTTTGATGATATGG | 6529 |
| Qy | 6481 | CAGGATGAAGGAAGTCCAGTATGAGATCTTCGGCTCGTCTCATGTATCTGGATGACCGTCCA | 6540 |
| Db | 6530 | CAGGATGAAGGAAGTCCAGTATGAGATCTTCGGCTCGTCTCATGTATCTGGATGACCGTCCA | 6589 |
| Qy | 6541 | GTATGATTAACATGGGCGGAGTAGTGAAGAAAGAGCTGAAGGTAGGACCCCTACGCCAATAC | 6600 |
| Db | 6590 | GTATGATTAACATGGGCGGAGTAGTGAAGAAAGAGCTGAAGGTAGGACCCCTACGCCAATAC | 6649 |
| Qy | 6601 | CACCTCGCTACTCCTATGATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA | 6660 |
| Db | 6650 | CACCTCGCTACTCCTATGATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA | 6709 |
| Qy | 6661 | CAAGCCACTCTGCGCTACAGCTACGACCTCAATGGGAACCTTGCACTTACGAGCCCTGG | 6720 |
| Db | 6710 | CAAGCCACTCTGCGCTACAGCTACGACCTCAATGGGAACCTTGCACTTACGAGCCCTGG | 6769 |
| Qy | 6721 | GAACAGTGACGGCTCACACCACTACGGTATGACATCCGCGACCCGATCATCTCGGCTGG | 6780 |
| Db | 6770 | GAACAGTGACGGCTCACACCACTACGGTATGACATCCGCGACCCGATCATCTCGGCTGG | 6829 |
| Qy | 6781 | TGACGTGCAATACAGATCGATGAGATGGCTTCTTGAGGACGGGCGGTGATATCTT | 6840 |
| Db | 6830 | TGACGTGCAATACAGATCGATGAGATGGCTTCTTGAGGACGGGCGGTGATATCTT | 6889 |
| Qy | 6841 | TGAGTACAACTCAGCTGGGCTGTCTCATCAAGGCCCTACAAACGGGCTGGCAGCTGGAGTGT | 6900 |
| Db | 6890 | TGAGTACAACTCAGCTGGGCTGTCTCATCAAGGCCCTACAAACGGGCTGGCAGCTGGAGTGT | 6949 |
| Qy | 6901 | CAGGTACCGCTACGATGGCTGGGGCGGCGGTGTCAGAAAGAGACGCCACAGCCACCA | 6960 |
| Db | 6950 | CAGGTACCGCTACGATGGCTGGGGCGGCGGTGTCAGAAAGAGACGCCACAGCCACCA | 7009 |
| Qy | 6961 | CCTGCAGTTCTTCTATGACAGCTGACCAACCCACCAAGGTCACCACTGTACAAACCA | 7020 |
| Db | 7010 | CCTGCAGTTCTTCTATGACAGCTGACCAACCCACCAAGGTCACCACTGTACAAACCA | 7069 |
| Qy | 7021 | CTCCAGCTCTGAGATCACTCTCTCTACTACGACTTGAAGGACACCTCTTTTGGCATGGA | 7080 |
| Db | 7070 | CTCCAGCTCTGAGATCACTCTCTCTACTACGACTTGAAGGACACCTCTTTTGGCATGGA | 7120 |
| Qy | 7081 | GCTGAGCAGTGGTGTGATGAGTTTTTATACATGCTTTGTGACAAACATCGGGAACCCCTCTTGTCTGT | 7140 |
| Db | 7130 | GCTGAGCAGTGGTGTGATGAGTTTTTATACATGCTTTGTGACAAACATCGGGAACCCCTCTTGTCTGT | 7189 |
| Qy | 7141 | CTTTAGTGGAAACAGGTTTGTGATGATCAAGCAAAATCCTGTACACAGCCTATCGGGGAGATCTA | 7200 |
| Db | 7190 | CTTTAGTGGAAACAGGTTTGTGATGATCAAGCAAAATCCTGTACACAGCCTATCGGGGAGATCTA | 7249 |
| Qy | 7201 | CATGATATACCAACCCCAACTTTTCAGATCATCATAGGCTTACATGGTGGCCTCTATGATCC | 7260 |
| Db | 7250 | CATGATATACCAACCCCAACTTTTCAGATCATCATAGGCTTACATGGTGGCCTCTATGATCC | 7309 |
| Qy | 7261 | ACTCAACCAAGCTTGTCCAATGGCCGCGAGATTTATGATGTGCTGCCCGGACGCTGGAC | 7320 |
| Db | 7310 | ACTCAACCAAGCTTGTCCAATGGCCGCGAGATTTATGATGTGCTGCCCGGACGCTGGAC | 7369 |
| Qy | 7321 | TAGCCCAACACAGCTGTGTGGAAGCACCTTTAGTAGCAGCAACGTCTATGCTCTTTTAATCT | 7380 |
| Db | 7370 | TAGCCCAACACAGCTGTGTGGAAGCACCTTTAGTAGCAGCAACGTCTATGCTCTTTTAATCT | 7429 |
| Qy | 7381 | CTATATGTTCAAAAACACAAACCCCATCAGCAATCCCCAGGACATCAAGTGTCTTCATGAC | 7440 |
| Db | 7430 | CTATATGTTCAAAAACACAAACCCCATCAGCAATCCCCAGGACATCAAGTGTCTTCATGAC | 7489 |
| Qy | 7441 | AGATGTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTGATCCCTGGTTA | 7500 |
| Db | 7490 | AGATGTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTGATCCCTGGTTA | 7549 |
| Qy | 7501 | TCCCAAAACACAGATGAGATGGAAACCCCTCTCTACAGCTCATCACACACAGATGAA | 7560 |
| Db | 7550 | TCCCAAAACACAGATGAGATGGAAACCCCTCTCTACAGCTCATCACACACAGATGAA | 7609 |
| Qy | 7561 | AACGACAGAGTGGGACACAGCAAGTCTATCCTCGGGGTACAGTGTCAAGTACAGAAGCA | 7620 |
| Db | 7610 | AACGACAGAGTGGGACACAGCAAGTCTATCCTCGGGGTACAGTGTCAAGTACAGAAGCA | 7669 |
| Qy | 7621 | GCTCAAGGCTTTGTCACTTTAGAAACGGTTTTGACAGCTCTATATGGCTCCCAATCACCAG | 7680 |
| Db | 7670 | GCTCAAGGCTTTGTCACTTTAGAAACGGTTTTGACAGCTCTATATGGCTCCCAATCACCAG | 7729 |
| Qy | 7681 | CTGCCACAGGCTCCAAAGACCAAGAGTTTGCATTCACAGGGCTCAGTCTTTTGGCAAGGG | 7740 |
| Db | 7730 | CTGCCACAGGCTCCAAAGACCAAGAGTTTGCATTCACAGGGCTCAGTCTTTTGGCAAGGG | 7789 |
| Qy | 7741 | GGTCAAGTTTGGCTTGAAGGATGGCCGAGTACACACAGACATCATAGTGTGGCCCAATGA | 7800 |
| Db | 7790 | GGTCAAGTTTGGCTTGAAGGATGGCCGAGTACACACAGACATCATAGTGTGGCCCAATGA | 7849 |
| Qy | 7801 | GGATGGCGAAGGGTTGCTGCATCTTGAACCATGCCACATACCTAGAGAACCTTGCACTT | 7860 |
| Db | 7850 | GGATGGCGAAGGGTTGCTGCATCTTGAACCATGCCACATACCTAGAGAACCTTGCACTT | 7909 |
| Qy | 7861 | CACCATTTGATGGGGTGGATACCCATTTACTTTGTGAACACGGAACCTTCAGAAGGTGACCT | 7920 |
| Db | 7910 | CACCATTTGATGGGGTGGATACCCATTTACTTTGTGAACACGGAACCTTCAGAAGGTGACCT | 7969 |
| Qy | 7921 | GGCCATCTCGGCCCTCAGTGGGGGGCGGGAACCTCTGGAGNAATGGGGTCAACGTCACCTGT | 7980 |
| Db | 7970 | GGCCATCTCGGCCCTCAGTGGGGGGCGGGAACCTCTGGAGNAATGGGGTCAACGTCACCTGT | 8029 |
| Qy | 7981 | GTCCCAGATCAACACAGTACTTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA | 8040 |
| Db | 8030 | GTCCCAGATCAACACAGTACTTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA | 8089 |
| Qy | 8041 | GTACGGGGCACTGTGCTTTGAAACACACACGCTACGGGACAAACGTTTGGATGAGGAAGGACCG | 8100 |
| Db | 8090 | GTACGGGGCACTGTGCTTTGNAACACACGCTACGGGACAAACGTTTGGATGAGGAAGGACCG | 8149 |
| Qy | 8101 | GGTCTCGAGCTGGGCCCGGACAGAGCCGTGGCCCAAGCTGGGGCCCGCGAGACGACGAG | 8160 |
| Db | 8150 | GGTCTCGAGCTGGGCCCGGACAGAGCCGTGGCCCAAGCTGGGGCCCGCGAGACGACGAG | 8209 |

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QY      8161  ACTGCGGAGGGAGGAGGCTGCGGCGCTGGACAGAGGGGGAGAAACAGCAGGTGCT 8220
Db      8210  ACTGCGGAGGGAGGAGGAGGCTGCGGCGCTGGACAGAGGGGGAGAAACAGCAGGTGCT 8269
QY      8221  GAGCACAGGGCGGGTGCAGAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACC 8280
Db      8270  GAGCACAGGGCGGGTGCAGAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACC 8329
QY      8281  AGAATCTGCAGACAGCGCCAAACATCCACTTTCAGACAGAGCGAGATGGCGGGAG 8340
Db      8330  AGAATCTGCAGACAGCGCCAAACATCCACTTTCAGACAGAGCGAGATGGCGGGAG 8389
QY      8341  GTGACAGAGGAG 8354
Db      8390  GTGACAGAGGAG 8403

RESULT 4
US-10-383-201-55
; Sequence 55, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 55
; LENGTH: 8355
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(8325)
US-10-383-201-55

Query Match      95.7%; Score 7991.2; DB 7; Length 8355;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 8248; Conservative 0; Mismatches 18; Indels 126; Gaps 12;

QY      35  ATGGACGTGAAGGAGGAGGAGCCTTACCGCTCGCTGACCGCGCGCGCGCGCGCGCGCGCG 94
Db      1  ATGGACGTGAAGGAGGAGGAGCCTTACCGCTCGCTGACCGCGCGCGCGCGCGCGCGCGCG 60
QY      95  CGCTACACAGCTCGTCCGCGGACAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 154
Db      61  CGCTACACAGCTCGTCCGCGGACAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY      155  TCCAGGAGACCCCTGAAGGCTTACGACGAGGAGCGCCCGCTAGGCTATGGCAGCGCGTC 214
Db      155  TCCAGGAGACCCCTGAAGGCTTACGACGAGGAGCGCCCGCTAGGCTATGGCAGCGCGTC 214
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Db      121  TCCAGGAGAGCCCTGAAGGCTTACGACGAGAGCGCCCGCTAGCTTATGGCAGCGCGTC 180
QY      215  AAGGACATTTGTCGCGAGGAGGCGGAGAAATTTGCGCGCACAGGTGCAACTTTCACCGCTG 274
Db      181  AAGGACATTTGTCGCGAGGAGGCGGAGAAATTTGCGCGCACAGGTGCAACTTTCACCGCTG 240
QY      275  CGGAGAGCTGGGGCTGGAGAGTAACCGCCCTCACCGGACCCCTGTATCCGGACAGACATTT 334
Db      241  CGGAGAGCTGGGGCTGGAGAGTAACCGCCCTCACCGGACCCCTGTATCCGGACAGACATTT 300
QY      335  GGCCTGCCCAATCGCGCTACTCCATGGGGCTGGCTTCTGATGCCGACATGGAGGCTGAC 394
Db      301  GGCCTGCCCAATCGCGCTACTCCATGGGGCTGGCTTCTGATGCCGACATGGAGGCTGAC 360
QY      395  ACGGTGCTGTCCCTGAGCACCCTGCTGCTGTGTGGGGCCGGAGCAACCGGTTCAGGGCGC 454
Db      361  ACGGTGCTGTCCCTGAGCACCCTGCTGCTGTGTGGGGCCGGAGCAACCGGTTCAGGGCGC 420
QY      455  AGCTCTGCTGTCCAGCGGGGCAATTCCAATCTCACACTCACCGACACCGAGCATGAA 514
Db      421  AGCTCTGCTGTCCAGCGGGGCAATTCCAATCTCACACTCACCGACACCGAGCATGAA 480
QY      515  AACACTGAGACTGATCATCCGGGGCGCTGCAGAACCCACGCGGGCTCCGAGCGCGCG 574
Db      481  AACACTGAGACTGATCATCCGGGGCGCTGCAGAACCCACGCGGGCTCCGAGCGCGCG 540
QY      575  CCGCGCTCTCGACGCCACACCCCOAACAGACACACCGGGCTCCATTAATCTCCCTG 634
Db      541  CCGCGCTCTCGACGCCACACCCCOAACAGACACACCGGGCTCCATTAATCTCCCTG 600
QY      635  AACCGGGGCAACTTTCAGCGGAGGAGCAACCCAGCGCGCGCCCGCCACGGACCATCTGCTC 694
Db      601  AACCGGGGCAACTTTCAGCGGAGGAGCAACCCAGCGCGCGCCCGCCACGGACCATCTGCTC 660
QY      695  TCGGAGAGCGCCCTGCGCGCGCGCGCGCGAGGAGCTGCCACGCCAGGAGAACTGGCTG 754
Db      661  TCGGAGAGCGCCCTGCGCGCGCGCGCGAGGAGCTGCCACGCCAGGAGAACTGGCTG 720
QY      755  CTCAGAGAGAACATCCCGCTGGAGACGAGGAACTTAGGGAAGCAGGCAATTCCTAGGACA 814
Db      721  CTCAGAGAGAACATCCCGCTGGAGACGAGGAACTTAGGGAAGCAGGCAATTCCTAGGACA 780
QY      815  TTGAGGAGCAACCTCATTGAGATGGACATTTCTGGGCGCTCCCGCCATGATGGGGCTTAC 874
Db      781  TTGAGGAGCAACCTCATTGAGATGGACATTTCTGGGCGCTCCCGCCATGATGGGGCTTAC 840
QY      875  AGTGAAGGCACTTCTCTTCAAGCCTGGAGGACCTTCCCGCTCTTCTGCAACACATCA 934
Db      841  AGTGAAGGCACTTCTCTTCAAGCCTGGAGGACCTTCCCGCTCTTCTGCAACACATCA 900
QY      935  CCAGGTACCCACTGACGTCAGCAGTGATCTCTCTCCCGCGCGAGCCCTGCGCCCGC 994
Db      901  CCAGGTACCCACTGACGTCAGCAGTGATCTCTCTCCCGCGCGAGCCCTGCGCCCGC 960
QY      995  AGCACCTTTCCCGCGCGCGCTTTTAACTCAAGAGCCCTTCCAAAGTACTGTAAGTGAAG 1054
Db      961  AGCACCTTTCCCGCTGGCGCGCTTTAACTCAAGAGCCCTTCCAAAGTACTGTAAGTGAAG 1020
QY      1055  TGCGAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGTGTATCTGTGTGGATATCTTT 1114
Db      1021  TGCGAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGTGTATCTGTGTGGATATCTTT 1080
QY      1115  GTGGCCATGCACTGTGTGGCCCTAAACTGACCTGACCGGATGGAGGGGAGATGTAT 1174
Db      1081  GTGGCCATGCACTGTGTGGCCCTAAACTGACCTGACCGGATGGAGGGGAGATGTAT 1140
QY      1175  GAGATCACGAGGACACAGCCAGTGGCCCTGTGCGCAACCGACGCTCTCCCTATACCCC 1234
Db      1141  GAGATCACGAGGACACAGCCAGTGGCCCTGTGCGCAACCGACGCTCTCCCTATACCCC 1200
QY      1235  TCAGGGGGCACTGGCTTAGAGACCCCTGACAGAAAGGCAAGAAACCAAGAGGAAAG 1294
Db      1201  TCAGGGGGCACTGGCTTAGAGACCCCTGACAGAAAGGCAAGAAACCAAGAGGAAAG 1260
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|----|------|---|------|----|------|--|------|
| Qy | 1295 | CCAGTAGTTTCTTTCCAGAGGACAGTTTTCATAGATTTCTGAGAAATTGATGCGAAGG | 1354 | Qy | 2375 | TGGAATGGCGAAACATGCAACCATC-----GCTCACTATCTGGATAGGCTAGTTAA----- | 2424 |
| Dd | 1261 | CCAGTAGTTTCTTTCCAGAGGACAGTTTTCATAGATTTCTGAGAAATTGATGCGAAGG | 1320 | Dd | 2332 | TGGAATGGCGAAACATGCAACCATCCTCCCTAGCTCACTATCTGGATAGGCTAGTTAACTT | 2391 |
| Qy | 1355 | CGAGCCTCCAGAGATTTCTCTCGGCACATTTCTGGAGATCTCAAGTGTTCATAGACCAT | 1414 | Qy | 2425 | --AGAGGTTGCTCCCTGGGTTGCAATGCGAAGCGCAGATGTACCTTAGACCTGGAATGGT | 2482 |
| Dd | 1321 | CGAGCTTCCAGAAAGATTCTCTCGGCACATTTCTGGAGATCTCAAGTGTTCATAGACCAT | 1380 | Dd | 2392 | TCAGAGGGTTGCTCCCTGGGTTGCAATGCGAAGCGCAGATGTACCTTAGACCTGGAATGGT | 2451 |
| Qy | 1415 | CTGTGATCTGAAATTCATATGTTCTCTGGGAAAGCGCAGCCCTGTTGGCATTTATGCC | 1474 | Qy | 2483 | TGGCACTGGGTCTGCCAGCTGGCTGGAGAGGAGCTGGCTGTGACACTTCCATGGAGACT | 2542 |
| Dd | 1381 | CCTGTGATCTGAAATTCATATGTTCTCTGGGAAAGCGCAGCCCTGTTGGCATTTATGCC | 1440 | Dd | 2452 | TGGCACTGGGTCTGCCAGCTGGCTGGAGAGGAGCTGGCTGTGACACTTCCATGGAGACT | 2511 |
| Qy | 1475 | AGAAAGGCTCTCCCTCTCCATACACAGTTTGTACTTTGTGAGCTGCTGGATGGCAGG | 1534 | Qy | 2543 | GCCTCGGTGACAGCAAAAGCAATGATGAGATGGCTCGGTGGAATGCACTGAGACCTGAC | 2602 |
| Dd | 1441 | AGAAAGGCTCTCCCTCTCCATACACAGTTTGTACTTTGTGAGCTGCTGGATGGCAGG | 1500 | Dd | 2512 | GCCTCGGTGACAGCAAAAGCAATGATGAGATGGCTCGGTGGAATGCACTGAGACCTGAC | 2571 |
| Qy | 1535 | AGGCTCTTAACCCAGGAGGCGGAGCTTAGAGGGGACCCCGGCCAGTCTCGGGAACT | 1594 | Qy | 2603 | TGCTGCTCCAGCCCTGTGCCATATCAACCCGCTGTGGCTTGGCTCCCTAACCCCTCTG | 2662 |
| Dd | 1501 | AGGCTCTTAACCCAGGAGGCGGAGCTTAGAGGGGACCCCGGCCAGTCTCGGGAACT | 1560 | Dd | 2572 | TGCTGCTCCAGCCCTGTGCCATATCAACCCGCTGTGGCTTGGCTCCCTAACCCCTCTG | 2631 |
| Qy | 1595 | GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGAATTCAGGAATCTGGCAC | 1654 | Qy | 2663 | GACATCATCAGAGACACAGGTCCCTGTGTCAAGCAGAACTTACACTCTCTCTATGAC | 2722 |
| Dd | 1561 | GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGAATTCAGGAATCTGGCAC | 1620 | Dd | 2632 | GACATCATCAGAGACACAGGTCCCTGTGTCAAGCAGAACTTACACTCTCTCTATGAC | 2691 |
| Qy | 1655 | TTGGCTTTTACATGACGGAAGGCTCAGAAAGTGGTTTCTTCTCACCACCTGCCATT | 1714 | Qy | 2723 | CGCATCAAGTTCTCTGTTGGGACAGCAGCACAATAATCCCGGGGAGAAACCCCTTT | 2782 |
| Dd | 1621 | TTGGCTTTTACATGACGGAAGGCTCAGAAAGTGGTTTCTTCTCACCACCTGCCATT | 1674 | Dd | 2692 | CGCATCAAGTTCTCTGTTGGGACAGCAGCACAATAATCCCGGGGAGAAACCCCTTT | 2751 |
| Qy | 1715 | GAGTCGGTGGATAACTCCCCCAGCAACTGCTATGGCAATGGTGAAGTCTCTGGGACC | 1774 | Qy | 2783 | GATGAGGGCATGCTTGTGTATTCTGTGGCAAGTGTACATCAGATGGAAACCCCTCTG | 2842 |
| Dd | 1675 | GAGTCGGTGGATAACTCCCCCAGCAACTGCTATGGCAATGGTGAAGTCTCTGGGACC | 1734 | Dd | 2752 | GATGAGGGCATGCTTGTGTATTCTGTGGCAAGTGTACATCAGATGGAAACCCCTCTG | 2811 |
| Qy | 1775 | TGCCACTGCTTCTGGGTTTCTGGGCCCCGACGTGGCGAGAGCTCTCTGCCCGCTGCTC | 1834 | Qy | 2843 | GTTGGTGTCAACATCAGTTTGTCAATAACCCCTCTCTTTGGATATACAAATCAGCAGCAA | 2902 |
| Dd | 1735 | TGCCACTGCTTCTGGGTTTCTGGGCCCCGACGTGGCGAGAGCTCTCTGCCCGCTGCTC | 1794 | Dd | 2812 | GTTGGTGTCAACATCAGTTTGTCAATAACCCCTCTCTTTGGATATACAAATCAGCAGCAA | 2871 |
| Qy | 1835 | TGTAGCGGAATGGCCAAATACATGAAGGACAGATGCTTGTGCCACAGTGGCTGGAAGGC | 1894 | Qy | 2903 | GATGGCAGCTTTGACTTTGGTGACAAATGGCGGCATCTCCATCATCTCGCGGTTGAGCGG | 2962 |
| Dd | 1795 | TGTAGCGGAATGGCCAAATACATGAAGGACAGATGCTTGTGCCACAGTGGCTGGAAGGC | 1854 | Dd | 2872 | GATGGCAGCTTTGACTTTGGTGACAAATGGCGGCATCTCCATCATCTCGCGGTTGAGCGG | 2931 |
| Qy | 1895 | GCTGAGTGCATGTGCCACCAACCAAGTGTATCGATGTGGCTCGACCAACCATGGCACC | 1954 | Qy | 2963 | GCACCTTTTATCACAAGAGGACACCCCTGTGGCTGCCATGGGATGGCTTCTTTGTGATG | 3022 |
| Dd | 1855 | GCTGAGTGCATGTGCCACCAACCAAGTGTATCGATGTGGCTCGACCAACCATGGCACC | 1914 | Dd | 2932 | GCACCTTTTATCACAAGAGGACACCCCTGTGGCTGCCATGGGATGGCTTCTTTGTGATG | 2991 |
| Qy | 1955 | TGCATCACGGGCACCTGCATCTGCAACCTCTGGCTTACAAAGGCGAGAGCTGTGAGGAA | 2014 | Qy | 3023 | GAAACCATCATCATGAGACATGAGGAGAAATGAGATTTCCAGCTGTGACCTGAGCAATTTT | 3082 |
| Dd | 1915 | TGCATCACGGGCACCTGCATCTGCAACCTCTGGCTTACAAAGGCGAGAGCTGTGAGGAA | 1971 | Dd | 2992 | GAAACCATCATCATGAGACATGAGGAGAAATGAGATTTCCAGCTGTGACCTGAGCAATTTT | 3051 |
| Qy | 2015 | GACTGCATGACCCCAATGTTTCAGGCGGGGTGTCTGCGTGAAGGCGAATGCCATTGC | 2074 | Qy | 3083 | GCCCGCCCCAACCCCACTGCTCTCCATCCCCCACTGACGTCTTTCGCCAGCTCCTGTGCA | 3142 |
| Dd | 1972 | GACTGCATGACCCCAATGTTTCAGGCGGGGTGTCTGCGTGAAGGCGAATGCCATTGC | 2031 | Dd | 3052 | GCCCGCCCCAACCCCACTGCTCTCCATCCCCCACTGACGTCTTTCGCCAGCTCCTGTGCA | 3111 |
| Qy | 2075 | TTTGTGGATGGGAGGACCAACTGCGAGACCCCGAGGCGCAATGCTTTAGACCAAGTGT | 2134 | Qy | 3143 | GAGAAAGGCCCAATTTGTGCGGAAATTCAGGCTTTGCGAGGAGAAATCTCTATCTCTGGC | 3202 |
| Dd | 2032 | TCTGTGGATGGGAGGAGCAACCACTGCGAGNCCCGAGGGCCACATGCTTTAGACCAAGTGT | 2091 | Dd | 3112 | GAGAAAGGCCCAATTTGTGCGGAAATTCAGGCTTTGCGAGGAGAAATCTCTATCTCTGGC | 3171 |
| Qy | 2135 | TCAGGCCACGGAACCTTCTCTCCGGAACACCGGGCTTTTGCAGCTGTGACCCCAAGCTGCACT | 2194 | Qy | 3203 | TGCAAGATGAGGCTGAGCTTACCTGAGCGCGGACCCCTGGGCTACAAATCTGTCTCTGAGG | 3262 |
| Dd | 2092 | TCAGGCCACGGAACCTTCTCTCCGGAACACCGGGCTTTTGCAGCTGTGACCCCAAGCTGCACT | 2151 | Dd | 3172 | TGCAAGATGAGGCTGAGCTTACCTGAGCGCGGACCCCTGGGCTACAAATCTGTCTCTGAGG | 3231 |
| Qy | 2195 | GGACACAGCTGTTCTATCGAGATCTGTGTCGCACTGTGGTGGCCATGGGCTGTGCGTA | 2254 | Qy | 3263 | ATCAGGCTCACCCACCCGACCATCCCTTTCAACCTCATGAAGGTGCACTCATGGTAGCG | 3322 |
| Dd | 2152 | GGACACAGCTGTTCTATCGAGATCTGTGTCGCACTGTGGTGGCCATGGGCTGTGCGTA | 2211 | Dd | 3232 | ATCAGGCTCACCCACCCGACCATCCCTTTCAACCTCATGAAGGTGCACTCATGGTAGCG | 3291 |
| Qy | 2255 | GGGGGCACTTCCGCTCGAGGATGGCTTGAATGGGGCAGGCTTCGACACCAAGCGGCTCTGC | 2314 | Qy | 3323 | GTGAGGGCGGCTCTTTCAGGAAAGTGGTTCGTGTGAGCGCCCCAGACCTGTCTATTATTTTC | 3382 |
| Dd | 2212 | GGGGGCACTTCCGCTCGAGGATGGCTTGAATGGGGCAGGCTTCGACACCAAGCGGCTCTGC | 2271 | Dd | 3292 | GTGAGGGCGGCTCTTTCAGGAAAGTGGTTCGTGTGAGCGCCCCAGACCTGTCTATTATTTTC | 3351 |
| Qy | 2315 | CACCCGGCTGTGCGAGCATGGGACCTTCCGCGACGGCAAGTGCAGTGCAGCCCTTGGC | 2374 | Qy | 3383 | ATTTGGGACAGACACAGCTCTACAAACCAAGAGGTGTTTGGGCTTTTCAGAAAGCTTTGTT | 3442 |
| Dd | 2272 | CACCCGGCTGTGCGAGCATGGGACCTTCCGCGACGGCAAGTGCAGTGCAGCCCTTGGC | 2331 | Dd | 3352 | ATTTGGGACAGACACAGCTCTACAAACCAAGAGGTGTTTGGGCTTTTCAGAAAGCTTTGTT | 3411 |
| Qy | | | | Qy | 3443 | TCCGTGGGTTTATGAATATGAATCTCTGCCAGATCTAATCTCTGTGGGAAAAAAGAACACA | 3502 |

|||||
3412 TCGTGGTTATGAATATGAATCTCGCCAGATCTAATCTGTGGGAAAGAAACAA 3471
QY GTGCTGAGGGCTATGAATTTGACGGCTTCAAGCTTTGGAGGATGGAGCTTAGACAAACAT 3562
Db GTGCTGAGGGCTATGAATTTGATGCGTCAAGCTTTGGAGGATGGAGCTTAGACAAACAT 3531
QY CATGCCCTCAACATTTCAAGTGTG--ATCCTGCACAAAGGGGAATGGGAGAACCAAGTTT 3619
Db CATGCCCTCAACATTTCAAGTGTGGCATCTCGACAAAGGGGAATGGGAGAACCAAGTTT 3591
QY GTGTCTCAGCAGGCTCTGTCTCATTTGGAGCATCATGGCAATGGGCGCGGAGAGCATC 3679
Db GTGTCTCAGCAGGCTCTGTCTCATTTGGAGCATCATGGCAATGGGCGCGGAGAGCATC 3651
QY TCGTGGCCCAAGCTGCAACGGCCCTTGTGACGGCAACAAAGCTCTGCGCCCAAGTGGCCCTC 3739
Db TCGTGGCCCAAGCTGCAACGGCCCTTGTGACGGCAACAAAGCTCTGCGCCCAAGTGGCCCTC 3711
QY ACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAACTTACATTAAGAAGGATCTTC 3799
Db ACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAACTTACATTAAGAAGGATCTTC 3771
QY CCTCTGGAATGTCAACCAATCTTAGAGCTGAGGTCAGAAATAAAGATTTCAAGCAT 3853
Db CCTCTGGAATGTCAACCAATCTTAGAGCTGAGGTCAGAAATAAAGATTTCAAGCAT 3831
QY AGTCACAGTCCAGCACACAAATACTAGCTGGCCACAGACCCCATGAGTGGGCGCTCTTC 3913
Db AGTCACAGTCCAGCACACAAATACTAGCTGGCCACAGACCCCATGAGTGGGCGCTCTTC 3891
QY CTTTCTGACAGCAACAGCGGGGTCTTTAAATCAAGTCCACTGTGGTGGTGAAGGAC 3973
Db CTTTCTGACAGCAACAGCGGGGTCTTTAAATCAAGTCCACTGTGGTGGTGAAGGAC 3951
QY CTTTCTCAAGAACTCTGAGTGTGTGGGGGACAGGTGACAGTGCTCCCTTTGATGAC 4033
Db CTTTCTCAAGAACTCTGAGTGTGTGGGGGACAGGTGACAGTGCTCCCTTTGATGAC 4011
QY ACTCGTGGGGGATCGTGGGAAGGCCACAGAAAGCCACACTCACCNAATCCAGGGGT--- 4090
Db ACTCGTGGGGGATCGTGGGAAGGCCACAGAAAGCCACACTCACCNAATCCAGGGGTCCC 4071
QY -----ATTACAGTGCAAGTTTGGGCTGATCTACTTCTGGATGGCAACCATGATCAGA 4144
Db CCAGGCATTTACAGTGACAAAGTTTGGGCTGATCTACTTCTGGATGGCAACCATGATCAGA 4131
QY CGCATCGATCAGNATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCAATCAGCC 4204
Db CGCATCGATCAGNATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCAATCAGCC 4191
QY CGGCCACTCAGCTGTGATTTCTGTCTATGGATATTTCCAGGTTAAGACAGGTTCACTGGAG 4255
Db CGGCCACTCAGCTGTGATTTCTGTCTATGGATATTTCCAGGTTAAGACAGGTTCACTGGAG 4251
QY TGGCCACAGACTTAGCCATCAACCAATGGCAACTCACTTTATGTCTCGACAAACAT 4315
Db TGGCCACAGACTTAGCCATCAACCAATGGCAACTCACTTTATGTCTCTCGACAAACAT 4311
QY GTGGTCTCTGCAATCTCTGAAACCAACAGGTGGCCATTTGCGCGGAGGCCCATGAC 4375
Db GTGGTCTCTGCAATCTCTGAAACCAACAGGTGGCCATTTGCGCGGAGGCCCATGAC 4371
QY TGGCAGGTCCTTGGCATTTGACCACTTCTGTCTAAGCAAGGTGGCCATCCAGCAACCTG 4435
Db TGGCAGGTCCTTGGCATTTGACCACTTCTGTCTAAGCAAGGTGGCCATCCAGCAACCTG 4431
QY GAGTCAGCCACCGCTTTGGCTGTTTCAACAATGGGGTCTGTATATTGCTGAGACTGAT 4495
Db GAGTCAGCCACCGCTTTGGCTGTTTCAACAATGGGGTCTGTATATTGCTGAGACTGAT 4491
QY GAGAAAAGATCAACCGCATCAGGAGGTCAACCACTAGTGGAGATCTCACTGTTGCT 4555

Db 4492 GAGAAAAGATCAACCGCATCAGGACGGTCACCACTAGTGGAGAGATCTCACTCGTTGCT 4551
QY GGGGCCCCCAGTGGCTGTGACTGTAAATATGATGCCAACTGTGTGATTTGTTTCTGGAGAC 4615
Db GGGGCCCCCAGTGGCTGTGACTGTAAATATGATGCCAACTGTGTGATTTGTTTCTGGAGAC 4611
QY GATGGTTATGCCAAGGATGCAAGTAAATACCCCATCTTCTCTTGGCTGTGTGTGCTGAT 4675
Db GATGGTTATGCCAAGGATGCAAGTAAATACCCCATCTTCTCTTGGCTGTGTGTGCTGAT 4671
QY GGGGAGCTCTACGTGGCGGACCTTTGGGAACATCCGAATTCGGTTTATCCGGAAGAAACAAG 4735
Db GGGGAGCTCTACGTGGCGGACCTTTGGGAACATCCGAATTCGGTTTATCCGGAAGAAACAAG 4731
QY CCTTTCTCAACACCCAGAACATGTATGAGTGTCTTCAACAATTTGACAGGAGCTCTAT 4795
Db CCTTTCTCAACACCCAGAACATGTATGAGTGTCTTCAACAATTTGACAGGAGCTCTAT 4791
QY CTGTTTGTATACCCCGCAAGCACCTGTACACCCAAAGCCTGCCACAGGAGACTACCTG 4855
Db CTGTTTGTATACCCCGCAAGCACCTGTACACCCAAAGCCTGCCACAGGAGACTACCTG 4851
QY TACAACCTTCACTACCTGAGGAGCGGACATCACTCATCAGACAAACAATGGCAAC 4915
Db TACAACCTTCACTACCTGAGGAGCGGACATCACTCATCAGACAAACAATGGCAAC 4911
QY ATGTTAATGTCCGCCAGACTCTACTGGGATGGCCCTCTGGCTGGTGGTCCAGATGGC 4975
Db ATGTTAATGTCCGCCAGACTCTACTGGGATGGCCCTCTGGCTGGTGGTCCAGATGGC 4971
QY CAGTGTACTGGGTGACCATGGGCAACCAAGTGCACCTCAAGAGTGTGACCAACAAGGA 5035
Db CAGTGTACTGGGTGACCATGGGCAACCAAGTGCACCTCAAGAGTGTGACCAACAAGGA 5031
QY CACGAGTGGCCATGATGACATACCATGGCAATTCGGGCTTCTGGCAACCAAAAGCAAT 5095
Db CACGAGTGGCCATGATGACATACCATGGCAATTCGGGCTTCTGGCAACCAAAAGCAAT 5091
QY GAAAACGGATGGACAACTTTTATGATGATACAGACAGTTCGGCCCTGACAAATGTGACC 5155
Db GAAAACGGATGGACAACTTTTATGATGATACAGACAGTTCGGCCCTGACAAATGTGACC 5151
QY TTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTATACAGACAGTTCAGTGCATGTCCAG 5215
Db TTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTATACAGACAGTTCAGTGCATGTCCAG 5211
QY GTAGAGACTTCCAGAGAGGATGATGACCAATAAACCAACCACTGTCTGCTCAGGCGCC 5275
Db GTAGAGACTTCCAGAGAGGATGATGACCAATAAACCAACCACTGTCTGCTCAGGCGCC 5271
QY TTCTACACACTGCTGCAAGACCAAGTCCGGAAACAGCTACTACATCGGGGCGGATGGCTCC 5335
Db TTCTAC-----GACCAAGTCCGGAAACAGCTACTACATCGGGGCGGATGGCTCC 5319
QY TTGGGCTGTCTGTGGCCAAACGGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTGGCTG 5395
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QY GCTGGGCAACCGTCAACCCCAAGAGAGAAATGTCACTGCTGCCCATCGACAAACGGC 5455
Db GCTGGGCAACCGTCAACCCCAAGAGAGAAATGTCACTGCTGCCCATCGACAAACGGC 5439
QY CTCAACTGTGGAGTGGCGCCAGCAAGAGCAGGCTCGGGGCGAGGTCACTGTCTTT 5515
Db CTCAACTGTGGAGTGGCGCCAGCAAGAGCAGGCTCGGGGCGAGGTCACTGTCTTT 5499
QY GGGCGCGGCTGGGGTG-----CACAAACCGAAATCTCCTATCTCTGGACTTTGAT 5566
Db GGGCGCGGCTGGGGTGCTCCAGGTTCAACCCGAAATCTCCTATCTCTGGACTTTGAT 5559
QY CGGTTAACGACGACAGAGAAATCTATGATGACCCAGCAAGTTCAACCTTGGATCTG 5626
Db CGGTTAACGACGACAGAGAAATCTATGATGACCCAGTTCAACCTTGGATCTG 5619

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|----|------|---|------|----|------|---|------|
| QY | 5627 | TACGACAGCGGGGGGGCCAGCCTCTGGTCAACCAGCAGCAGGCTGAATGGTGTCAAC | 5686 | QY | 6707 | TTACTGAGCCCTGGGAAACAGTGCACGGCTCACACCACTACGGTATGACATCCCGGACCGC | 6766 |
| Db | 5620 | TACGACAGCGGGGGGGCCAGCCTCTGGTCAACCAGCAGCAGGCTGAATGGTGTCAAC | 5679 | Db | 6667 | TTACTGAGCCCTGGGAAACAGTGCACGGCTCACACCACTACGGTATGACATCCCGGACCGC | 6726 |
| QY | 5687 | GTGACATACTCCCTCTGGGGTTACATGTGTGGCATCCAGAGGGGCATCATGTCTGAAGA | 5746 | QY | 6767 | ATCACTCGGCTGGGTGACGTGCAATACAAAGATGATGAGGATGGCTTCTCTGAGGACGCG | 6826 |
| Db | 5680 | GTGACATACTCCCTCTGGGGTTACATGTGTGGCATCCAGAGGGGCATCATGTCTGAAGA | 5739 | Db | 6727 | ATCACTCGGCTGGGTGACGTGCAATACAAAGATGATGAGGATGGCTTCTCTGAGGACGCG | 6786 |
| QY | 5747 | ATGGAATACGACAGCGGGGCCGATCACATCAGGATCTTCGCTGATGGGAAGACATGG | 5806 | QY | 6827 | GGCGGTGATATCTTTGAGTACAACTCAGCTGGCTGCTCATCAAGGCTTACAAACCGGGCT | 6886 |
| Db | 5740 | ATGGAATACGACAGCGGGGCCGATCACATCAGGATCTTCGCTGATGGGAAGACATGG | 5799 | Db | 6787 | GGCGGTGATATCTTTGAGTACAACTCAGCTGGCTGCTCATCAAGGCTTACAAACCGGGCT | 6846 |
| QY | 5807 | AGCTACACATACTTAGAAGTGCATGTGTGCTACTACACAGCCAGAGGAGTATATC | 5866 | QY | 6887 | GGCAGCTGGAGTGTCAAGTACCGCTACGATGGCGGGCGGCGGTGTCCAGCAAGAGC | 6946 |
| Db | 5800 | AGCTACACATACTTAGAAGGAGGTG----- | 5827 | Db | 6847 | GGCAGCTGGAGTGTCAAGTACCGCTACGATGGCGGGCGGCGGTGTCCAGCAAGAGC | 6906 |
| QY | 5867 | TTTGAGTTGCAAGAATGACCGCTCTCTTCTGTGACGATGCCCAACGTTGGCGGGCAG | 5926 | QY | 6947 | AGCCACAGCCACCACTGCTGAGTTCCTTATGACAGCTTCACCAACCCCAAGGTCACC | 7006 |
| Db | 5828 | -TCGAGTTGCAAGAATGACCGCTCTCTTCTGTGACGATGCCCAACGTTGGCGGGCAG | 5886 | Db | 6907 | AGCCACAGCCACCACTGCTGAGTTCCTTATGACAGCTTCACCAACCCCAAGGTCACC | 6966 |
| QY | 5927 | ACACTAGACCAATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGC | 5986 | QY | 7007 | CACCTGTACAAACACTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTTCGAAGGACAC | 7066 |
| Db | 5887 | ACACTAGACCAATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGC | 5946 | Db | 6967 | CACCTGTACAAACACTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTTCGAAGGACAC | 7026 |
| QY | 5987 | AATGCCCTCAGTACACAGGACTTCACTGAGGATGGGCACCTCTTTCACACCTTCTACCTG | 6046 | QY | 7067 | CTCTTTGCCATGGAGCTGAGCTGAGTGGTGTGATGATTTTACATAGCTTGTGACAAACCTGGG | 7126 |
| Db | 5947 | AATGCCCTCAGTACACAGGACTTCACTGAGGATGGGCACCTCTTTCACACCTTCTACCTG | 6006 | Db | 7027 | CTCTTTGCCATGGAGCTGAGCTGAGTGGTGTGATGATTTTACATAGCTTGTGACAAACCTGGG | 7086 |
| QY | 6047 | GGCACTGGCGCGAGGTTATACAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTC | 6106 | QY | 7127 | AGCCCTCTTGTCTCTTTAGTGGAAACAGGTTTGTGATCAAGCAAACTCTGTACACAGCC | 7186 |
| Db | 6007 | GGCACTGGCGCGAGGTTATACAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTC | 6066 | Db | 7087 | AGCCCTCTTGTCTCTTTAGTGGAAACAGGTTTGTGATCAAGCAAACTCTGTACACAGCC | 7146 |
| QY | 6107 | TATGACACCAACCAAGTCACTTCACTATGACAGCGCAGGCTGCTGAAGACCATC | 6166 | QY | 7187 | TATGGGAGATCTACATGGATACCAACCCCAACTTTTCAGATCATCATAGGCTACCATGGT | 7246 |
| Db | 6067 | TATGACACCAACCAAGTCACTTCACTATGACAGCGCAGGCTGCTGAAGACCATC | 6126 | Db | 7147 | TATGGGAGATCTACATGGATACCAACCCCAACTTTTCAGATCATCATAGGCTACCATGGT | 7206 |
| QY | 6167 | AACTACAGAAATGAGGGCTTCACTGCACCATCCGCTACCGTACGATTTGGGCCCTTGAT | 6226 | QY | 7247 | GGCCTCTATGATCCACTCACTCAAGCTTGTCCATATGGCGCGGAGATTATGATGTGCTG | 7306 |
| Db | 6127 | AACTACAGAAATGAGGGCTTCACTGCACCATCCGCTACCGTACGATTTGGGCCCTTGAT | 6186 | Db | 7207 | GGCCTCTATGATCCACTCACTCAAGCTTGTCCATATGGCGCGGAGATTATGATGTGCTG | 7266 |
| QY | 6227 | GACCGACAGATCTTCCGCTTCACTGAGGAAGGATGTTCAACGCCGTTTGTACTACAAC | 6286 | QY | 7307 | GGCGAGCTGTGACTAGCCAGACCCAGAGCTGTGGAAGCACCTTTAGTACGCAACGCTC | 7366 |
| Db | 6187 | GACCGACAGATCTTCCGCTTCACTGAGGAAGGATGTTCAACGCCGTTTGTACTACAAC | 6246 | Db | 7267 | GGCGAGCTGTGACTAGCCAGACCCAGAGCTGTGGAAGCACCTTTAGTACGCAACGCTC | 7326 |
| QY | 6287 | TATGACAAACAGCTTCCGGGTGACAGCATGAGAGGCTGTGATCAACGAGACCCCACTGCC | 6346 | QY | 7367 | ATGCTCTTTAATCTCTATATGTTTCAAAAACCAACCCCACTCAGCAACTCCCAGGACATC | 7426 |
| Db | 6247 | TATGACAAACAGCTTCCGGGTGACAGCATGAGAGGCTGTGATCAACGAGACCCCACTGCC | 6306 | Db | 7327 | ATGCTCTTTAATCTCTATATGTTTCAAAAACCAACCCCACTCAGCAACTCCCAGGACATC | 7386 |
| QY | 6347 | ATTGATCTCTATCGCTATGATGTGTGAGGCAAGACAGCAGGATTTGGGAAGTTTGGT | 6406 | QY | 7427 | AACTGCTTTCATGACAGATGTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTTACAAAC | 7486 |
| Db | 6307 | ATTGATCTCTATCGCTATGATGTGTGAGGCAAGACAGCAGGATTTGGGAAGTTTGGT | 6366 | Db | 7387 | AACTGCTTTCATGACAGATGTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTTACAAAC | 7446 |
| QY | 6407 | GTCAATTTACTATGACATTAACCAAGATCATCAACAGCTGTGATCAACCAACCAAGCAT | 6466 | QY | 7487 | GTGATCCCTGGTTATCCCAAAACAGACATGGATGCCATGGAACTCTTACAGAGCTCATC | 7546 |
| Db | 6367 | GTCAATTTACTATGACATTAACCAAGATCATCAACAGCTGTGATCAACCAACCAAGCAT | 6426 | Db | 7447 | GTGATCCCTGGTTATCCCAAAACAGACATGGATGCCATGGAACTCTTACAGAGCTCATC | 7506 |
| QY | 6467 | TTTGATGCATATGGCAGGATGAAGAGTGCAGTATGAGATCTTCCGCTCGCTCATGTAC | 6526 | QY | 7547 | CACACACAGATGAAAACGAGGAGTGGGCAACAGCA----- | 7583 |
| Db | 6427 | TTTGATGCATATGGCAGGATGAAGAGTGCAGTATGAGATCTTCCGCTCGCTCATGTAC | 6486 | Db | 7507 | CACACACAGATGAAAACGAGGAGTGGGCAACAGCAAGGTAATTCCTGCACAAGGCTGC | 7566 |
| QY | 6527 | TGGATGACCTCCAGTATGATTAACATGGGGGAGTAGTGAAGAGGAGCTGAAGGTAGGA | 6586 | QY | 7584 | -AGCTCTATCCTCGGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGGCTTTGTCACTTA | 7642 |
| Db | 6487 | TGGATGACCTCCAGTATGATTAACATGGGGGAGTAGTGAAGAGGAGCTGAAGGTAGGA | 6546 | Db | 7567 | CAGTCTATCCTCGGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGGCTTTGTCACTTA | 7626 |
| QY | 6587 | CCCTACGCCAATACCACTCGCTACTCTCTATGAGTATGATGCTGACGCCAGCTGCAGACA | 6646 | QY | 7643 | GAAAGGTTTGAACAGCTCTATGGCTCCCAATCACCAGCTGCCAGAGGCTCCAAAGACC | 7702 |
| Db | 6547 | CCCTACGCCAATACCACTCGCTACTCTCTATGAGTATGATGCTGACGCCAGCTGCAGACA | 6606 | Db | 7627 | GAAAGGTTTGAACAGCTCTATGGCTCCCAATCACCAGCTGCCAGAGGCTCCAAAGACC | 7686 |
| QY | 6647 | GTCTCCATCAATGACAAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCAC | 6706 | QY | 7703 | AAGAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGGGCTCAAGTTTGCCTTGAAGGAT | 7762 |
| Db | 6607 | GTCTCCATCAATGACAAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCAC | 6666 | Db | 7687 | AAGAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGGGCTCAAGTTTGCCTTGAAGGAT | 7746 |

Db 7747 GCGCGAGTACACACACATCATCAGTGTGGCAATGAGATGGCGAAGGCTTGCTGCC 7806
Qy ATCTTGAACATGCCCACTACCTAGAGAACCTGCACTTACCATTTGATGGGTGGATACC 7882
Db ATCTTGAACATGCCCACTACCTAGAGAACCTGCACTTACCATTTGATGGGTGGATACC 7866
Qy CATTACTTTGTGAACACGAGACCTTCAGAAAGTGTGACCTGGCCATCCTGGCCCTCAGTGGG 7942
Db CATTACTTTGTGAACACGAGACCTTCAGAAAGTGTGACCTGGCCATCCTGGCCCTCAGTGGG 7926
Qy GGGCGCGAACCCTCGAGAAATGGGTCAAACGTCCTGCTGCCAGATCAACACAGTACTT 8002
Db GGGCGCGAACCCTCGAGAAATGGGTCAAACGTCCTGCTGCCAGATCAACACAGTACTT 7986
Qy AATGGCAGACTAGACGCTACACAGACATCCAGCTCCAGTACGGGGCACTGTGCTTGAAC 8062
Db AATGGCAGACTAGACGCTACACAGACATCCAGCTCCAGTACGGGGCACTGTGCTTGAAC 8046
Qy ACACGCTACGGACACACGTTGGATGAGGAGAGGACGCGGTCTTGAGCTGGCCCGGAG 8122
Db ACACGCTACGGACACACGTTGGATGAGGAGAGGACGCGGTCTTGAGCTGGCCCGGAG 8106
Qy AGAGCCGCTGCGCAACGCTGGGCGCGGACGACGAGACTCGCGGAAGGGGAGGAAGGC 8182
Db AGAGCCGCTGCGCAACGCTGGGCGCGGACGACGAGACTCGCGGAAGGGGAGGAAGGC 8166
Qy CTGCGGGCTGACAGAGAGGGGAGAGACGAGAGTGTGAGACACAGGGGGGTGCAAGGC 8242
Db CTGCGGGCTGACAGAGAGGGGAGAGACGAGAGTGTGAGACACAGGGGGGTGCAAGGC 8226
Qy TAGCAGCGCTTTTTCGTGATCTCTGTGAGCAGTATCCAGAGACTGTGACAGAGCCCAAC 8302
Db TAGCAGCGCTTTTTCGTGATCTCTGTGAGCAGTATCCAGAGACTGTGACAGAGCCCAAC 8286
Qy AACATCCACTTCATGAGACAGAGCGAGATGGCGGAGGTGACAGAGGAC 8354
Db AACATCCACTTCATGAGACAGAGCGAGATGGCGGAGGTGACAGAGGAC 8338

RESULT 5

US-10-042-865-1
; Sequence 1, Application US/10042865
; Publication No. US20040029216A1

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; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8438
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-042-865-1

Query Match 93.1%; Score 7779.2; DB 7; Length 8438;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 811; Conservative 0; Mismatches 203; Indels 100; Gaps 11;

Qy 32 GCCATGGACGTGAAGGAGAGAAAGCCTTACCGCTCGCTGACCCCGCGCGCGCGAG 91
Db 1 GCCATGGACGTGAAGGAGAGAAAGCCTTACCGCTCGCTGACCCCGCGCGCGCGAG 60

Qy 92 GCGCGCTACACCACTCGTCCGCGGACAGCAGAGAGGGCAAGCCCGCGCAAAATCCTAC 151
Db 61 GCGCGCTACACCACTCGTCCGCGGACAGCAGAGAGGGCAAGCCCGCGCAAAATCCTAC 120

Qy 152 AGCTCCAGCAGACCCCTGAAGGCTTACGACAGAGACCCCGCTTAGCTTATGGCAGCGC 211
Db 121 AGCTCCAGCAGACCCCTGAAGGCTTACGACAGAGACCCCGCTTAGCTTATGGCAGCGC 180

Qy 212 GTCAAGGACATTTGCGCGCAGGAGGCGAGAAATTTGCGCGCACAGTGCACATTCAAC 271
Db 181 GTCAAGGACATTTGCGCGCAGGAGGCGAGAAATTTGCGCGCACAGTGCACATTCAAC 240

Qy 272 CTGCGGAGCTGGGGCTGGAGAGTAACCGCCCTTACCGGACCCCTGTACCGGACAGAC 331
Db 241 CTGCGGAGCTGGGGCTGGAGAGTAACCGCCCTTACCGGACCCCTGTACCGGACAGAC 300

Qy 332 ATTGGCCTGCCCAATGCGGCTACTCCATGGGGCTGGCTCTGATGCCGACATGGAGGCT 391
Db 301 ATTGGCCTGCCCAATGCGGCTACTCCATGGGGCTGGCTCTGATGCCGACATGGAGGCT 360

Qy 392 GACACGCTGTCTCCCTGAGCACCCGCTGCTGTGTGGGGCGGAGACACAGGTCAGGG 451
Db 361 GACACGCTGTCTCCCTGAGCACCCGCTGCTGTGTGGGGCGGAGACACAGGTCAGGG 420

Qy 452 CGCAGCTCTGCTGCTCCAGCGGGCAATTCACAACTTCACTACCGGACACCGAGCAT 511
Db 421 CGCAGCTCTGCTGCTCCAGCGGGCAATTCACAACTTCACTACCGGACACCGAGCAT 480

Qy 512 GAAAAACACTGAGACTGATCATCCGGGCGGCTCGAGAACCCAGCGGGCTCCGAGACCGCG 571
Db 481 GAAAAACACTGAGACTGATCATCCGGGCGGCTCGAGAACCCAGCGGGCTCCGAGACCGCG 540

Qy 572 CCGCGCGCTCTTGCACGCGCCACACCCCAACACAGACACACCGCGGCTCCATTAACTCC 631
Db 541 CCGCGCGCTCTTGCACGCGCCACACCCCAACACAGACACACCGCGGCTCCATTAACTCC 600

Qy 632 CTGAACCGGGGCAACTTACCGCGGAGGACCAACCCAGCGCCCGCCCGGACCACTCG 691
Db 601 CTGAACCGGGGCAACTTACCGCGGAGGACCAACCCAGCGCCCGCCCGGACCACTCG 660

Qy 692 CTCTCCGGAGAGCCCTCTGCGGCGGCGCCAGGAGCTTSCCCACGCGCCAGAGAACTGG 751

QY 2893 CAGCAGCAAGATGGCAGCTTTGACTTGGTGAACAATGGCGCATCTCCATCATCTCTGGC 2952
Db 2872 CAGCAGCAAGATGGCAGCTTTGACTTGGTGAACAATGGCGCATCTCCATCATCTCTGGC 2931
QY 2953 GTTCGAGCGGCACCTTTTATCATCACAGGAGCACCCCTGTGGCTGCCATGGGATCGCTT 3012
Db 2932 GTTCGAGCGGCACCTTTTATCATCACAGGAGCACCCCTGTGGCTGCCATGGGATCGCTT 2991
QY 3013 CTTTGTGATGGAACCATCATCATGAGACATGAGAGGAATGAGATTCAGCTGTGACCT 3072
Db 2992 CTTTGTGATGGAACCATCATCATGAGACATGAGAGGAATGAGATTCAGCTGTGACCT 3051
QY 3073 GAGCAATTTTGGCGGCCCAACCAAGTCTCTCCATCCCACTGACGTCTCTGGCAG 3132
Db 3052 GAGCAATTTTGGCGGCCCAACCAAGTCTCTCCATCCCACTGACGTCTCTGGCAG 3111
QY 3133 CTCCTGTGCAGAAAGGCCCAATTGTGCCGGAATTCAGGCTTTTGCAGAGGAATCTC 3192
Db 3112 CTCCTGTGCAGAAAGGCCCAATTGTGCCGGAATTCAGGCTTTTGCAGAGGAATCTC 3171
QY 3193 TATCTCTGGCTGCAAGATGAGGCTGAGCTACTGTAGCAGCGCGAAGCCCTGGCTACAAATC 3252
Db 3172 TATCTCTGGCTGCAAGATGAGGCTGAGCTACTGTAGCAGCGCGAAGCCCTGGCTACAAATC 3231
QY 3253 TGTCTTGAGGATCAGCTCAACCCAGCCGACCATCCCTTCAACCTCATGAAGGTGACCT 3312
Db 3232 TGTCTTGAGGATCAGCTCAACCCAGCCGACCATCCCTTCAACCTCATGAAGGTGACCT 3291
QY 3313 CATGGTAGCGGTGAGGGCGGCTCTTTAGGAAGTGGTTTCGCTGAGCGCCAGACCTGTC 3372
Db 3292 CATGGTAGCGGTGAGGGCGGCTCTTTAGGAAGTGGTTTCGCTGAGCGCCAGACCTGTC 3351
QY 3373 CTATTATTTCATTTGGGACAGACAGACGTCTACACAGAAAGGTGTTTGGGCTTTTCAGA 3432
Db 3352 CTATTATTTCATTTGGGACAGACAGACGTCTACACAGAAAGGTGTTTGGGCTTTTCAGA 3411
QY 3433 AGCCTTTGTTTCGCTGGGTATGAATATGAATCTCTGCCAGATCTAATCTCTGGGAA 3492
Db 3412 AGCCTTTGTTTCGCTGGGTATGAATATGAATCTCTGCCAGATCTAATCTCTGGGAA 3471
QY 3493 AGAACAAACAGTCTGAGGCTATGAATATGAATCTCTGCCAGATCTAATCTCTGGGAA 3552
Db 3472 AGAACAAACAGTCTGAGGCTATGAATATGAATCTCTGCCAGATCTAATCTCTGGGAA 3531
QY 3553 AGAACAAACATGCTCCCTCAACATTCAAAGTGGT---ATCTGCAACAAGGAATGGGA 3609
Db 3532 AGAACAAACATGCTCCCTCAACATTCAAAGTGGTGGCATCTCTGCAACAAGGAATGGGA 3591
QY 3610 GAACCAAGTTTGTCTCAGCAGCTCTCTGATTTGGGAGCATCATGGGCAATGGGCGCG 3669
Db 3592 GAACCAAGTTTGTCTCAGCAGCTCTCTGATTTGGGAGCATCATGGGCAATGGGCGCG 3651
QY 3670 GAGAGCATCTCTGCGCCAGCTGCAACGGCTTCTGTCAGCGCAACAAGCTCTCTGGCCCC 3729
Db 3652 GAGAGCATCTCTGCGCCAGCTGCAACGGCTTCTGTCAGCGCAACAAGCTCTCTGGCCCC 3711
QY 3730 AGTGGCCCTCACCTGTGGCTCTGAGGGAGCCTCTATGTGGGTGATTTCAACTACATTAG 3789
Db 3712 AGTGGCCCTCACCTGTGGCTCTGAGGGAGCCTCTATGTGGGTGATTTCAACTACATTAG 3771
QY 3790 AAGGATCTTCCCTCTGGAAATGTCCACCAACATCTCTAGAGCTGAGG-----AATAAGA 3843
Db 3772 AAGGATCTTCCCTCTGGAAATGTCCACCAACATCTCTAGAGCTGAGGCTCAGAAATAGA 3831
QY 3844 TTTTCAGACATGTCAGTCTCAGACACAAATATCTACTTGGCCACAGACCCCATGAGTGG 3903
Db 3832 TTTTCAGACATGTCAGTCTCAGACACAAATATCTACTTGGCCACAGACCCCATGAGTGG 3891
QY 3904 GGCCGTCTTCTTCTGACAGCAACAGCGCGGGTCTTTTAAATCAAGTCCACTGTGGT 3963
Db 3892 GGCCGTCTTCTTCTGACAGCAACAGCGCGGGTCTTTTAAATCAAGTCCACTGTGGT 3951

QY 3964 GGTGAAGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGGTGACCAAGTGCCTCCC 4023
Db 3952 GGTGAAGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGGTGACCAAGTGCCTCCC 4011
QY 4024 CTTTGTGACACTCGCTGCGGGGATGGTGGGAAGCCACAGAAAGCCACACTCACCAATCC 4083
Db 4012 CTTTGTGACACTCGCTGCGGGGATGGTGGGAAGCCACAGAAAGCCACACTCACCAATCC 4071
QY 4084 CAGGGT-----ATTACAGTGGCAAGATTTGGGCTGATCTACTTCTGTTGGATGGCAC 4134
Db 4072 CAGGGTCCCCCAGGCAATTAAGTGGCAAGTTTTGGGCTGATCTACTTCTGTTGGATGGCAC 4131
QY 4135 CATGATCAGAGCGCATCGATCAGAATGGGATCATCTCACCCCTGCTCGGCTCTAATGATCT 4194
Db 4132 CATGATCAGAGCGCATCGATCAGAATGGGATCATCTCACCCCTGCTCGGCTCTAATGATCT 4191
QY 4195 CACATCAGCCCGGCACTCAGCTGTGATTTCTGTCATGGATATTTCCAGGTAAGA---- 4249
Db 4192 CACATCAGCCCGGCACTCAGCTGTGATTTCTGTCATGGATATTTCCAGGTAAGAAGGT 4251
QY 4250 ----CTGAGTGGCCCAAGATTTAGCCATCAACCCCAATGGACAACTCACCTTTATGCTCT 4305
Db 4252 TCACCTGGAGTGGCCCAAGATTTAGCCATCAACCCCAATGGACAACTCACCTTTATGCTCT 4311
QY 4306 CGAACAAATGTGGTCTCTGCAAAATCTCTGAAACCACAGGTGGCATTTCTGCGCGGAG 4365
Db 4312 CGAACAAATGTGGTCTCTGCAAAATCTCTGAAACCACAGGTGGCATTTCTGCGCGGAG 4371
QY 4366 GCCCATGCACTGCCAGGTCCCTGGCATTGACCACTTCTCTTAAGCAAGGTGGCCATCCA 4425
Db 4372 GCCCATGCACTGCCAGGTCCCTGGCATTGACCACTTCTCTTAAGCAAGGTGGCCATCCA 4431
QY 4426 CGAACCTCTGGAGTCAAGCCACCGCTTTGGCTGTTTTCACAATGGGGTCTCTATATGTC 4485
Db 4432 CGAACCTCTGGAGTCAAGCCACCGCTTTGGCTGTTTTCACAATGGGGTCTCTATATGTC 4491
QY 4486 TGAGACTGATGAGAAAGATCAACCGCATCAGCGAGGTCAACACTAGTGGAGAGATCTC 4545
Db 4492 TGAGACTGATGAGAAAGATCAACCGCATCAGCGAGGTCAACACTAGTGGAGAGATCTC 4551
QY 4546 ACTGTTGCTGGGCGCCCAAGTGGCTGTGACTGTGATAAATAATGATGCCAACTGTGATTGTT 4605
Db 4552 ACTGTTGCTGGGCGCCCAAGTGGCTGTGACTGTGATAAATAATGATGCCAACTGTGATTGTT 4611
QY 4606 TTTCTGAGACGATGGTTATGCGCAAGGATGCAAAATTAATACCCCATCTCTCTTGGCTGT 4665
Db 4612 TTTCTGAGACGATGGTTATGCGCAAGGATGCAAAATTAATACCCCATCTCTCTTGGCTGT 4671
QY 4666 GTGTGCTGATGGGAGCTCTACGTGGCGGACCTTTGGGAACATCCGAATTCGGTTTATCCG 4725
Db 4672 GTGTGCTGATGGGAGCTCTACGTGGCGGACCTTTGGGAACATCCGAATTCGGTTTATCCG 4731
QY 4726 GAAGAACAAAGCCTTTCTCAACACCCAGAACATGTATGAGCTGTCTTCAACCAATGACCA 4785
Db 4732 GAAGAACAAAGCCTTTCTCAACACCCAGAACATGTATGAGCTGTCTTCAACCAATGACCA 4791
QY 4786 GGAGCTCTATCTGTTGATACACCGGACAGCCTGTACACCAAGCCTGCCACAGG 4845
Db 4792 GGAGCTCTATCTGTTGATACACCGGCAAGCCTGTACACCAAGCCTGCCACAGG 4851
QY 4846 AGACTACCTGTACAACTTCACTTACCTGAGGAGCGGACATCACACTCATACAGACAA 4905
Db 4852 AGACTACCTGTACAACTTCACTTACCTGAGGAGCGGACATCACACTCATACAGACAA 4911
QY 4906 CAATGGCAACATGGTAAATGTCCGCGAGACTCTACTGGGATGCCCTCTGGCTGTGGT 4965
Db 4912 CAATGGCAACATGGTAAATGTCCGCGAGACTCTACTGGGATGCCCTCTGGCTGTGGT 4971
QY 4966 CCAGATGCGCAGGTGCTACTGGGTGACCATGGGCAACAGTGGCATCAAGTGTGAC 5025
Db 4972 CCAGATGCGCAGGTGCTACTGGGTGACCATGGGCAACAGTGGCATCAAGTGTGAC 5031
QY 5026 CACAAAGGACACAGGTTGGCCATGATGACATACCATGGCAATTCGGGCTTCTGGCAAC 5085

| | | | |
|------|----|--|------|
| 5032 | Db | CACAAAGGACACAGAGTTGGCCATGATGACATACCATGGCAAATCCGGCCCTTCTGGCAAC | 5091 |
| 5086 | Qy | CMAAGCAATGMAAACCGATGGCAACAATTTTATGAGTACGACAGCTTTTGCGCGCCTGAC | 5145 |
| 5092 | Db | CMAAGCAATGMAAACCGATGGCAACAATTTTATGAGTACGACAGCTTTTGCGCGCCTGAC | 5151 |
| 5146 | Qy | AAATGTGACCTTCCCTACTCGCCAGGTGAGCAGTTTCCGAAGTGATAACAGACAGTTTCAGT | 5205 |
| 5152 | Db | AAATGTGACCTTCCCTACTCGCCAGGTGAGCAGTTTCCGAAGTGATAACAGACAGTTTCAGT | 5211 |
| 5206 | Qy | GCATGTCCAGGTAGAGACCTCCAGCAAGGATGATGCCAATAAACCAACCTGCTGTCG | 5265 |
| 5212 | Db | GCATGTCCAGGTAGAGACCTCCAGCAAGGATGATGCCAATAAACCAACCTGCTGTCG | 5271 |
| 5266 | Qy | CTCAGGCGCTTCTACACACTGCTGCAAGACCAAGTCCGGAAACAGCTACTACATCGGGG | 5325 |
| 5272 | Db | CTCAGGCGCTTCTACACACTGCTGCAAGACCAAGTCCGGAAACAGCTACTACATCGGGG | 5331 |
| 5326 | Qy | CGATGGCTCTCTTGGCGCTGCTGCTGGCCAAACCGCATGGAGGTGGCGTGCAGACTGAGCC | 5385 |
| 5332 | Db | CGATGGCTCTCTTGGCGCTGCTGCTGGCCAAACCGCATGGAGGTGGCGTGCAGACTGAGCC | 5391 |
| 5386 | Qy | CCACTTGTGCTGGCTGGCAACCGTCAAACCGTGGGCAAGAGAAATGTCAAGTGCCTCAT | 5445 |
| 5392 | Db | CCAATTGCTGGCTGGCAACCGTCAAACCGTGGGCAAGAGAAATGTCAAGTGCCTCAT | 5451 |
| 5446 | Qy | CGACAAACGGCTCAACCTGCTGGAGTGGCGCCACGCGCAAGAGACAGCTCGGGGCGAGGT | 5505 |
| 5452 | Db | CGACAAACGGCTCAACCTGCTGGAGTGGCGCCACGCGCAAGAGACAGCTCGGGGCGAGGT | 5511 |
| 5506 | Qy | CACGTCTTTTGGGCGCGCGCTGCGGGTG-----CACAAACCGAAATCTCTATCTCT | 5556 |
| 5512 | Db | CACGTCTTTTGGGCGCGCGCTGCGGGTGCTCCAGGTTCAACACCGAAATCTCTATCTCT | 5571 |
| 5557 | Qy | GGACTTTTGATCGCGTAAACAGCAACAGAGAAGATCTATGATGACACACGCAAGTTACCCCT | 5616 |
| 5572 | Db | GGACTTTTGATCGCGTAAACAGCAACAGAGAAGATCTATGATGACACACGCAAGTTACCCCT | 5631 |
| 5617 | Qy | TCGGATTTCTGTACACACAGCGCGGGCGGCCAGCCCTGTGTCACCCAGCAGCAGGCTGAA | 5676 |
| 5632 | Db | TCGGATTTCTGTACACACAGCGCGGGCGGCCAGCCCTGTGTCACCCAGCAGCAGGCTGAA | 5691 |
| 5677 | Qy | TGGTGTCAAAGTGACATACTCCCTCTGGGGGTTACATTTGCTGGCATCCAGAGGGGCATCAT | 5736 |
| 5692 | Db | TGGTGTCAAAGTGACATACTCCCTCTGGGGGTTACATTTGCTGGCATCCAGAGGGGCATCAT | 5751 |
| 5737 | Qy | GTCTGAAGAATGGAATACGACAGCGGGCGCGCATCACATCCAGGATTTTCGCTGATGG | 5796 |
| 5752 | Db | GTCTGAAGAATGGAATACGACAGCGGGCGCGCATCACATCCAGGATTTTCGCTGATGG | 5811 |
| 5797 | Qy | GAAGACATGGAGCTTACATACTTAGAGA-----AGTCCATGGTGGCTACT | 5844 |
| 5812 | Db | GAAGACATGGAGCTTACATACTTAGAGAAGCGAGGTGTCCAGTCCATGGTGGCTACT | 5871 |
| 5845 | Qy | ACAGACCCAGAGGAGTATATCTTTTGGTTCCGACAGAAAGACCGCTCTCTCTGTGAC | 5904 |
| 5872 | Db | ACAGACCCAGAGGAGTATATCTTTTGGTTCCGACAGAAAGACCGCTCTCTCTGTGAC | 5931 |
| 5905 | Qy | GATGCCAACGTTGGCGCGGACACATAGAGACCATCCGCTCAGTGGGCTACTACAGAAA | 5964 |
| 5932 | Db | GATGCCAACGTTGGCGCGGACACATAGAGACCATCCGCTCAGTGGGCTACTACAGAAA | 5991 |
| 5965 | Qy | CATCTATCAGCCCCCTGAGGCAATGCTCAGTCAATACAGAGCTTCTACTGAGGATGGGCA | 6024 |
| 5992 | Db | CATCTATCAGCCCCCTGAGGCAATGCTCAGTCAATACAGAGCTTCTACTGAGGATGGGCA | 6051 |
| 6025 | Qy | CCTCCTTCAACCTTCTACCTGGGCACTGGCGGAGGGTGATATACAGATATGCAAACT | 6084 |
| 6052 | Db | CCTCCTTCAACCTTCTACCTGGGCACTGGCGGAGGGTGATATACAGATATGCAAACT | 6111 |
| 6085 | Qy | GTCAAAGCTGGCAGAGACGCTCTATGACCAACCAAGGTCAAGTTTACCTATGACGAGAC | 6144 |

| | | | |
|------|----|---|------|
| 6112 | Db | GTCAAAGCTGGCAGAGCGCTCTATGACACCAAGGTACAGTTTACCTATGACGAGAC | 6171 |
| 6145 | Qy | GGCAGGCATGCTGAAGACCAATCAACCTTACAGAAATGAGGGCTTCACTGCAACCAATCCGCTA | 6204 |
| 6172 | Db | GGCAGGCATGCTGAAGACCAATCAACCTTACAGAAATGAGGGCTTCACTGCAACCAATCCGCTA | 6231 |
| 6205 | Qy | CCGTCAAGATTGGGCCCTGATTGACCGACAGATCTTCGCTTCACTGAGGAAAGGCATGGT | 6264 |
| 6232 | Db | CCGTCAAGATTGGGCCCTGATTGACCGACAGATCTTCGCTTCACTGAGGAAAGGCATGGT | 6291 |
| 6265 | Qy | CAACGCCGTTTGTAGCTTACAACCTATGACAAACAGCTTCCGGGTGACCAAGCATGACGGCTGT | 6324 |
| 6292 | Db | CAACGCCGTTTGTAGCTTACAACCTATGACAAACAGCTTCCGGGTGACCAAGCATGACGGCTGT | 6351 |
| 6325 | Qy | GATCAACGAGACCCCACTGCCCCATTGATCTCTATCGCTATGATGATGTGTGTCAGCAAGAC | 6384 |
| 6352 | Db | GATCAACGAGACCCCACTGCCCCATTGATCTCTATCGCTATGATGATGTGTGTCAGCAAGAC | 6411 |
| 6385 | Qy | AGAGCAGTTTGGGAAGTTTGGTGTCTATTACTATGACATTTAAACAGATCATCAACACAGC | 6444 |
| 6412 | Db | AGAGCAGTTTGGGAAGTTTGGTGTCTATTACTATGACATTTAAACAGATCATCAACACAGC | 6471 |
| 6445 | Qy | TGTCATGACCCACACCAAGCATTTTGTGTCATTTGATGCATATGGCAGGATGAAGGAAGTGCAGTATGA | 6504 |
| 6472 | Db | TGTCATGACCCACACCAAGCATTTTGTGTCATTTGATGCATATGGCAGGATGAAGGAAGTGCAGTATGA | 6531 |
| 6505 | Qy | GATCTTCCGCTCGCTCATGTACTGGATGACCGCTCCAGTATGATAAATGATGGGCGAGTAGT | 6564 |
| 6532 | Db | GATCTTCCGCTCGCTCATGTACTGGATGACCGCTCCAGTATGATAAATGATGGGCGAGTAGT | 6591 |
| 6565 | Qy | GAAGAAGGAGCTGAAGGTAGGAACCTTAGGCCAATACCACTCGCTACTCTTATGATGATGA | 6624 |
| 6592 | Db | GAAGAAGGAGCTGAAGGTAGGAACCTTAGGCCAATACCACTCGCTACTCTTATGATGATGA | 6651 |
| 6625 | Qy | TGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGACAAGCCACTCTGGCGCTACAGCTA | 6684 |
| 6652 | Db | TGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGACAAGCCACTCTGGCGCTACAGCTA | 6711 |
| 6685 | Qy | CGACCTCAATGGGAACCTGCACCTTACTGAGCCCTGGGAACAGTGCACGGCTCACACCACT | 6744 |
| 6712 | Db | CGACCTCAATGGGAACCTGCACCTTACTGAGCCCTGGGAACAGTGCACGGCTCACACCACT | 6771 |
| 6745 | Qy | ACGGTATGACATTCGCGAACCGCATCACTCGGCTGGGTGACGTGCAATACAGATGGATGA | 6804 |
| 6772 | Db | ACGGTATGACATTCGCGAACCGCATCACTCGGCTGGGTGACGTGCAATACAGATGGATGA | 6831 |
| 6805 | Qy | GGATGGCTTCTTGAGGCAGCGGGCGGTGATATCTTTGAGTACAACTCAGCTGCGCTGCT | 6864 |
| 6832 | Db | GGATGGCTTCTTGAGGCAGCGGGCGGTGATATCTTTGAGTACAACTCAGCTGCGCTGCT | 6891 |
| 6865 | Qy | CATCAAGGCCTACAAACCGGGCTGGCAGCTGGAGTGTGAGGTACCGCTACGATGGCCTGGG | 6924 |
| 6892 | Db | CATCAAGGCCTACAAACCGGGCTGGCAGCTGGAGTGTGAGGTACCGCTACGATGGCCTGGG | 6951 |
| 6925 | Qy | CGCGCGGTGTCCAGAAAGACAGCCACAGCCACAACCTGAGTTCCTTCTATGACAGACCT | 6984 |
| 6952 | Db | CGCGCGGTGTCCAGAAAGACAGCCACAGCCACAACCTGAGTTCCTTCTATGACAGACCT | 7011 |
| 6985 | Qy | GACCAACCCCAACCAAGTCAACCACTGTAACCACTCCAGCTCTCGAGATCACTCCCT | 7044 |
| 7012 | Db | GACCAACCCCAACCAAGTCAACCACTGTAACCACTCCAGCTCTCGAGATCACTCCCT | 7071 |
| 7045 | Qy | CTACTACGACTTGCAAAGACACCTCTTTTGCCATGGAGCTGAGCAGTGGTGTATGATTTTA | 7104 |
| 7072 | Db | CTACTACGACTTGCAAAGACACCTCTTTTGCCATGGAGCTGAGCAGTGGTGTATGATTTTA | 7131 |
| 7105 | Qy | CATAGCTTGTGACAAACATCGGGACCCCTCTTTGCTGTCTTTAGTGGAAACAGGTTTGATGT | 7164 |
| 7132 | Db | CATAGCTTGTGACAAACATCGGGACCCCTCTTTGCTGTCTTTAGTGGAAACAGGTTTGATGT | 7191 |
| 7165 | Qy | CAAGCAAAATCCTGTACACAGCCTATGGGAGATCTCATGATGATCAACCAACCCCACTTTCA | 7224 |
| 7192 | Db | CAAGCAAAATCCTGTACACAGCCTATGGGAGATCTCATGATGATCAACCAACCCCACTTTCA | 7251 |

QY 7225 GATCATCATAGGCTACCATGGTGGCTCTATGATCCACTCACCAAGCTTGTCCACATGGG 7284
DB 7252 GATCATCATAGGCTACCATGGTGGCTCTATGATCCACTCACCAAGCTTGTCCACATGGG 7311
QY 7285 CCGCGAGATTATGATGTGTGCGCGGAGCGCTGGACTAGCCACAGACACGAGCTGTGGAA 7344
DB 7312 CCGCGAGATTATGATGTGTGCGCGGAGCGCTGGACTAGCCACAGACACGAGCTGTGGAA 7371
QY 7345 GCACCTTAGTAGAGCAACGTCATGCTTTTAATCTCTATATGTTCAAAAAACAACCC 7404
DB 7372 GCACCTTAGTAGAGCAACGTCATGCTTTTAATCTCTATATGTTCAAAAAACAACCC 7431
QY 7405 CATCAGCAACTCCAGGACATCAAGTCTTCATGACAGATGTTAAACAGTGGCTGCTCAC 7464
DB 7432 CATCAGCAACTCCAGGACATCAAGTCTTCATGACAGATGTTAAACAGTGGCTGCTCAC 7491
QY 7465 CTTTGGATTCCAGCTACCAACGTCATGCTGCTTATCCCAACAGACATGGATGCCAT 7524
DB 7492 CTTTGGATTCCAGCTACCAACGTCATGCTGCTTATCCCAACAGACATGGATGCCAT 7551
QY 7525 GGAACCTCTACGAGCTATCCACACAGATGAAACGCAAGGATGGGAACAACAGCA - 7583
DB 7552 GGAACCTCTACGAGCTATCCACACAGATGAAACGCAAGGATGGGAACAACAGCAA 7611
QY 7584 -----AGTCTATCTCGGGTACAGTGTGAAGTACAGAACA 7620
DB 7612 GGTAATTCCTGCACAGGCTGCCAGTCTATCTCGGGGTACAGTGTGAAGTACAGAACA 7671
QY 7621 GCTCAAGGCTTTGTCACTTAGAAGGTTGACAGCTCTATGGCTCCACAATCACCAG 7680
DB 7672 GCTCAAGGCTTTGTCACTTAGAAGGTTGACAGCTCTATGGCTCCACAATCACCAG 7731
QY 7681 CTGCCAGAGCTCCAAAGCAAGAGTTTGCATCCAGCGCTCAGTCTTTGGCAAGGG 7740
DB 7732 CTGCCAGAGCTCCAAAGCAAGAGTTTGCATCCAGCGCTCAGTCTTTGGCAAGGG 7791
QY 7741 GGTCAAGTTTGGCTTGAAGGATGGCGAGTGACACAGACATCATCAGTGTGGCCAAATGA 7800
DB 7792 GGTCAAGTTTGGCTTGAAGGATGGCGAGTGACACAGACATCATCAGTGTGGCCAAATGA 7851
QY 7801 GGATGGGCAAGGGTTGTGCACTTTGAACCATGCCACTACCTAGAGAACCTGCACTT 7860
DB 7852 GGATGGGCAAGGGTTGTGCACTTTGAACCATGCCACTACCTAGAGAACCTGCACTT 7911
QY 7861 CACCATTTGATGGGTGGATACCCATTACTTTGTGAAACCAAGACCTTCAGAGGTGACCT 7920
DB 7912 CACCATTTGATGGGTGGATACCCATTACTTTGTGAAACCAAGACCTTCAGAGGTGACCT 7971
QY 7921 GGCCATCTCTGGGCTCAGTGGGGGGCGGCAACCTGGAGAAATGGGGTCAACGTCACCTGT 7980
DB 7972 GGCCATCTCTGGGCTCAGTGGGGGGCGGCAACCTGGAGAAATGGGGTCAACGTCACCTGT 8031
QY 7981 GTCCAGATCAACACAGTACTTAATGGCAGGACTAGAGCTTACACAGACATCCAGTCCA 8040
DB 8032 GTCCAGATCAACACAGTACTTAATGGCAGGACTAGAGCTTACACAGACATCCAGTCCA 8091
QY 8041 GTACGGGGCACTGTCTTGAACACAGCTACGGGCAACGTTGGATGAGGAGAGGCACG 8100
DB 8092 GTACGGGGCACTGTCTTGAACACAGCTACGGGCAACGTTGGATGAGGAGAGGCACG 8151
QY 8101 GGTCTCGAGCTGGCCCGGACAGAGCCGTGCGCAAGCGTGGGCCCGGACGAGCAGAG 8160
DB 8152 GGTCTCGAGCTGGCCCGGACAGAGCCGTGCGCAAGCGTGGGCCCGGACGAGCAGAG 8211
QY 8161 ACTGGGCAAGGGAGGAGGCTTCGGGCTTGACAGAGGGGAGAGCAGAGGTGCT 8220
DB 8212 ACTGGGCAAGGGAGGAGGCTTCGGGCTTGACAGAGGGGAGAGCAGAGGTGCT 8271
QY 8221 GAGCACAGGGGGTGCAGGCTACGAGCGCTTTTTCGTGATCTCTGTCGAGCAGTACCC 8280
DB 8272 GAGCACAGGGGGTGCAGGCTACGAGCGCTTTTTCGTGATCTCTGTCGAGCAGTACCC 8331

QY 8281 AGAACTGTACAGAGCGCCAAACATCCACTTTCATGAGACAGAGCGAGATGGGCCGAG 8340
DB 8332 AGAACTGTACAGAGCGCCAAACATCCACTTTCATGAGACAGAGCGAGATGGGCCGAG 8391
QY 8341 GTGACAGAGAGGAC 8354
DB 8392 GTGACAGAGAGGAC 8405
RESULT 6
US-10-723-860-3169
; Sequence 3169, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05982.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3169
; LENGTH: 8624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-3169

Query Match 44.1%; Score 3680.8; DB 8; Length 8624;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 3775; Conservative 0; Mismatches 2; Indels 83; Gaps 1;

QY 4578 GTAAATATGATGCAACTGTGATTGTTTCTCGAGACGATGCTTATGCCAAGGATGCAA 4637
DB 1 GTAAATATGATGCAACTGTGATTGTTTCTCGAGACGATGTTATGCCAAGGATGCAA 60
QY 4638 AGTTAAATACCCATCTTCCTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACC 4697
DB 61 AGTTAAATACCCATCTTCCTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACC 120
QY 4698 TTGGGACATCCGAATCGGTTATCCGGAAGAACAAAGCTTCTCTCAACACCAGAACA 4757
DB 121 TTGGGACATCCGAATTCGGTTTATCCGGAAGAACAAAGCTTCTCTCAACACCAGAACA 180
QY 4758 TGATGAGCTGTCTTCAACCAATTGACAGAGCTCTATCTGTTTGATACACCGGCAAGC 4817
DB 181 TGATGAGCTGTCTTCAACCAATTGACAGAGCTCTATCTGTTTGATACACCGGCAAGC 240
QY 4818 ACCTGTACACCCAAAGCCTGCCACAGGAGACTACCTGTACAACTTCACTACACTGGGG 4877
DB 241 ACCTGTACACCCAAAGCCTGCCACAGGAGACTACCTGTACAACTTCACTACACTGGGG 300
QY 4878 ACGGCGACATCACTCATCAGACAAACAATGGCAACATGTTAAATGTCGCCGAGACT 4937
DB 301 ACGGCGACATCACTCATCAGACAAACAATGGCAACATGTTAAATGTCGCCGAGACT 360
QY 4938 CTACTGGGATGCCCTCTGGCTGCCAGATGGCAGGTGTACTGGGTGACCATGG 4997
DB 361 CTACTGGGATGCCCTCTGGCTGGTCCAGATGGCCAGGTGTACTGGGTGACCATGG 420
QY 4998 GCACCAACAGTGCATCAAGAGTGTGAACCAACAGGACACGAGTTGGCCATGATGACAT 5057
DB 421 GCACCAACAGTGCATCAAGAGTGTGAACCAACAGGACACGAGTTGGCCATGATGACAT 480
QY 5058 ACCATGGCAATTCGGGCTTCTGGCAACCAAGCAATGAAACCGATGGAACAATTTT 5117
DB 481 ACCATGGCAATTCGGGCTTCTGGCAACCAAGCAATGAAACCGATGGAACAATTTT 540
QY 5118 ATGA----- 5121

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|----|------|---|------|
| Qy | 7255 | TGATCCACTCACCAGCTTGTTCACATGGCCGGCGAGATTATGATGTCTGCGCGGACG | 7314 |
| Db | 2761 | TGATCCACTCACCAGCTTGTTCACATGGCCGGCGAGATTATGATGTCTGCGCGGACG | 2820 |
| Qy | 7315 | CTGAGCTAGCCACAGACGAGCTGTGGAAGCACCTTAGTAGCAGCAACGTCATGCCTTT | 7374 |
| Db | 2821 | CTGAGCTAGCCACAGACGAGCTGTGGAAGCACCTTAGTAGCAGCAACGTCATGCCTTT | 2880 |
| Qy | 7375 | TAATCTCTATATGTTCAAAAAACAACCCCATCAGCAACTCCACAGGACATCAAGTGCTT | 7434 |
| Db | 2881 | TAATCTCTATATGTTCAAAAAACAACCCCATCAGCAACTCCACAGGACATCAAGTGCTT | 2940 |
| Qy | 7435 | CATGACAGATGTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAAGCTATCCC | 7494 |
| Db | 2941 | CATGACAGATGTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAAGCTATCCC | 3000 |
| Qy | 7495 | TGTTATCCAAACACAGACATGGATGCCATGGAACCCCTCTACGAGCTCATCCACACACA | 7554 |
| Db | 3001 | TGTTATCCAAACACAGACATGGATGCCATGGAACCCCTCTACGAGCTCATCCACACACA | 3060 |
| Qy | 7555 | GATGAAAACGACAGAGTGGACACAACGAAAGTCTATCTCGGGGTACAGTGTGAAGTACA | 7614 |
| Db | 3061 | GATGAAAACGACAGAGTGGACACAACGAAAGTCTATCTCGGGGTACAGTGTGAAGTACA | 3120 |
| Qy | 7615 | GAGCAGCTCAAGGCCCTTTGTCACTTTAGAAACGTTTGACCAAGCTCTATGGCTCCACAAT | 7674 |
| Db | 3121 | GAGCAGCTCAAGGCCCTTTGTCACTTTAGAAACGTTTGACCAAGCTCTATGGCTCCACAAT | 3180 |
| Qy | 7675 | CACAGCTGCCAGCGGCTCCAAAGACCAAGAAGTTTGATCCAGCGGCTCAGTCTTTGG | 7734 |
| Db | 3181 | CACAGCTGCCAGCGGCTCCAAAGACCAAGAAGTTTGATCCAGCGGCTCAGTCTTTGG | 3240 |
| Qy | 7735 | CAAGGGGTCAAGTTTGCCTTGAAGATGGCGGAGTGACCAAGATCATCATCAGTGTGCG | 7794 |
| Db | 3241 | CAAGGGGTCAAGTTTGCCTTGAAGATGGCGGAGTGACCAAGATCATCATCAGTGTGCG | 3300 |
| Qy | 7795 | CAATGAGGATGGCGAAGGGTTGCTGCCATCTTGAACATGCGCCACTACCTAGAGAACT | 7854 |
| Db | 3301 | CAATGAGGATGGCGAAGGGTTGCTGCCATCTTGAACATGCGCCACTACCTAGAGAACT | 3360 |
| Qy | 7855 | GCATTCACATATGATGGGGTGATACCCATTTACTTTGTGAAACAGGACCTTCAGAAAG | 7914 |
| Db | 3361 | GCATTCACATATGATGGGGTGATACCCATTTACTTTGTGAAACAGGACCTTCAGAAAG | 3420 |
| Qy | 7915 | TGACCTGGCCATCCTGGGCTCAGTGGGGGGCGGAGAACCTTGGAGATGGGGTCAAAGT | 7974 |
| Db | 3421 | TGACCTGGCCATCCTGGGCTCAGTGGGGGGCGGAGAACCTTGGAGATGGGGTCAAAGT | 3480 |
| Qy | 7975 | CACTGTGTCCAGATCAACACAGTACTTTAAATGGCAGGACTAGACGCTACACAGACATCCA | 8034 |
| Db | 3481 | CACTGTGTCCAGATCAACACAGTACTTTAAATGGCAGGACTAGACGCTACACAGACATCCA | 3540 |
| Qy | 8035 | GCTCCAGTACGGGGCACTGTGTTGAAACACAGCTACGGGACAAAGTTGGATGAGGAGAA | 8094 |
| Db | 3541 | GCTCCAGTACGGGGCACTGTGTTGAAACACAGCTACGGGACAAAGTTGGATGAGGAGAA | 3600 |
| Qy | 8095 | GGCAGGGTCTGGAGCTGGCCCGCAGAGAGCGGTGGCCCAAGCGTGGGGCCCGGAGCA | 8154 |
| Db | 3601 | GGCAGGGTCTGGAGCTGGCCCGCAGAGAGCGGTGGCCCAAGCGTGGGGCCCGGAGCA | 3660 |
| Qy | 8155 | GCAGAGACTGCGGGGAAGGGAGGAGGCTTGGGGCTCTGGACAGAGGGGGAGAGCAGCA | 8214 |
| Db | 3661 | GCAGAGACTGCGGGGAAGGGAGGAGGCTTGGGGCTCTGGACAGAGGGGGAGAGCAGCA | 3720 |
| Qy | 8215 | GGTGTGTAGCACAGGGCGGGTCAAGGCTACGACGGCTTTTTTGTGATCTCTGTGAGCA | 8274 |
| Db | 3721 | GGTGTGTAGCACAGGGCGGGTCAAGGCTACGACGGCTTTTTTGTGATCTCTGTGAGCA | 3780 |
| Qy | 8275 | GTACCAGAACTGTACAGACGGCCCAACAATCCACTTTCATGACAGACGAGATGGG | 8334 |
| Db | 3781 | GTACCAGAACTGTACAGACGGCCCAACAATCCACTTTCATGACAGACGAGATGGG | 3840 |

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|---|------|--|------|
| Qy | 8335 | CCGGAGGTGACAGAGAGGAC | 8354 |
| Db | 3841 | CCGGAGGTGACAGAGAGGAC | 3860 |
| RESULT 7 | | | |
| US-10-756-149-2959 | | | |
| ; Sequence 2959, Application US/10756149 | | | |
| ; Publication No. US20050181375A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Aziiz, Natasha | | | |
| ; APPLICANT: Zlotnik, Albert | | | |
| ; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND | | | |
| ; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER | | | |
| ; FILE REFERENCE: file | | | |
| ; CURRENT APPLICATION NUMBER: US/10/756,149 | | | |
| ; CURRENT FILING DATE: 2004-01-12 | | | |
| ; NUMBER OF SEQ ID NOS: 5818 | | | |
| ; SOFTWARE: PatentIn version 3.2 | | | |
| ; SEQ ID NO 2959 | | | |
| ; LENGTH: 8624 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Homo Sapiens | | | |
| US-10-756-149-2959 | | | |
| Query Match | | | |
| Best Local Similarity 44.18; Score 3680.8; DB 9; Length 8624; | | | |
| Matches 3775; Conservative 0; Mismatches 2; Indels 83; Gaps 1; | | | |
| Qy | 4578 | GTAAAAATGATGCCAACTGTGATGTTTCTGGAGACGATGGTTATGCCAAGGATGCAA | 4637 |
| Db | 1 | GTAAAAATGATGCCAACTGTGATGTTTCTGGAGACGATGGTTATGCCAAGGATGCAA | 60 |
| Qy | 4638 | AGTTAAATACCCCATCTTCCTTGGCTGTGTGTGATGGGAGCTCTACGTGGCCGACC | 4697 |
| Db | 61 | AGTTAAATACCCCATCTTCCTTGGCTGTGTGTGATGGGAGCTCTACGTGGCCGACC | 120 |
| Qy | 4698 | TTGGGAACATCCGAATTCGGTTCATCGGAAGACAGACCTTCTCCTCAACACCCAGAAC | 4757 |
| Db | 121 | TTGGGAACATCCGAATTCGGTTCATCGGAAGACAGACCTTCTCCTCAACACCCAGAAC | 180 |
| Qy | 4758 | TGTATGAGCTGTCTTACCAATTTGACCAGGAGCTCTATCTGTTGTATACCACCGGCAAGC | 4817 |
| Db | 181 | TGTATGAGCTGTCTTACCAATTTGACCAGGAGCTCTATCTGTTGTATACCACCGGCAAGC | 240 |
| Qy | 4818 | ACCTGTACACCAAGGCTGCCACAGGAGACTACCTGTACAACCTTCACTGAGG | 4877 |
| Db | 241 | ACCTGTACACCAAGGCTGCCACAGGAGACTACCTGTACAACCTTCACTGAGG | 300 |
| Qy | 4878 | ACGGCGACATCACACTCATCACAGACAAACAAATGGCAACATGGTAAATGTCCGGCGAGACT | 4937 |
| Db | 301 | ACGGCGACATCACACTCATCACAGACAAACAAATGGCAACATGGTAAATGTCCGGCGAGACT | 360 |
| Qy | 4938 | CTACTGGGATGCCCTCTGGCTGGTCCAGATGGCCAGGTGTACTTGGGTGACCATGG | 4997 |
| Db | 361 | CTACTGGGATGCCCTCTGGCTGGTCCAGATGGCCAGGTGTACTTGGGTGACCATGG | 420 |
| Qy | 4998 | GCACCAACAGTCACTCAAGAGTGTGACACACAGGACACGAGTTGGCCATGATGACAT | 5057 |
| Db | 421 | GCACCAACAGTCACTCAAGAGTGTGACACACAGGACACGAGTTGGCCATGATGACAT | 480 |
| Qy | 5058 | ACCATGGCAATTCGGGCTTCTGGCAACCAAAAGCAATGAAAACGGATGGACAACATTTT | 5117 |
| Db | 481 | ACCATGGCAATTCGGGCTTCTGGCAACCAAAAGCAATGAAAACGGATGGACAACATTTT | 540 |
| Qy | 5118 | ATGA----- | 5121 |
| Db | 541 | ATGACAACTTCAGATGGCAGGAATTTATCACCACATTTTTTACATATAGATGACAGAG | 600 |
| Qy | 5122 | -----GTACGACAGCTTTGGCCGCTGACCAATGTGAC | 5154 |
| Db | 601 | ATTAGATAAACAGCCTTGAAACCAACGAGTACGAGCTTTGGCCGCTGACAAATGTGAC | 660 |

| | | | |
|----|------|--|------|
| QY | 5155 | CTTCCCTACTGGCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCACTGATGTCCA | 5214 |
| Db | 661 | TTTTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCACTGATGTCCA | 720 |
| QY | 5215 | GGTAGAGACTTCAGACAAAGATGATGTACACATAACCAACCACTGTCTGCTTCAAGCGC | 5274 |
| Db | 721 | GGTAGAGACTTCAGACAAAGATGATGTACACATAACCAACCACTGTCTGCTTCAAGCGC | 780 |
| QY | 5275 | CTTCTACACACTGCTGCAAGACCAAGTCCGGAAACAGTACTACATCGGGGCCGATGGCTC | 5334 |
| Db | 781 | CTTCTACACACTGCTGCAAGACCAAGTCCGGAAACAGTACTACATCGGGGCCGATGGCTC | 840 |
| QY | 5335 | CTTGGCGCTCTGCTGGCCCAACGGCATGGAGGTGGCGCTCAGACCTGAGCCCCACTTGTCT | 5394 |
| Db | 841 | CTTGGCGCTCTGCTGGCCCAACGGCATGGAGGTGGCGCTCAGACCTGAGCCCCACTTGTCT | 900 |
| QY | 5395 | GGCTGGCACCGTCAACCCCCACCGTGGGCAAGAGGAATGTCACTGCGCCCATGCAACCGG | 5454 |
| Db | 901 | GGCTGGCACCGTCAACCCCCACCGTGGGCAAGAGGAATGTCACTGCGCCCATGCAACCGG | 960 |
| QY | 5455 | CCTCAACCTGGTGGAGTGGCGGCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTT | 5514 |
| Db | 961 | CCTCAACCTGGTGGAGTGGCGGCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTT | 1020 |
| QY | 5515 | TGGCGCGCGCTGCGGGTGCAACACCGAAATCTCTATCTCTGGACTTTTGTATCGCGTAAC | 5574 |
| Db | 1021 | TGGCGCGCGCTGCGGGTGCAACACCGAAATCTCTATCTCTGGACTTTTGTATCGCGTAAC | 1080 |
| QY | 5575 | ACGCACAGAGAAGATCTATGATGACCAACCGCAAGTTTCAACCTTGGATTTGTAGCACCA | 5634 |
| Db | 1081 | ACGCACAGAGAAGATCTATGATGACCAACCGCAAGTTTCAACCTTGGATTTGTAGCACCA | 1140 |
| QY | 5635 | GGCGGGCGCGCCAGCTCTGGTCAACCCAGCAGGAGCTGAATGGTGTCAACCTGACATA | 5694 |
| Db | 1141 | GGCGGGCGCGCCAGCTCTGGTCAACCCAGCAGGAGCTGAATGGTGTCAACCTGACATA | 1200 |
| QY | 5695 | CTCCCTGGGGGTTTACATGCTGSCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATA | 5754 |
| Db | 1201 | CTCCCTGGGGGTTTACATGCTGSCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATA | 1260 |
| QY | 5755 | CGACACGGCGGGCGCATCATCCAGGATCTTGGCTGTATGGGAAGACATGGAGCTACAC | 5814 |
| Db | 1261 | CGACACGGCGGGCGCATCATCCAGGATCTTGGCTGTATGGGAAGACATGGAGCTACAC | 1320 |
| QY | 5815 | ATACTTAGAGAGTCCATGTGTGCTACTACACAGCAGGAGCAGTATCTTTGAGTT | 5874 |
| Db | 1321 | ATACTTAGAGAGTCCATGTGTGCTACTACACAGCAGGAGCAGTATCTTTGAGTT | 1380 |
| QY | 5875 | CGACAAGAAATGACCGCTCTCTTCTGTGACGATGCCCAAAGTGGCGGGCGAGACACTAGA | 5934 |
| Db | 1381 | CGACAAGAAATGACCGCTCTCTTCTGTGACGATGCCCAAAGTGGCGGGCGAGACACTAGA | 1440 |
| QY | 5935 | GACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTCAGGGCAATGCCTC | 5994 |
| Db | 1441 | GACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTCAGGGCAATGCCTC | 1500 |
| QY | 5995 | AGTCATACAGACTTCTCAGTGGAGTGGGCCTCTCTTCAACCTTCTACCTTGGGCACTGG | 6054 |
| Db | 1501 | AGTCATACAGACTTCTCAGTGGAGTGGGCCTCTCTTCAACCTTCTACCTTGGGCACTGG | 1560 |
| QY | 6055 | CCGAGGGTGATATACAAAGTATGCAAACTGTCAAAGCTGGCAGAGAGCTCTATGACAC | 6114 |
| Db | 1561 | CCGAGGGTGATATACAAAGTATGCAAACTGTCAAAGCTGGCAGAGAGCTCTATGACAC | 1620 |
| QY | 6115 | CACCAAGGTCAAGTTTCACTATGACGAGACGGCAGGATGCTGAAGACCATCAACCTTACA | 6174 |
| Db | 1621 | CACCAAGGTCAAGTTTCACTATGACGAGACGGCAGGATGCTGAAGACCATCAACCTTACA | 1680 |
| QY | 6175 | GAATGAGGGTTCACCTTGACACCATCCGGTACCGTACAGATTGGGGCCCTGATTGACCGACA | 6234 |
| Db | 1681 | GAATGAGGGTTCACCTTGACACCATCCCGTACCGTACAGATTGGGGCCCTGATTGACCGACA | 1740 |
| QY | 6235 | GATCTTCCGCTTCACTTAGGAAGGCATGGTCAACGCCCGTTTTTGACTACAACTATGACAA | 6294 |

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|----|------|---|------|
| Db | 1741 | GATCTTCCGCTTCACTGAGGAAGGATGGTCAACGCCCGTTTTTGACTACAACTATACCAA | 1800 |
| QY | 6295 | CAGCTTCCGGGTGACCAGCATCGAGCTGTGATCAACGAGACCCCACTGCCCCATTGATCT | 6354 |
| Db | 1801 | CAGCTTCCGGGTGACCAGCATCGAGCTGTGATCAACGAGACCCCACTGCCCCATTGATCT | 1860 |
| QY | 6355 | CTATCGCTATGATGATGTCTCAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTA | 6414 |
| Db | 1861 | CTATCGCTATGATGATGTCTCAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTA | 1920 |
| QY | 6415 | CTATGACATTAACAGATCATCACACAGCTGTATGATGACCCACACCAAGCATTTTATGTC | 6474 |
| Db | 1921 | CTATGACATTAACAGATCATCACACAGCTGTATGATGACCCACACCAAGCATTTTATGTC | 1980 |
| QY | 6475 | ATATGGCAGGATGAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTTGGATGAC | 6534 |
| Db | 1981 | ATATGGCAGGATGAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTTGGATGAC | 2040 |
| QY | 6535 | CGTCCAGTATGATAACATGGGGCGAGTAGTGAAGAAAGGAGCTGAAGGTAGGACCCCTACGC | 6594 |
| Db | 2041 | CGTCCAGTATGATAACATGGGGCGAGTAGTGAAGAAAGGAGCTGAAGGTAGGACCCCTACGC | 2100 |
| QY | 6595 | CAATACCACTCGCTACTCTCTATGAGTATGATGCTGACGGCCAGCTGCAGACGTCTCCAT | 6654 |
| Db | 2101 | CAATACCACTCGCTACTCTCTATGAGTATGATGCTGACGGCCAGCTGCAGACGTCTCCAT | 2160 |
| QY | 6655 | CAATGACAGCCACTCTGGGCTTACAGCTACGACCTCAATGGGAACCTGCACCTTACTGAG | 6714 |
| Db | 2161 | CAATGACAGCCACTCTGGGCTTACAGCTACGACCTCAATGGGAACCTGCACCTTACTGAG | 2220 |
| QY | 6715 | CCCTGGGAAACAGTGACGGCTCACACCACTACCGGTATGACATCCGGGACCGCATCTCG | 6774 |
| Db | 2221 | CCCTGGGAAACAGTGACGGCTCACACCACTACCGGTATGACATCCGGGACCGCATCTCG | 2280 |
| QY | 6775 | GCTGGGTGACGTGCAATAACAAGATGATGAGGATGGCTTCTGAGGAGCGGGCGGTGA | 6834 |
| Db | 2281 | GCTGGGTGACGTGCAATAACAAGATGATGAGGATGGCTTCTGAGGAGCGGGCGGTGA | 2340 |
| QY | 6835 | TATCTTTGAGTACAACTCAGCTGGCTGTCTCAACAGGCTTCAACCGGCTGCGAGCTG | 6894 |
| Db | 2341 | TATCTTTGAGTACAACTCAGCTGGCTGTCTCAACAGGCTTCAACCGGCTGCGAGCTG | 2400 |
| QY | 6895 | GAGTGTGAGTACCGCTACGATGGCTGGGGCGCGCTGTCTCCAGCAAGAGCAGCCACAG | 6954 |
| Db | 2401 | GAGTGTGAGTACCGCTACGATGGCTGGGGCGCGCTGTCTCCAGCAAGAGCAGCCACAG | 2460 |
| QY | 6955 | CCACCACTGCAAGTTCTTCTATGACAGCTTGACAAACCCCAACCAAGGTCAACCACTGTA | 7014 |
| Db | 2461 | CCACCACTGCAAGTTCTTCTATGACAGCTTGACAAACCCCAACCAAGGTCAACCACTGTA | 2520 |
| QY | 7015 | CAACCACTCCAGCTCTGAGATCACCTCCCTCTACTACGATTCGCAAGGACACCTCTTTTC | 7074 |
| Db | 2521 | CAACCACTCCAGCTCTGAGATCACCTCCCTCTACTACGATTCGCAAGGACACCTCTTTTC | 2580 |
| QY | 7075 | CATGGAGCTGAGCAGTGGTGTGATGAGTTTACATAGCTTTGTGACAAATCGGGACCCCTCT | 7134 |
| Db | 2581 | CATGGAGCTGAGCAGTGGTGTGATGAGTTTACATAGCTTTGTGACAAATCGGGACCCCTCT | 2640 |
| QY | 7135 | TGCTGTCTTTTGTGGAAACAGTTTGTATGATCAAGCAAAATCCTGTACACAGCTTATGGGGA | 7194 |
| Db | 2641 | TGCTGTCTTTTGTGGAAACAGTTTGTATGATCAAGCAAAATCCTGTACACAGCTTATGGGGA | 2700 |
| QY | 7195 | GATCTACATGGATACCAACCCCAACTTTCAGATCATCATAGGCTACCATGGTGGCTCTTA | 7254 |
| Db | 2701 | GATCTACATGGATACCAACCCCAACTTTCAGATCATCATAGGCTACCATGGTGGCTCTTA | 2760 |
| QY | 7255 | TGATCACTACCAAGCTTGTCCACATGGGCCGGCGAGATTATGATGTGTGCGCGGACG | 7314 |
| Db | 2761 | TGATCACTACCAAGCTTGTCCACATGGGCCGGCGAGATTATGATGTGTGCGCGGACG | 2820 |
| QY | 7315 | CTGAGCTAGCCACAGACCAAGAGCTGTGGAAAGCACTTGTAGTAGCAGCAACCTCATGCTTTT | 7374 |

Db 2821 CTGGACTAGCCAGACCGAGCTGTGGAAGCACCTTAGTAGCAGCAAGCTCATGCCTTT 2880
Qy 7375 TAAATCTCTATATGTTCAAAAAACAACCCCATCAGCAACTCCCAAGGACATCAAGTGCTT 7434
Db 2881 TAAATCTCTATATGTTCAAAAAACAACCCCATCAGCAACTCCCAAGGACATCAAGTGCTT 2940
Qy 7435 CATGACAGATGTTAAACAGCTGCTGCTACCTTTTGATTTCCAGCTACACAAGCTCATCCC 7494
Db 2941 CATGACAGATGTTAAACAGCTGCTGCTACCTTTTGATTTCCAGCTACACAAGCTCATCCC 3000
Qy 7495 TGGTTATCCCAACACAGACATGATGCAATGGAACCTCTACGAGCTCATCCACACACA 7554
Db 3001 TGGTTATCCCAACACAGACATGATGCAATGGAACCTCTACGAGCTCATCCACACACA 3060
Qy 7555 GATGAACACGAGGAGTGGGACAAACGCAAGTCTATCTCGGGGTACAGTGTGAAGTACA 7614
Db 3061 GATGAACACGAGGAGTGGGACAAACGCAAGTCTATCTCTCGGGGTACAGTGTGAAGTACA 3120
Qy 7615 GAAGCAGCTCAAGGCTTTTGTACCTTTAGAACGGTTTGACCAAGCTCTATGGCTCCACAAT 7674
Db 3121 GAAGCAGCTCAAGGCTTTTGTACCTTTAGAACGGTTTGACCAAGCTCTATGGCTCCACAAT 3180
Qy 7675 CACCAAGCTGCCAGAGGCTCCAAAGACCAAGAAAGTTTGATCCAGCGGCTCAGTCTTTGG 7734
Db 3181 CACCAAGCTGCCAGAGGCTCCAAAGACCAAGAAAGTTTGATCCAGCGGCTCAGTCTTTGG 3240
Qy 7735 CAAGGGGTCAAGTTTGCCTTGAAGATGGCCGAGTGACCAAGACATCATCAGTGTGGC 7794
Db 3241 CAAGGGGTCAAGTTTGCCTTGAAGATGGCCGAGTGACCAAGACATCATCAGTGTGGC 3300
Qy 7795 CAATGAGGATGGCGAAGGTTTGTGCCATCTTGAACCATGCCACTACCTAGAGAACT 7854
Db 3301 CAATGAGGATGGCGAAGGTTTGTGCCATCTTGAACCATGCCACTACCTAGAGAACT 3360
Qy 7855 GCACCTTACCATTTGATGGGGTGGATACCCATTACTTTGTGAACACAGGACCTTCAGAGG 7914
Db 3361 GCACCTTACCATTTGATGGGGTGGATACCCATTACTTTGTGAACACAGGACCTTCAGAGG 3420
Qy 7915 TGACCTGGCCATCTTGGGCTCAGTGGGGGGGGGGAACCTTGGAGAAATGGGTCAGCT 7974
Db 3421 TGACCTGGCCATCTTGGGCTCAGTGGGGGGGGGGAACCTTGGAGAAATGGGTCAGCT 3480
Qy 7975 CACTGTGTCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCA 8034
Db 3481 CACTGTGTCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCA 3540
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Db 3841 CCGGAGGTGACAGAGGAGC 3860

; Sequence 7176, Application US/10723860
; Publication No. US20040253608A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7176
; LENGTH: 8774
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4015)..(4029)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6561)..(6580)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-7176

Query Match 43.4%; Score 3621.6; DB 8; Length 8774;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 3758; Conservative 0; Mismatches 14; Indels 88; Gaps 4;

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Qy 5945 TCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTTGAGGGCAATGCTCAGTCAATACAG 6004
Db 5935 TCCATTTGGCTACTTACCGCAACATATACAACCCCGGAAAGCAACGCTCCATCATCAGC 5994
Qy 6005 GACTTCACTGAGATGGGCACCTCTTTCACACCTTCTACCTGGGCACCTGCGCGCAGGTC 6064
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Qy 6125 AGTTTCACCTATGACAGAGCGGAGGATGCTGGAAGCAATCAACCTTACAGAAATGAGGGC 6184
Db 6115 AGTTTACCTATGATGAACAGCAGGAGTCTTAAAGACAGTAAACCTTCCAGAGTGAATGGT 6174
Qy 6185 TTCACCTGCACCATCCGCTACCGTCAAGTTGGGCGCCCTGATTCGCCAGCAGATCTCCGC 6244
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Qy 6365 GATGATGTGTACGGCAAGACAGACAGTGTGGGAAGTTTGGTGTCTTACTTACTAGCAT 6424
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Db 6415 AACCAAGATCATTTTACAGCTGTANTGACCTATACGAAGCACTTTGATGCTCATGGCCGT 6474
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Qy 6545 GATAACATTTGGGCGAGTAGTGAAGGAGGACTGAAGGTAGGACCCCTACGCCAATACCAC 6604
Db 6535 GATAACATTTGGGTCGGGTAAACCAAGAGAGAGATTAATAATAGGGCCCTTTTGCCACACACC 6594


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; APPLICANT: Burgess, Catherine E
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; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 35
; LENGTH: 8675
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-038-854-35

Query Match 41.6%; Score 3473.8; DB 7; Length 8675;
Best Local Similarity 65.2%; Pred. No. 0;
Matches 5445; Conservative 0; Mismatches 2692; Indels 216; Gaps 14;

Qy 35 ATGACGTGAAGGAGAGAGACCTTACGGCTCGCTGACCCGGCGC---CGGACCGCGAG 91
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Qy 151 ATGGATGTGAAGAAGCAGCGCCTTACTGCTCCCTGACCAAGAGCAGCAGAGAGAGAA 210
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 92 CGCGCTACACAGCTCGTCCGGCAGCAGCGAGGAGGCAAG---CCCGCAGAAATCG 148
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 211 CGGCGCTACACAAATTCCTCCGAGACANATGAGAGTGCGGGGTACCCACACAGAGTCC 270
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 149 TACAGCTCCACGAGACCTGAAAGCCTACGACCAGGA---CGCCCGCTAGCCTATGGC 205
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 206 AGCCGCTCAAGGACATGTGCCCGAGGAGCCAGGAATTCGCCCGCAGAGTGCACAC 265
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 331 AACAGAGTGAAGGATTTGGTTTCACAGAGAAGCAGACGAGTTTCACTAGACAAGGACAGAAT 390
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 266 TTCAACCTCGGGAGCTGGGCTCGAAGAGTAAACGCCCTCACGGAGCCCTGTACCGG 325
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 391 TTTTACCCTTAGGCAAGTTAGGAGTTTGTAACCAAGCACTCGAAGAGACTGGCAATTTGT 450
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 326 ACAGACATTTGGCTCCGCCAATCGGCTACTCCATGGGGGTGGCTCTGATGCCGACATG 385
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 451 GCGAAATGGGCTCCCTCACAGAGGTTACTCTATAGTCAGGAGTCTGATGCTGATACT 510
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 386 GAGGCTGACACGGTGTGCTCCCTGAGCACCCCTGGCTGTGTGGGCGCGGAGCACAGG 445
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 511 GAAATGAAGCAGTGATGTCCCGAGAGCATGCCATGAGACTTTTGGGCGCAGGGGGTCAAA 570
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 446 TCAGGGCGCAGCTCCTGCTGTCCAGCGCGGCCCAATTCCAATCTCACACTCACCGACACC 505
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

571 TCAGGCGCGCAGCTCCTGCTGTCAAGTCGGTCAACTCAGCCCTCACTGACAGATACG 630
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
506 GAGCATGAATAACAACACTGAGACTGATCATCGGGGGGCTGCAGAACACACGCGCGCTCCG 565
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
631 GAGCAGCAATAACAAGTCCGACAGTGAAGTGAACACCTGCAAGCAATCAAGGCCAGTCT 690
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
566 ACGCCGCGCGCGCTCTGCGACAGCGCCACACCCCAACAGCAGCAGCAGCGCGCTCCATT 625
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
691 ACCCTGAGCCCTTGGCGCTTCCATAGCAGCACTCTGCAAGCATATCATCATCCATC 750
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
626 AACTCCCTGAACCGGGGCAACTTACGCCGAGAGAGAACCCAGCCCGGCGCGCCACGAGAC 685
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
751 ACTTCTCTCAACAGAAACTCCCTGAGCAATAGAAGGAACAGAGTCCGGCGCGCGCGCT 810
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
686 CACTCGCTCTCGGAGAGCCCTGCGCGCGCGCCAGGAGCTGCGCCACGCGCCAGGAG 745
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
811 GCTTTGCCCGCCGAGCTGCAAC-----CACACCGAGTCCGTCAGCTGCAGGAC 861
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
746 AACTGGCTGCTCAACAGCAACATCCCGCTGGAGACAGCAACCTAGCAAGCAGCCATTC 805
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
862 AGCTGGTCTCTGGCAGTAATGTACCACCTGGAAGCAGGCATTT----- 905
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
806 CTAGGACATTTGAGGACAACTCATTTAGATGACATTTCTCGCGGCTCCCGCCATGAT 865
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
906 ----- 905
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
866 GGGGCTTACAGTGACGGGCACTTCTTCAAGCTGGAGGCACCTCCCGCTCTTCTGTC 925
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
906 -----CCTATTCAAAACAGGAACAGGTACACGCCACATGTTTCACT 945
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
926 ACCACATCACAGGGTACCCACTGAGCTCCAGCACAGTGTACTCTCTCCGCCCGGACCC 985
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
946 ACTGCAACCCAGGATACACAAATGGCATCTGGCTCTGTTTATTCACCACCTACTCGGCA 1005
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
986 CTGCCCCGAGACCTTTGCGCGCGCGCTTTAACTCAAGAAGCCCTCCAAGTACTGT 1045
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1006 CTACCTAGAAACACCCCTATCAAGAAGTGTCTTTAAATTCAGAAGTCTTCAAGTACTGT 1065
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1046 AACTGGAAGTGCAGCCCTGAGCGCATCTCATCTCAGCCACTCTGGTTCATCTGCTG 1105
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1066 AGCTGAAATGCACTGCACTGTGTGCGGTAGGGGTCTCGGTGCTCTGCGCATACTCTG 1125
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1106 GCATCTTTGTGCGCATGCACTGTTTGGCTTAACTGGCACTGACGCGATGAGAGGGG 1165
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1126 TCTTTATTTATAGCAATGCACTCTTTGGCTCAACTGSCAGCTTACAGCAGACTGAAAT 1185
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1166 CAGATGTATGAGATTCAGGAGGACACAGCCAGCAGTTGGCTGTGCCAACCGAGCTTCC 1225
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1186 GACACATTTGAGA-----ATGGAAGAGTGAATTTCTGATACCATGCGCAACAAACACTGTG 1239
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1226 CTATACCCCTCAGGGGCACTGGCTTAGAGACCCCTGACAGGAAGGCAAGGAACACCA 1285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1240 TCATTACCTTCTGGAGACA----- 1258
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1286 GAAGGAAGCCCACTAGTTTCTTTCCAGAGGACAGATTTTCATAGATTTCTGGAGAAATGAT 1345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1259 -ATGGAATAATTAGTGTGATTTACGCAAGAAATAACACCATAGATTCCGAGAACTTGAT 1317
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1346 GTGGGAAGCGAGCCTCCAGAAATTCCTCTGGCACTTTCTGGGAGATCTCAAGTGTTC 1405
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1318 ATTGGCGAAGAGCAATTCAGAGATTCCTCCCGGATCTTCTGGAGATCAAGCTCTTC 1377
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1406 ATAGACCATCTGTGCATCTGAAATTCATATGCTCTGGAAGAGGAGCCCTCGTGTGGC 1465
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1378 ATTGATCAGCCACAGTTTCTTAAATTCATATCTCTCTCAGAAGGATGCAATTTGATGGA 1437
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1438 GTATATGGCGGAAGAGTTACCGCTTCCCATACTCAGTCTCTCCCGGATGATGACTTC 1497
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1514 GTGAGCTGTGATGTCAGGAGGCTCTTAACCCAGAGGCGCGGAGCCCTAGAGGGAGCC 1573
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 1498 GTGAGCTCCTGGAGCGCAGGCTGATTGTCAGAGAGCAGCGGAGCTGCTTGAGACG 1557
Qy 1574 CCGCGCCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAGACAGGCTTATCCAGTAT 1633
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Qy 1634 TTGGATTCAGGAATCTGGGACATGTGCTTTTACAATGACGGAAGAGTCAAGAGTGGTT 1693
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Qy 1694 TCTTTTCAACACATGCCATTCAGTTCGGTGAATACTGCCAGAACTGCTATAGCAAT 1753
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Qy 1874 TGCCACAGTGGTGGAAAGCGCTGAGTCCGATGTCGATGTCGCCACAAACAGTGTATCGATGTG 1933
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Qy 1934 GCGTCGACCAACCATGGCACCCTGATCATCAGGGCACCTGCATCTGCAACCTTGGCTTACAG 1993
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Qy 2234 GGTGACCATGGCGTGTGCGTAGGGGCACTTCCGCTCGAGGATGGCTGGATGGGGCA 2293
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Qy 2294 GGCTGGACCGGGCGCTGCCACCGGCGCTGTGCCGAGCATGGGACCTGGCGGACGGC 2353
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Qy 2414 AGGGTAGT-----TAAAGAGGTTGCCCTGGGTGTGCAATGGCAAC 2455
Db 2398 AAGATAGTTAAAGACAAGATAGGATATAAAGAGGTTGTCTGTGCTGTGCAACAGCAAT 2457
Qy 2456 GGCAGATGATCTTAGACTGAATGGTTGGGCACTCGCTGTGCCAGCTGGGCTGGAGAGA 2515
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Db 2578 GGACTCATTTGACTGATGGATCCCGATTTGCTGCTTACAGAGTTCTCTGCCAGAAATCAGCCC 2637

Qy 2636 CTGTGCTTGGCTCCCCTAAACCCTCTGACATCATCCAGGAGACACAGGTCCTGTGTCA 2695
Db 2638 TATTGTGGGACTGCGGGATCCTCAGACATCATTAGCCAAAGCCTTCAATCGCTTCT 2697
Qy 2696 CAGCAGAACCTTACACTCTCTTATGACCGCATCAAGTTCCTCGTGGGAGGAGCAGACG 2755
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Qy 3056 ATTCAGAGCTGTGACCTGAGCAATTTTCCCGCGCCCAACCCAGTCTCTCTCCATCCCCA 3115
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Qy 3116 CTGACGCTCTTGGCAGCTCTGTGAGAGAAAGGCCCATTTGTGCGGAAATTCAGGCT 3175
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Qy 3296 CTATGAAAGTGCACCTCATGTGAGCGGTGAGGGCGCCCTTTCAGAGAGTGGTTCGCT 3355
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Qy 3356 GCAGCCCGCAGACCTGCTTATTTTCAATTTGGGACAAGACAGACGCTCTACAAACAGAG 3415
Db 3358 GCCTCAAACTTTGGCTATATCTTTTATATGGGATAAACAAGATGATATATCAGAAA 3417
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Db 3478 CTGACTCTGTGGGAAAAAGAGACTGCCATTTCTGAGGGCTATGAATTTGGATGCGTCCAAC 3537
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Qy 3596 AAAGGGAATGGGAGAACCCAGTTTGTCTCAGCAGGCTCTCTGTCAATTTGGAGCATCATG 3655
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Qy 3656 GGCAATGGGCGCCGGAAGAGCATCTCTGCCCCAGCTGCAACGGCCTTGTCTGAGCGCAAC 3715
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QY 3716 AAGCTCTGCGCCAGTGGCCCTCACCTGTGGCTCTGAOGGAGCCCTCTATGTGGTGAT 3775
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QY 4256 TGCCCAACAGACTTAGGCATCAACCCAAATGGACAACCTACTTATGTCTCGACAACAAT 4315
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Db 4318 GTAGTTTACAGATCACTGAAATCGTCAAGTTTCGATTCGCTGGACGGCCATGACAC 4377
QY 4376 TGCCAGGTCCCTGGCATTGACCACTTCTCTTAAGCAAGGTGGCCATCCACGCAACCCCTG 4435
Db 4378 TGTGAGTTCCTCGGAGTGG---AATATCTGTGTGGGGAAGCACGCGGTGCAGACAAACACT 4434
QY 4436 GAGTCAGCCACCGCTTTGGCTGTTTACACAATGGGGTCTGTATATTGCTGAGACTGAT 4495
Db 4435 GAATCAGCCACTGCGATTGCTGTCTTACAGTGGGGTCTGTACATTACTGAAACTGAT 4494
QY 4496 GAGAAAGAATCAACCGCATCAGGAGGTCAACCATAGTGGAGAGATCTCACTCGTTGCT 4555
Db 4495 GAGAGAAATTAACCGGATAAGGAGGTCAACAAGATGAGAGAAATCTCTTAGTGGCC 4554
QY 4556 GGGGCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATGTTTTCTGGAGAC 4615
Db 4555 GGAATACCTTTACAGATGTGACTGCAAAATGATGCCAACTGTGACTGTACCAGAGTGA 4614
QY 4616 GATGGTTATGCCAAGGATGAAAGTTAAATACCCCATCTTCTTGGCTGTGTGCTGTAT 4675
Db 4615 GATGGCTACGCCAAGGATGCAAACTCAGTGGCCCCATCTCTCCCTGGCTGTCTTCAGAT 4674
QY 4676 GGGGAGCTCTACGTGGCCGACTTTGGGAACATCCGAATTCGGTTTATCCGGAAAGAACAG 4735
Db 4675 GGTACATGTATATTGCAGATCTAGGGAATATCCGGATCCGGCTGTGTCAAGAAATAG 4734
QY 4736 CTTTCTCAACACCCAGAACATGTATGAGCTGTCTTCAACAAATGACAGGAGCTCTAT 4795
Db 4735 CTTTACTTAATCTATGAACCTCTATGAAGTTGCGTCTCCAACTGATCAAGAATCTTAC 4794
QY 4796 CTGTTTGTATACCACCGCAGCACCTGTACACCAACCAAGCCCTGCCACAGGAGACTACCTG 4855

Db 4795 ATCTTTGACATCAATGGTACTCACCAATATACTGTAAGTTTATGTCACCTGGTATTACCTT 4854
QY 4856 TACAACCTTCACTTACCTGGGACCGGACATCACACTCATCACAGACAAACAATGGCAAC 4915
Db 4855 TACAATTTTATGCTACAGCAATGCAATGATATCTCTGTGTACAGACAGCAATGGCAAC 4914
QY 4916 ATGTTAAATGTCCGCGAGACTCTTACTGGGATGCCCTCTGCTGGTGGTCCAGATGCC 4975
Db 4915 ACCCTTAGAATTTAGACGGGACCCAAATCGCATGCCAGTTTCGAGTGGTGTCTCTGATAAC 4974
QY 4976 CAGGTGTACTGGGTGACCAATGGGACCAACAAGTGCACCTCAAGAGTGTGACACACAGGA 5035
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QY 5036 CACGAGTTGGCCATGATGACATACCATGCAATTCGGGCTTCTGCAACCAAAAGCAAT 5095
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QY 5096 GAAAAACGATGGACAAACATTTTATGATACGACAGCTTTTGGCGCTGACAAATGTGACC 5155
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QY 5156 TTCCCTTACGTGGCCAGGTGAGCAGTTTTCGAAAGTATACAGACAGTTTCACTGATGATGCCAG 5215
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QY 5216 GTAGAGACTCCAGC---AAGGATGATGTACCAATAACCAACCACTGTCTGCCTCAGGC 5272
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QY 5333 TCTTGGCGCTGCTGTGGCCAAAGGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTG 5392
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QY 5393 CTGGCTGGCACCGTCAACCCACCGTGGGCAAGAGAAATGTCACTGCTGCCCTCGACAAC 5452
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QY 5453 GGCTCAACCTGTGGTGGCGCCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACCTGTC 5512
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QY 5513 TTTGGCGCGGCTGCGGTGCAACCCGAAATCTCTATCTCTGGAATTTTGTGATCGGTA 5572
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QY 5753 TAGCACCAGGGCGCGCATCATCTCAGGATCTTCGTGATGGGAGACATCGAGCTAC 5812
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Db 5815 ACATATTTAGAAAGTCCATGGTTCTTCTGCTTCATAGCCAGCGGACAGTACATCTTCGAA 5874
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Db 5935 CAGACCATCCGATCCATTTGGCTACTACCGCAACATATACACCCCGGGAAGCAACGCC 5994
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Qy 6053 GCGCGAGGGTGATATACAAAGTATGGCAAACTGTCAAAAGCTGGCAGAGACGCTCTATGAC 6112
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Qy 6113 ACCACCAAGGTCACTTACCTATGACGAGCGGAGGATGCTGGAAGCAACCTCAACCTA 6172
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Qy 6713 AGCCCTGGGAACAGTGCAAGGCTCACACCACTTACCGTATGATCATCCGCGACCGCATCACT 6772
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Qy 6773 CGGCTGGGTGACGTGCAATACAAAGATGATGATGAGTGTCTTCTGAGCAGCGGGCGGT 6832
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Qy 6953 AGCCACCACTGCACTTCTTCTATGACAGCTGTGACCAACCCCAACCAAGGTCAACCCACTG 7012
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Qy 7013 TACAACCACTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTTCGAAGGACACCTCTTTT 7072
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Db 7075 GCCATGAAATCAGCAGTGGGATGAATTTCTATATTCATCGGATTAACACAGGACACCA 7134
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Qy 7193 GAGATCTACATGGATCAACCCCACTTTTCAGATCATATAGGCTACCAATGCTGCTC 7252
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Qy 7253 TATGATCCACTCAACCAAGCTTGTCCATGCGCGCGGAGATTATATGATGTGCTGCGCGGA 7312
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Qy 8033 CAGCTCAGTACGGGGCACTGTGCTTGAACACAGCTTACGGGACAAAGTGTGGATGAGAG 8092
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QY 1777 CCACTGCTTCCCTGGGTTTCTGGGCCCGGACATGTGGCAGAGCCTCTGCCCCGCTGCTCTG 1836
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QY 1897 TGAGTCCGATGTGCCCAACCAACAGTGTATCGATGTGGCTGCACGAACCAATGGCACCTG 1956
DB 1697 CGAGTGTGATGTGCCAGTACTCCAGTGTATGACCCACAGTGTGGGGTGTGGGATTTG 1756
QY 1957 CATCACGGGACCTGCATCTGCAACCCCTGGCTTACAAAGGCGAGAGCTGTGAGGAAAGTGA 2016
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QY 2017 CTGCATGGACCCACATGTTTAGGCGGGGTGTCTGCTGAGAGGGAATGCCATGTGCTT 2076
DB 1817 CTGTATAGACCTCGGGTGTCTTAATCATGGTGTGTATCCACGGGGAAATGTCACTGCAG 1876
QY 2077 TGTGGATGGGAGGACCAAACTGCGAGACCCACGGGCCACATGCTTAGACCACTGTTTC 2136
DB 1877 TCAGGATGGGAGGTAGCAATGTGAAATCTGAAGACCATGTGTCCAGACCACTGCTC 1936
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DB 1937 CGGCCACGGAACGTATCTTCAAGAAAGTGGCTCCTGCAGTGTGACCCCTAATCTGGACTGG 1996
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DB 1997 CCCAGACTCTCAAAAGCAATATGTTCTGTGACTGTGCTCACAAGGCTGTGATGGAATGCAAGGCTG 2056
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QY 2422 ---TAAAGAGGTTGGCTGGGTTGTGCAATGGCAACGGCAGATGTACCTTAGACCTGAA 2478
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QY 2479 TGGTTGGCACTGGCTGCGCAGCTGGGCTGGAGAGAGCTGGCTGTGACACTTCCATGGA 2538
DB 2297 TGGCGGACATTTGTGTGTCGACGCTGGATGGAGAGGAGCAGGCTGTGACGTAGCCATGGA 2356
QY 2539 GACTGCTCGGTGACAGCAAAAGACAATGATGGAGATGGCCCTGGTGGACTGCATGGACCC 2598
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QY 2659 TCTGGACATCATCCAGGAGACAGGTCCCTGTGTACAGCAGAAACCTTACACTCCTTTCTA 2718
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QY 2719 TGACCGCATCAAGTTCCTCGTGGGAGGAGCAGCAGCAGACATAATCCCCGGGAGAACCC 2778
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DB 2657 ACTTATTTGGAGTAAATGTCTCGTTTTTTCATTACCCAGAAATATGGATATACTATTACCCG 2716
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QY 2959 GCGGGCACCTTTTATCACACAGAGGACACCCCTGTGTGCTGCCATTTGGGATCGCTTTTGT 3018
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QY 3019 CATGAAACCATCATATGAGACATGAGGAGATGAGATTTCCAGCTGTGACCTGAGCAA 3078
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Db 4694 CAATGATTAATCTGCTGTGACAGACAGCAATGGCAACACCCCTTGAATTTAGACGGHACCC 4753
Qy 4939 TACTGGGATGCCCTCTGGGTGGTCCAGATGGCGAGGTGACTGGGTGACCAATGGG 4998
Db 4754 AATCGCATGCCAGTTCCAGTGGTGTCTCCTGTATAACCAAGTGATATGTTTGAACAATAGG 4813

Qy 4999 CACCAACAGTGCACCTCAAGAGTGTGACCACACAAGGACACGAGTTGGCCATGATGACATA 5058
Db 4814 AACAAATGATGTTTGAAGGCGATGCTGCTCAAGGACTGGAATTAGTTTGTGTTACTTA 4873
Qy 5059 CCATGGCAATTCGGGCTCTTGGCAACCAAAAGCAATGAAAACGGATGGAACAATTTTA 5118
Db 4874 CCATGGCAATAGTGGGCTTTTAGCCACTAAAAGTGTATGAACCTGGATGGACAACTGTTT 4933
Qy 5119 TGAGTACGACAGCTTTGGCGGCTGACAAATGTGACCTTTCCCTACTTGGCCAGGTGAGCAG 5178
Db 4934 TGACTATGACAGTGAAGGCTGCTGACAAATGTTACGTTTCCAACTGGAGTGGTCAAAA 4993
Qy 5179 TTTCCGAAGTGTATACAGACAGTTCAGTGCATGTCCAGGTAGAGACCTCCAGC---AAGGA 5235
Db 4994 CTTGCATGGGACATGGAACAGGCTATCACAGTGGACATTGAGTCATCTAGCCGAGAGA 5053
Qy 5236 TGATGTCAACATAAACCAACCACTGTGCTCCTCAGCGGCTTCTACACACTGCTGCAAGA 5295
Db 5054 AGATGTGACATCACTTCAAAATCTGCTCGATCGATTTCTTCTACACCATGGTTCAGA 5113
Qy 5296 CCNAAGTCCGGAACAGACTACTACATCGGGCCGATGGCTCTTGGCGCTGCTGCGCCAA 5355
Db 5114 TCAGTTTAAAGAAACAGCTACAGATTGGTTATGACGGCTCCCTCAGAAATTAATCTACGCCAG 5173
Qy 5356 CGGCATGGAGGTGGCGCTGCAGACTGAGCCCACTTGTGGCTGGCAACCGTCAACCCAC 5415
Db 5174 TGGCCTGGACTCACATCAACACAGAGCGCACGCTTGTGGCTGGCACCCGCTAATCCGAC 5233
Qy 5416 CBTGGCAAGAGAAATGTCACTGCTGCCATTCGACAAACGGCTCAAACCTGTGGTGGAGTGGCG 5475
Db 5234 GGTGGCAAAAGAAACATGACTTTGGCTGGCGAGAACGGTCAAAAATTTGGTGGAAATGGAG 5293
Qy 5476 CCAGCCCAAGAGAGCGCTCGGGCCAGGCTCACTGCTTGGCGCGCGGCTGCGGGTGCA 5535
Db 5294 ATTTCCAAAGAGCAAGCCCAAGGAAAGTCAATGCTTTGGCGCGAAGCTCAGGGTTAA 5353
Qy 5536 CAACCCAAATCTCTATCTCTGACCTTGTATCGCTGAACACGCAAGAGAAAGATCTATGA 5595
Db 5354 TGGCAGAAACCTCTTTCAGTTGACTTTGATCGAACACAAAGAGAAAGATCTATGA 5413
Qy 5596 TGACCAACCGAAAGTTCACTGCTGGATTCGTAACGACGAGGCGGGGGCGGCGGCTCTG 5655
Db 5414 CGACCAACCGTAAATTTCTACTGAGGATCGCTACGACACGCTCTGGGCAACCGGCTCTCTG 5473
Qy 5656 GTCAACCCAGCAGGAGCTGNAATGGTGTCAACGTGACATCTCCCTGGGGGTTACATTCG 5715
Db 5474 GCTGCCAAGCAGCAAGCTGATGGCCGTCAATGTCATCTATTCACAGGTCAAAATTCG 5533
Qy 5716 TGGCATCCAGAGGGGATCATGTCTGAAAGAAATGGAATACGACGAGCGCGCGCATCAC 5775
Db 5534 CAGCATCCAGCGAGGACCACTAGCGAGAAAGTAGATTATGACGAGCAGGGAGGATCGT 5593
Qy 5776 ATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATCTTATAGAAAGTCCATGGT 5835
Db 5594 GTCTCGGGTCTTTGCTGATGGTAAAACATGGAGTTTACACATATTTAGAAAAGTCCATGGT 5653
Qy 5836 GCTGCTACTACAGCAGGAGGAGTATATCTTTGAGTTTCGACAAAGATGACCGGCTCTC 5895
Db 5654 TCTTCTGCTTCAATAGCAGCGGAGTACATCTTTCGAATAGGATATGTTGGACCGGCTGTC 5713
Qy 5896 TTTCTGTGAGCATGCCCAACGTTGGCGGCGAGACATAGAGACCATCCGCTCAGTGGGCTA 5955
Db 5714 TGCATCAACATGCCAGGTGGCTGCCACACCATGACAGACCATCCGATCCATTTGGCTA 5773
Qy 5956 CTAAGAAAACATCTATCAGCCCTCAGGGCAATGCTCAGTCAATACAGAGCTTCACTGA 6015
Db 5774 CTAACCGCAACATATACAAACCCCGGAAAGAACGCTCCATCATCACGAGCTACAAACGA 5833
Qy 6016 GATGGGCACTCTTTCACACTTCTTACCTGGGCACTGGCGGAGGTTGATATACAGTA 6075
Db 5834 GGAAGGGCTGCTTCTTCAAAACAGCTTTCTTGGGTACAAGTGGAGGGTCTTATTTCAAATA 5893

Db 8036 GCAGGGCTACGACGGGTACTACGTACTCTCGTGGAGCAGTACCCCGAGCTGGCCGACAG 8095
QY 8296 CGCCAAACATCCACTTCATGAGACAGACGAGATGGCGCGGAGGTGAC 8345
Db 8096 CGCCAAACATCCAGTTCCTCGGACGACGAGATCGGCAGGAGGTAAC 8145

RESULT 12

US-10-038-854-41

; Sequence 41, Application US/10038854

; Publication No. US20040022781A1

; GENERAL INFORMATION:

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; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-230

; CURRENT APPLICATION NUMBER: US/10/038,854

; CURRENT FILING DATE: 2003-01-22

; PRIOR APPLICATION NUMBER: 60/258,928

; PRIOR FILING DATE: 2000-12-29

; PRIOR APPLICATION NUMBER: 60/259,415

; PRIOR FILING DATE: 2001-01-02

; PRIOR APPLICATION NUMBER: 60/259,785

; PRIOR FILING DATE: 2001-01-04

; PRIOR APPLICATION NUMBER: 60/259,814

; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: 60/279,832

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/279,833

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/279,863

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/283,889

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/284,447

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: 60/286,683

; PRIOR FILING DATE: 2001-04-25

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 411

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 41

; LENGTH: 8487

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-038-854-41

Query Match

40.7%; . Score 3398.8; DB 7; Length 8487;

Best Local Similarity 67.0%; Pred. No. 0; Mismatches 2362; Indels 102; Gaps 9;
Matches 5008; Conservative 0;

QY 880 CGGGCAGCTTCCTCTTCAAGCCCTGG--AGGCACCTCCCGCTCTTCTTCGACACACATCACC 936
Db 766 CAGGCATTTCCCTATTCAAAACAGGACAGTCAACAGCCACTGTTTCAGTACTGCAACCCC 825

QY 937 AGGGTACCACCTGACGTCCAGCACAGTGTACTCTCTCCGCCCCCGACCCCTCGCCCGCAG 996
Db 826 AGGATAGACAATGGCATCTGGCTCTGTTTATTTCACCACTACTCGGCCACTACTAGAAA 885

QY 997 CACCTTGGCCCGCGGCTTTAACTCAAGAGCCCTCAAGTACTGTAACCTGGAAGTG 1056
Db 886 CACCCTATCAAGAAGTGCTTTTAAATTCAGAAGTCTTCANAAGTACTGTAGCTGGAATG 945

QY 1057 CGCAGCCCTGAGCGCATCGTCACTCTCAGCCACTCTGTCATCTCTGTCGTCATCTTTGT 1116
Db 946 CACTGCACTGTGTCCGTAGGGGTCTCGGTGCTCTCTGCAATACTCTCTCTTATTTAT 1005

QY 1117 GGCCATGCACTGTTTGGCTTAACTGGCACTCTGAGCCGATGGAGGGGAGATGTATGA 1176
Db 1006 AGCAATGCATCTTTTGGCTCACTGGCAGCTACAGCAGACTGAAATGACACATTTGA 1065

QY 1177 GATCAGGAGGACACAGCCAGTGGCTGTGTGCCAACCGAGCTCTCCCTATACCCCTC 1236
Db 1066 GA-----ATGGAAGAGTGAATTTCTGATACCATGTCACCAACAAACACTGTGTCTTACCTTC 1119

QY 1237 AGGGGCACTGGCTTAGAGACCCCTGACAGGAAGCAAGGACCAAGCAAGCAAGCAAGCC 1296
Db 1120 TGGAGACA-----ATGGAAGATTT 1137

QY 1297 CAGTAGTTCTTTCCAGAGGACAGATTTTCATAGATTTCTGAGAAATTTGATGTGGAAAGCG 1356
Db 1138 AGTGTGATTTAGCAAGAAATAACACCATAGATTTCCGAGAACTTGTATTTGCCGAG 1197

QY 1357 AGCTTCCCAAGATTTCTCTGGCACTTTCTGGAGATCTCAAGTGTTCATAGACCATCC 1416
Db 1198 AGCAATTTCAAGAGATTTCTCCCGGATCTTCTGGAGATCACAGCTCTTCTTATTCATCAGCC 1257

QY 1417 TGTGCATCTGAATTCATATGTCTCTGGAAGGAGCCCTGTTGGCATTTATGGCAG 1476
Db 1258 ACAGTTTCTAAATTTCAATATCTCTTCAGAGGATGATGATTTGGAGTATATGGCCG 1317

QY 1477 AAAAGSCCTCCCTCTTCATACATACAGATTTGATTTGAGCTGCTGGAGCGAGAG 1536
Db 1318 GAAAGCTTACCGCTTCCCATACTCAGTATGACTTCGTGGAGCTCTGGATGGCAGCAG 1377

QY 1537 GCTCTTAACCCAGAGGCGGAGCCTAGAGGGGACCCCGCGCAGTCTCGGGAACTGT 1596
Db 1378 GCTGATGTCAGAGACGAGCGGAGCTGCTTGAGACGAGAGCGCGGCGGAGCGAG 1437

QY 1597 GCGCCCTCCAGCATGACAGAGCTTCATCCAGTATTTGGATTCAGGAATCTGGCACTT 1656
Db 1438 ATCCGTGAGCTTTCATGAGCGCGCTTATCCAGTACTTGGATTTCTGGATCTGGCATCT 1497

QY 1657 GCGTTTTTACATGACGGAAGAGGATCAGAGTGGTTTCTCTTCTCACCCTGCCATTGA 1716
Db 1498 GCGTTTTTATATGATGGGAAATAATGCAGACGAGGTGCTTTTAAATACCATTTGTTATAGA 1557

QY 1717 GTCGGTGGATTAAGTGGCCAGCAACTGCTATGTCATATGTCATCTCTGGGACCTG 1776
Db 1558 GTCTGTGGTGGATGTCCCGGAAATTTGCCATGGAATGAGAAATGCGTTTCTCGAACTTG 1617

QY 1777 CCACTGCTTCTGGGTTTCTGGGCCCGAGCTGTGGCAGAGCCCTCTGCCCCCTGCTCTG 1836
Db 1618 CCATTGTTTCCAGGATTTCTGGGTCCGATTTCTCAAGAGCGCGCTGTCTCAGTGTATG 1677

QY 1837 TAGCGGAATGSCCAATACATGAAAGGAGATGCTTTGTGCCACAGTGGCTGGAAAGCGCG 1896
Db 1678 TAGTGGCAACGGGACAGTATCCCAAGGGCGCTGCTGTGTTTCAGCGGCTGGAAAGGCGAC 1737

QY 1897 TGAGTSCGATGTGCCCAACCAACAGTGTATCGATGTGGCTGTCAGCAACCATGGCACCTG 1956

Db 1738 CGAGTGTGATGTGCCGACTACCCAGTGTATTGACCCACAGTGTGGGGTCTGTGGATTTG 1797
Qy 1957 CATACGGGCACTGTCATCTGCAACCTTGGCTACNAGGGCCAGAGCTGTGAGGAATGGA 2016
Db 1798 TATCATGGGCTCCTGTGCTTGCATCTCAGGATACAAAGGAGAAAGTTGTGAAGAAGCTGA 1857
Qy 2017 CTGCATGACCCACATGTTTCAGGCGGGGTGTCTGCGTGAGAGCGGAATGCCATTGGCTT 2076
Db 1858 CTGTATAGACCTTGGGTGTCTTAATCATGTGTGTGTATCCACGGGGAAATGTCACTGCAG 1917
Qy 2077 TGTGGGATGGGAGGACCAAACTGCGAGACCCCAAGGCCCAATCTCTTAGACCAAGTGTTC 2136
Db 1918 TCCAGGATGGGAGGTAGCAATTGTGAATACTGAAGACCATGTGTCCAGACCAAGTGTCTC 1977
Qy 2137 AGGCCACGGAACCTTCTCCCGGACACCGGGCTTTGCAAGTTGTGACCCCAAGCTGGACTGG 2196
Db 1978 CGGCCACGGAAGCTATCTTCAAGAAAGTGGCTCTCTGCACGTTGTGACCCCTAACTGGACTGG 2037
Qy 2197 ACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGCGCTGTGCGTAGG 2256
Db 2038 CCCAGACTGTCTAAACGAAATATGTTCTGTGACTGTGGCTCACACGGCGTTTGCATGGG 2097
Qy 2257 GGGCACCTCGCGCTCGAGGATGGCTGGATGGGGCAGCCTGCGACCAAGCGGGCTTGCCA 2316
Db 2098 GGGGAGGTGTGCTGTGAAGAAGGCTGGACGGGCCAACTGTAACTCAGAGAGCCTGCCA 2157
Qy 2317 CCCGGCTGTGCCGAGCATGGGACCTGCGGGCAGCGGCAAGTGCAGTGCAGGCCCTGGCTG 2376
Db 2158 CCCCGCTGTGCGGAGCAGCGGACCTGCAAGGATGGCAAGTGTGAATCGACGCCATGGCTG 2217
Qy 2377 GAATGGCGAACTCCACCATCGCTCACTATCTGATAGGTAGTTAAAGAGGGTTTGCC 2436
Db 2218 GAATGGAGACACTGCATCTC-----GAGGGTTGTCC 2250
Qy 2437 TGGGTTGTGCAATGGCAACGGCAGATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTG 2496
Db 2251 TGGTCTGTGCAACAGCAATGGAAGATGTACCTCGGACCAAAATGGCTGGCATTTGTGTG 2310
Qy 2497 CCAGCTGGCTGGAGAGAGCTGGCTGTGACACTTCCATGGAGACTGCTGGGTGACAG 2556
Db 2311 CCAGCTGGATGGAGAGGAGCGGCTGTGACGTAGCCATGGAGACTTTTGCACAGATAG 2370
Qy 2557 CAAAGACAATGATGAGATGGCTGTGTGACTGCAATGACCTGACTGCTGCTCCAGCC 2616
Db 2371 CAAAGACAATGAGAGATGAGACTCATTTGACTGCAATGATCCCGATTGCTGCCTACAG 2430
Qy 2617 CCGTGGCCATATCAACCCGCTGTGCTTGGCTCCCTTAACCTCTGGACATCATCCAGGA 2676
Db 2431 TTCCCTGCCAGATCAGCCCTATTGTCCGGGACTGCGCGATCCTCAGGACATCATTAGCCA 2490
Qy 2677 GACAGAGTCCCTGTGTACAGCAGAACCTACACTCTCTTATGACCGCATCAAGTTCTT 2736
Db 2491 AAGCCTTCAATCGCCTTCTCAGCAAGCTGCCAAATCCTTTTATGATGAATCAAGTTTCT 2550
Qy 2737 CGTGGCAGGACACGACGACATAAATCCCGGGGAGAACCCCTTTGATGGAGGCATGC 2796
Db 2551 TATAGATCTGTATAGACCCATGTTATACCTGGAGAAAGTCTTTCAATATAGAGCCTTGC 2610
Qy 2797 TTGTGTTATTCTGTGGCCAAAGTGATGACATCAGATGGAAACCCCTCGTTGGTGTGAACAT 2856
Db 2611 ATCTGTATCAGAGGCCAAGTACTGACTGCTGATGGAACTCCACTTATTGGAGTAAATGT 2670
Qy 2857 CAGTTTTGTCAATAACCTCTCTTTGGATATACATCAGCAGGCAAGATGGCAGCTTTGA 2916
Db 2671 CTCGTTTTTCCATTACCCAGAAATATGGATATATTAATACCCCGCAGGACGGAATGTTGA 2730
Qy 2917 CTGTGTGACAAATGCGGCATCTCCATCATCTCGGGTTCCAGCGGCACCTTTTCATCAC 2976
Db 2731 CTTGGTGGCAATGTTGGGCTCTCTAACTTTGGTATTTGAAAGATCCCCATTCCTCAC 2790
Qy 2977 ACAGGACGACACCTGTGCTGCCATGGGATCGCTTCTTTGTCATGGAAACCATCATCAT 3036
Db 2791 TCAGTATCATCTGTGTGGATTCCATGGAAATGCTCTTTTATGTGATGGATACCCCTAGTCAT 2850

Qy 3037 GAGACATGAGGAGAAATGAGATTTCCAGCTGTGACCTGAGCAAAATTTTCCGCCCCCAACCC 3096
Db 2851 GGAGAAAGAGAGAAATGACATTTCCAGCTGTGATCTCAGTGGATTCGTGAGGCCAAATCC 2910
Qy 3097 AGTGTCTCTCTCCATCCCACTGACGTCTTTCGCCAGCTCTCTGTGCAGAGAAAGGCCCAT 3156
Db 2911 CATCATTTGTGTATCATCTTTATCCACTTTTATCCAGATCTTCTCTGAGACAGTCCCAT 2970
Qy 3157 TGTGCCGGAATTCAGGCTTTGAGGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCT 3216
Db 2971 CATTTCCGAAACACAGGTACTCCACGAGGAAATCAAAATTCAGGAAACAGATTTGAAACT 3030
Qy 3217 GAGCTACTCTGAGCAGCGGACCCCTGTGCTACAAATCTGTCTCTGAGGATCAGCCTCACCCA 3276
Db 3031 CTCCTACTTGAATTCCAGAGTGCAGGGTATAGTCAAGTCTCAAGATCACCATGACCCA 3090
Qy 3277 CCCAGCATCCCCCTTCAACCTCATGAAGTGCACCTCATGGTAGCGGTGGAGGCCGCT 3336
Db 3091 GTCTATTATTCCATTTAATTTAATGAAGTTTCATCTTATGGTAGCTGTAGTAGGAAGCT 3150
Qy 3337 CTTCAGAAAGTGTTCCTGTGAGCCCGCAGACCTGTCTCTATTATTTTCAATTTGGGACAGAC 3396
Db 3151 CTTCCAAAAGTGGTTTCTGCTCACCAACTTGGCCTATACCTTTCATATGGGATAAAAC 3210
Qy 3397 AGAGCTCTACAACAGAGAGGTGTTTGGCTTTTCAAGAGCCCTTTGTTCCGTGGGTATGA 3456
Db 3211 AGATGATATATATCAGAAAGTCTATGTTCTATCTGAAGCTGTGTGTCAAGTGGATGA 3270
Qy 3457 ATATGAATCTCGCCAGATCTAATCTGTGGGAAAAAGAACAAACAGTGTGCAAGGGCTA 3516
Db 3271 GTATGAGTGTGTTTGGACCTGACTCTGTGGAAAAAGAGGACTGCCATTTCTGCAAGGGCTA 3330
Qy 3517 TGAATTTGACGCTGCCAAGCTTGGAGGATGGAGCTTAGACAAACATCATGCCCTCAACAT 3576
Db 3331 TGAATGGATGCTGCTCCAAACATGCGTGGACATTAGATAAAACATCAGTGTGATGT 3390
Qy 3577 TCAAAGTGGTATCTCTGCACAAAGGAAATGGGGAAACAGTGTGTGTCTCAGCAGCCCTCC 3636
Db 3391 ACAGAACGTTATCTGTACAAAGGAAACGGGGAAACAGTGTATCTCCCAGCAGCCTCC 3450
Qy 3637 TGTCAITTTGGGAGCATATGGGCAATGGCGCCGGAGAGCATCTCTGCCCCAGTGCAG 3696
Db 3451 AGTCGTGAGTAGCATCATGGCAATGGCGAAGCGCAGCAGCATTTCTGCCCCAGTTCGAA 3510
Qy 3697 CGGCTTCTGACGGCAACAGCTCTTGGCCCGCAGTGGCCCTCACCTGTGCTCTGACGG 3756
Db 3511 TGGTCAAGCTGATGTTAAAGTTACTTGGCCCCAGTGGCGCTAGCTTGTGGGATCGATGG 3570
Qy 3757 GAGCTCTATGTGGGTGATTTCAAATACATTAGAAAGGATCTTCCCTCTGGAAATGTCAAC 3816
Db 3571 CAGTCTGTACGTAGCGCATTTCAACTACGTGGCGGGATATTCCCTTCTGGAAATGTAAC 3630
Qy 3817 CAACATCTTAGAGCTGAGGAATAAGATTTTCAGACATAGTACAGTCCAGCAGACAAATA 3876
Db 3631 AAGTGTCTTAGAACTAAGAAATAAAGATTTTAGACATAGCAGCAACCCAGCTCATAGATA 3690
Qy 3877 CTACTGCGCCACAGACCCCATGATGGGGCGTCTTCTTCTGACAGCAGACAGCCGCG 3936
Db 3691 CTACTTTGCAACGGATCCAGTCACGGGAGATCTGTACGTCTTCTGACAAACACCCCGAG 3750
Qy 3937 GGTCTTTAAAATCAAGTCCACTGTGGTGGTGAAGGACCTTGTCAAGAACTCTGAGGTTGT 3996
Db 3751 AATTTATCGCCCAAGTCACTTACGGGGCAAAAGACTTGAATAAAATGCAAGTCTGT 3810
Qy 3997 TGGCGGAGCAGGTGACCAAGTCCCTCCCTTTGTATGACACTCGCTCGGGGATGTGGGAA 4056
Db 3811 GCGAGGACAGGGGAGCAATGCCCTTCCCTTTGACGAGCGGAGATGTGGGGATGGAGGAA 3870
Qy 4057 GGCCACAGAGCCACACTCACCNAATCCAGGGGTATTACAGTGGACAGATTTGGGCTGAT 4116
Db 3871 GGCCGTGGAGGCCACACTCATGAGTCCCAAGGAAATGGCAGTTGATTAAGAAATGGATTAA 3930

| | | | |
|----|------|---|------|
| Db | 6088 | ATTTGACTATAGCTATAGCAACAGCTTTTCGAGTGCACGAGCATGCGGGTGTGATCAATGA | 6144 |
| Qy | 6334 | GACCCCACTGCCCATTTGATCTCTATCGCTATGATGATGTGTCAAGCAAGACAGACAGATT | 6393 |
| Db | 6148 | AACGCCACTGCCTATTGATCTGATCAGTTTGATGACATTTCTGGCAAGTTTGACGATT | 6207 |
| Qy | 6394 | TGGAAAGTTTGGGTGTCAATTTACTATGACATTAACCAAGATCATCACACGCTGTCAATGAC | 6453 |
| Db | 6208 | TGGAAGTTTGGAGTTATATATTATGATATTAACACGATCATTTTCTACAGCTGTAAATGAC | 6267 |
| Qy | 6454 | CCACCAACAGCATTTTGATGCATATGGCAGGATGAAGGAAGTGCAGTATGAGATCTTCGG | 6513 |
| Db | 6268 | CTATACGAAGCACTTTGATGCTCATGGCCGTATCAAGGAGATTCAATATGAGATATTTTCA | 6327 |
| Qy | 6514 | CTCCGTCAATGACTGGAATGACCGGTCCAGTATGATAACATGGGGCGAGTGTGAAGAAGGA | 6573 |
| Db | 6328 | GTCGCTCATGTACTTGGATTACAAATTCAGTATGATTAACATGGGTCCGGTAAACCAAGAGA | 6387 |
| Qy | 6574 | GCTGAAGGTAGGACCCCTACGCGCAATACCACTCGCTACTCCTCATGAGTATGATGCTGACGG | 6633 |
| Db | 6388 | GATTAAAAATAGGGCCCTTTGCCAACACCCACCAATAATGCTTATGAAATATGATGTTGATGG | 6447 |
| Qy | 6634 | CCAGCTGCAGACAGTCTCCATCAATGACAGGCCACTCTGGGGCTACAGCTACGACCTCAA | 6693 |
| Db | 6448 | ACAGCTCCAAACAGTTTACCTCAAATGAAGAAAGATAATGTGGCGGTACAACTACGATCTGAA | 6507 |
| Qy | 6694 | TGGAAACCTGCACATTTACTGAGCCCTGGGAAACAGTGACGGCTCACACCCTACGGTATGA | 6753 |
| Db | 6508 | TGGAAACCTCTCATTTTACTGAAACCCAGTAAACAGTGCCTGCTGACACCCCTTTCGCTATGA | 6567 |
| Qy | 6754 | CATCCGGACCGCATCACTCGGCTGGGTGAGCTGCAATACAAGATGATGAGGATGGCTTT | 6813 |
| Db | 6568 | CCTCGAGACAGATCACTCGACTGGGTGATGTTTCAATATACGGTTGGATGAAGATGGTTT | 6627 |
| Qy | 6814 | CCTGAGGACGGGGGGGGTGNATTCATTGTGAGTACAACTCAGCTGGCCCTGCTCATCAAGGC | 6873 |
| Db | 6628 | CCTACGTCAAAGGGGCGACGGAAATCTTTGAAATATAGCTCCAAGGGGCTTTCTAATCGAGT | 6687 |
| Qy | 6874 | CTACAAACGGGCTCGCAGCTGGAGTGTCAAGTACCGCTACGATGGCCCTGGGGGGGGCGGT | 6933 |
| Db | 6688 | TTACAGTAAAGGCAGTGGCTGGACAGTGATCTACCGTTTATGACGGCTCTGGGAAGGGCGTGT | 6747 |
| Qy | 6934 | GTCAGCAAGACAGCACACGCCACCACTGCACTTCTTCTATGCGACAGCTGACCAACCC | 6993 |
| Db | 6748 | TTCTAGCAAAACCAAGTCTAGACAGACCTCGAGCTTTTTTATGCTGACTTAACCTATACC | 6807 |
| Qy | 6994 | CACCAAGGTCAACCACTGTACAAACACTCCAGCTCTGAGATCACTCCCTCTACTACGA | 7053 |
| Db | 6808 | CACCTAGGATTACTCATGTCTACAAACCAATTCGAGTTTCAGAAATTAACCTCCCTGTATTATGA | 6867 |
| Qy | 7054 | CTTCGACGACACCTCTTTGCGATGGAGCTCAGCAGTGGTGTAGTGTGATTTACATAGCTTG | 7113 |
| Db | 6868 | TCTCCAAAGGACATCTTTTGGCATGGAAATCAGCAGGTGGGGATGAAATCTCATATTTGCATC | 6927 |
| Qy | 7114 | TGACAAACATCGGGACCCCTCTTGCTGTCTTTAGTGGAAACAGGTTTGATGATCAAGCAAAAT | 7173 |
| Db | 6928 | GGATAACACAGGGACACCACTGGCTGTGTTCACTAGTAGCAATGGGCTTATGCTGAAACGAT | 6987 |
| Qy | 7174 | CCTGTACACAGCCTATGGGGAGATCTACATGGATACCAACCCCAACTTTTCAGATCATCAT | 7233 |
| Db | 6988 | TCAGTACACTGCATATGGGGAATCTATTTTGACTCTAATATTGACTTTTCAACTGGTAAAT | 7047 |
| Qy | 7234 | AGGCTACATGGTGGCCTCTATGATCACTCAACCAAGCTTGTCCACATGGGGCGGGGAGA | 7293 |
| Db | 7048 | TGGAATTTCTAGTGGTGGCTGTATGATGCCACTCACCAATTAATCCACTTTTCGAGAAAGAGA | 7107 |
| Qy | 7294 | TTATGATGTGCTGGCCGGAGCTGGAGCTAGCCCCAGACCAAGCTGTGGGAAGCACCTTAG | 7353 |
| Db | 7108 | TTATGACATTTTGGCAGACGGTGGACAAACACCTGACATAGAAATCTGGA---AAGAAAT | 7164 |
| Qy | 7354 | TAGCAGCAACGTCAATGCCCTTTTAACTCTATATGTTCCAAAAACAAACCCCATCAGCAA | 7413 |
| Db | 7165 | TGGGAAGGACCCAGCTCCTTTTACTTTGTGATGTCATGTTTAGAAATAACAACTCTGCAAGCAA | 7224 |

| | | | |
|----|------|---|------|
| Qy | 7414 | CTCCAGGACATCAAGTGTCTTCAATGACAGATGTTTAAACAGCTGGCTGCTCACTTTGGATT | 7473 |
| Db | 7225 | AATCCATGACGTGAAAGATTACATACAGATGTTTAAACAGCTGGCTGGTACATTTGGTTT | 7284 |
| Qy | 7474 | CGAGCTACAAACGTGATCCCTGGTTATCCCAAACAGACATGGATGCCATGGAAACCTC | 7533 |
| Db | 7285 | CCATCTGCACAAATGCTATTCTCTGGATTCCCTGTTCCTCAAAATTTGATTTAAACAGAACCTTC | 7344 |
| Qy | 7534 | CTACGAGCTCATCCACACACAGATGAAAAACGAGGAGTGGGACAAACAGCAAGTCTATCCT | 7593 |
| Db | 7345 | TTACGA-----ACTTGTGAAGAGTCAGCAGTGGGATGATATACCGCCCATCTT | 7392 |
| Qy | 7594 | CGGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGGCCTTTGTCACTTAAAGACGGTTTGA | 7653 |
| Db | 7393 | CGAGTCCAGCAGCAAGTGGCGCGCAGGCCAAGGCCTTCCTGTCTGCTGGGAAGATGCG | 7452 |
| Qy | 7654 | CGAGCTTATGGCTCCACAATCACACAGCTGCCAGCAGGCTCCAAAGACCAGAAAGTTTGC | 7713 |
| Db | 7453 | CGAGGTGCAGGTGAGCCGCGCGCGGCCGCGC-----GGCGCGCAGTCTCTGGCTGTGGTTCGC | 7509 |
| Qy | 7714 | ATCCAGCGGCTCAGTCTTTGGCAAGGGGGTCAAGTTTGCCTTTGAAGGATGGCGGAGTAC | 7773 |
| Db | 7510 | CAGGTCAGTCTGCTCATCGGCNAAGGCGTCATGTCGCCGTCAGCCAGCGCGCGTGCA | 7569 |
| Qy | 7774 | CACAGACATCATCAGTGTGGCCAAATGAGATGGCGAAAGGTTGTGCCATCTTGAAACA | 7833 |
| Db | 7570 | GACCAACGTGCTCAACATCGCCAAACGAGGACTGCATCAAGGTGGCGGCCGTGCTCAACAA | 7629 |
| Qy | 7834 | TGCCCACTACCTAGAACTCGACTTCACCATTGATGGGGTGGATACCCATTACTTTGT | 7893 |
| Db | 7630 | CGCTCTTCTACCTGGAGAACTGCACTTCCACATCGAGGGCAAGGACACGCATCTTTCAT | 7689 |
| Qy | 7894 | GAACACAGGACCTTCAGAAAGGTGACCTGGGCCCTCTGGGCCCTCAGTGGGGGGCGGCGAAC | 7953 |
| Db | 7690 | CAAGACCAACCCCGCAGAGCGACTTGGGCAACGTCGCGTTGACCGCGCGCGAAGGC | 7749 |
| Qy | 7954 | CTTGGAGAAATGGGGTCAACGTCATCTGTGTCCAGATCAACACAGTACTTTAATGGCAGGAC | 8013 |
| Db | 7750 | GCTTGGAGAACGGCATCAACGTTACCGTGTGCGAGTCCACACGGTGGTGAACGGCAGGAC | 7809 |
| Qy | 8014 | TAGACGCTACACAGATCCAGTCCAGTACGGGGACCTGTCTTGAACACACGCTACGG | 8073 |
| Db | 7810 | GCGCAGGTTTCGGGAGCGTGAGATGAGTTCGGCGCGCTGGCGCTGCGCTGCGCTACGG | 7869 |
| Qy | 8074 | GACAACTTGGATGAGGAGAAAGCACGGTCTCTGGAGCTGGCCCCGCGCAGAGACCGTGGC | 8133 |
| Db | 7870 | CATGACCTTGGACGAGGAGNAGGCGCGCATCTCTGAGCAGGCGCGCAGCGCGCTCGC | 7929 |
| Qy | 8134 | CCAAGCGTGGCCCCGCGAGCAGAGAGATGTCGGGGAAGGGGAGGAAGGCTCTCGGGCCCTG | 8193 |
| Db | 7930 | CCGGGCTCTGGGCGCGCAGCAGCGCGCTGCGCACGCGCAGGAGGGCGCGCGCTCTG | 7989 |
| Qy | 8194 | GACAGAGGGGAGAACACAGCTGCTGAGCACAGCGCGGGTGCAGGCTACGACGGCTT | 8253 |
| Db | 7990 | GACGAGGGCGAGAACGGCAGCTGCTGAGCGCGCGCAAGTGTGAGGGCTACGACGGTA | 8049 |
| Qy | 8254 | TTTTCGTGATCTCTGTGAGCAGTACCAGAACTGTGACAGCGGCCAACCAATCCACTT | 8313 |
| Db | 8050 | CTACGTACTCTCGGTGAGCAGTATCCCGCAGCTGGCCGACAGCGCCAAACATCCAGTT | 8109 |
| Qy | 8314 | CATGACACAGACGAGATGGCGCGGAGGTGAC | 8345 |
| Db | 8110 | CCTTGGCGCAGACGAGATCGGACGAGAGTAAAC | 8141 |

RESULT 13
US-09-808-602-78
; Sequence 78, Application US/09808602
; Patent No. US2002015115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma

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; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 78
; LENGTH: 8689
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-09-808-602-78

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Query Match          40.7%; Score 3397.8; DB 3; Length 8689;
Best Local Similarity 64.8%; Pred. No. 0;
Matches 5469; Conservative 0; Mismatches 2712; Indels 254; Gaps 19;

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| | | | |
|----|-----|---|-----|
| QY | 35 | ATGAGCTGAGAGAGAGAGCTTACCGCTCGCTGACCGCGCGCGCGAGCGCGC | 94 |
| Db | 133 | ATGGATGTGAAGATCGGCGACATCGCTCTTTGACCAAGGGACGGTGTGCAAGGAGTGT | 192 |
| QY | 95 | CGCTACACAGCTCTGTCGCGGACAGCGAGGAGGGGCAAG-CCCGCGAGAAATCGTAC | 151 |
| Db | 193 | CGCTACACAGCTCTCTCTGGACAGTAGAGACTGCGGTGCGCCAGCAGAGTCTCTAC | 252 |
| QY | 152 | AGCTCCAGCGAGACCTCTGAAGGCTACGACCGAGCGCCGCTAGCCTATGGAGCGCG | 211 |
| Db | 253 | AGTTCCAGTCAGACCTCTGAAGCTTATGACCATGACAGAGAGTGCATATGGAACCGA | 312 |
| QY | 212 | GTCAGGACATTTGCGCGAGGAGGCGAGGAATTCGCGCAGAGTGCACACTTCAC | 271 |
| Db | 313 | GTCACAGACTGGTGACCGGGAGTCCGATGAGTTTCTAGACAAGGGCTAATTTTACC | 372 |
| QY | 272 | CTCGGGAGCTGGGGCTGGAAGAGTAAAGCCCGCTCACGGGACCTGTATCCGACAGAC | 331 |
| Db | 373 | CTGGCAGANTTGGGAATCTGGAG-CCCTCCCGACACCGAAGTGTACTGTTCGAC | 429 |
| QY | 332 | ATTGGCTGCCCCAATCGCGCTACTCCATGGGGCTGGCTCTGATGCCGACATGGAGGT | 391 |
| Db | 430 | ATGGGGATCTCCACAGGGCTACTCTCTGAGCACTGGGTCTGATGGGACTCGGACAC | 489 |
| QY | 392 | GACACGTGTCTCCCTGAGACCCCGTGGGTCTGTGGGCGGGAGCACACGGTCAAGG | 451 |
| Db | 490 | GAGGGAGGATGTCTCCAGAACATGCCATCAGACTGTGGGGACGAGGGATAAATTCAGG | 549 |
| QY | 452 | CGAGCTCTGCTGTCGCGCGGCGCAATTCCAATCTCACTTCACCGACACCGAGCAT | 511 |
| Db | 550 | CGCAGCTCTGCTTGTCCAGCGCGAGAACTCAGCCCTTACTCTGACTGATTTCTGACAAT | 609 |
| QY | 512 | GAAACACTGAGACTGATCATTCGGGCGGCC-TCGAGAACACCGCGGCTCGGAC | 567 |
| Db | 610 | GAAATAAATCGGATGACGACAATGTGTCGACCCATTCACATCTCTGTAGCCTC | 669 |
| QY | 568 | CGCGCGCGCGCTCTCGACGCGCCACACCCCGAACACGACACACCGGCGCTCCATTA | 627 |
| Db | 670 | CTCCCATCTGTCTGAGCTGCTAGCTCCCAATAATCTCCACAGTTAGTGC-AGATGCC | 728 |
| QY | 628 | CTCCCTGACCGGGGCACTTTCAGCGGAGAGCAACCCAGGCCG-674 | 674 |
| Db | 729 | ATTGCTAGACAGCAACACTTCCATCAGATCATGGACACCAACCCCGATGAGGAATTC | 788 |
| QY | 675 | -----CCCCACGAGCACCTCTCTCCGGAGAGCCCTCTCGCGGCGCGGCC | 722 |
| Db | 789 | CCCTAATTCATCTGCTCAGAGCATGCTCAGGGCCCCAGCAGCCTCCAGTAGTGGGCC | 848 |

| | | | |
|----|------|---|------|
| QY | 723 | AGGAGCCTGCCACGCCAGGAGAACTGGCTGTCTCAACAGCAACATCCCCCTGGAGCCA | 782 |
| Db | 849 | TCCGAAACACACACAGCCAGTCAACGCTGAGGGCCCCCTCTGCCACCTCTCATAAACACAC | 908 |
| QY | 783 | GGAACTTAGGCAAGCAGCACTTCCTAGGACATTTGAGGACATTCATTTGAGATGACA | 842 |
| Db | 909 | CCTGTCCCAACCACTCTCTCTGCCAACTCCCTCTCAACAGAACTCACTACCAATCGCG | 968 |
| QY | 843 | TTCTCGGCGCTCCGSCCA-861 | 861 |
| Db | 969 | GAGTCAATCCAGCGCCCCAGCTCTGACCCCAATGACCTGGGCCACACGCGGAGTCCGT | 1028 |
| QY | 862 | -----TGATGGGGCTTTACAGTGAAGCGGCACTTCCT | 891 |
| Db | 1029 | TCAGCTCCAGGACAGCTGGGTGTGAACGAGTGGCGCTGCGAGACGCGGCACTTCCT | 1088 |
| QY | 892 | CTTCAA-CCCTGGAGGACCTCCCGCTCTTCTGCACCAATCACCAGGTTACCACT | 948 |
| Db | 1089 | CTTCAAGAGCTCTCCGGAAGCACACCCCTGTTTTCAGCAGCTCTTCTCCAGGATACCCCT | 1148 |
| QY | 949 | GAGCTCCAGCAGTGTACTCTCTCGCGCCGACCCCTGCGCGCAGCAGCTTCGCGCG | 1008 |
| Db | 1149 | GACCTCAGGACCGTTTATACACCAACCCCGCTGCTGCCACGGAATACATTTCTAG | 1208 |
| QY | 1009 | GCGGCTTTTAACTCAAGAAAGCCCTCAAGTACTGTAACTGGAAGTGGCAGCCCTGAG | 1068 |
| Db | 1209 | GAGGCTTCAAGCTGAAGAAACCTTCAAACTATCGAGTTGGAATGGCCGCGCTGTC | 1268 |
| QY | 1069 | CGCATCTGTCATCTCAGCCTCTCTGTCATCTCTGTCGTCGTCATCTTTGTGGCCATGCACT | 1128 |
| Db | 1269 | TGCCATTTGCGCTCTCTCTGCGCACTTTTGTGGCCATTTTGTGGCCATTTTATGATCAATGCACT | 1328 |
| QY | 1129 | GTTTGGCTTAACTGCGACCTGCGAGCGGATGGAGGGGAGATGATGAGATCAGCGAGGA | 1188 |
| Db | 1329 | GCTCGGACTCAATTTGGCACTCCAGCGCGGAGATGAGACACCTTTTAACT-ATGG | 1382 |
| QY | 1189 | CACAGCAGCAGTGTGGCTGTGCAACCGACGCTCTCCCTATACCCCTCAGGGGCACTGG | 1248 |
| Db | 1383 | CGTAAGGACCGGCTTACAGGAAACGATGATGTCGCAACAGTGCCTCTCGAGGCAAGT | 1442 |
| QY | 1249 | CTTAGAGACCCCTGACAGGAAAGCAAGCAACAGAAAGAAAGCCAGTAGTTTCTT | 1308 |
| Db | 1443 | GCCCTGCTGTTGAAAA-1459 | 1459 |
| QY | 1309 | TCCAGAGGACAGTTTCTATAGATTTCTGAGAAATGATGTGGAAAGCGAGCTCCACAGAA | 1368 |
| Db | 1460 | -----ACAGCAGCATAGACAGCGCGGAGGAGAGTGGTGCAGCGGTGACACAGGA | 1511 |
| QY | 1369 | GATTCTCTCTGGCACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTCTGTGATCTGAA | 1428 |
| Db | 1512 | AGTCCACACAGGGGTGTTTGGAGGTCAGATTCACATCAGTCAGCTCAGTTCTTAAA | 1571 |
| QY | 1429 | ATTCAATGTCTCTGGGAAAGCAGCCCTGGTGGCATTTATGGCAGAAAGGCTCC | 1488 |
| Db | 1572 | GTTCACACATCTCCCTGGGAAAGATGCCCTCTTCGGCGTCTACATAGAGAGAGACTGCC | 1631 |
| QY | 1489 | TCCTTACATACAGTTTTCAGCTTTGAGCTGCTGGAGCTGCTGGAGGAGGCTCCTAACCCA | 1548 |
| Db | 1632 | ACCATCTCATGACAGTATGACTTTCATGGAACCCCTGGACGGAA-----A | 1676 |
| QY | 1549 | GAGGGCGGAGGCTTAGAGGGGACCCCGCGCAGTCTCGGGGAACTGTGCCCCCTCCAG | 1608 |
| Db | 1677 | GGAAAGTGAGGTGGTTCAGTTCACCCAGGGAACCGCGGAGCATCCAGACCTGTGCA | 1736 |
| QY | 1609 | CCATGAGACAGGCTTATCCAGTATTGGATTCAGGAATTCGGACCTTGGCTTTTACAA | 1668 |
| Db | 1737 | GAACGAGGCTGTCTCGTGCAGTACTTGGATGTTGGGCTGTGGCAGCTCGCTTCTACAA | 1796 |
| QY | 1669 | TGACGGAAGGAGTTCAGAGTGTTCCTTCTTCAACCACTGCCATTTGAGTTCGGTGATA | 1728 |
| Db | 1797 | TGACGCGCAGGACGAAGGAGATGGTCTCTTCAATACGGTTGTCTTAGATTTCAGTGCAGGA | 1856 |

| | | | |
|----|------|---|------|
| QY | 1729 | CTGCCCAAGCAACTGCTATATGGCAATATGTTGACTGCAATCTCTGGGACCTTGCACATGCTTTCCT | 1788 |
| Db | 1857 | CTGTCCAGAAACTGCCACGGGAACGGCGAATGCGTGTCTGGACTGTGTCACTGTCTTCCC | 1916 |
| QY | 1789 | GGGTTTCTCGGCCCCGACTGTGCGAGAGCCCTCTGCCCGCTCTCTGTAGCGGAATGG | 1848 |
| Db | 1917 | AGGATTTCTAGTGGAGACTCGCTTAAAGTCGCTTGCCTTCTCTGTGAGTGGGAATGG | 1976 |
| QY | 1849 | CCAAATACATGAAGCGCAGATGCTTTTGCCACAGTGGCTTGGAAAGCGCGCTGAGTGCAGTGT | 1908 |
| Db | 1977 | ACAGTATTTCCAAAGGACATGCCAGTGTCTACAGTGGCTGGAAAGGAGCAGAAATGCCAGTGT | 2036 |
| QY | 1909 | GCCCAACCAACAGTGTATCGATGTGGCTTCGACAGCAACATATGGCAGCTGTGCATCAGGGCAC | 1968 |
| Db | 2037 | GCCCATGAACCAAGTGCATCGATCTCTTGTGGGGGCCACGGGTCTCTGCATATGATGGGAA | 2096 |
| QY | 1969 | CTGCATCTTGCAACCTTGCTTACAAAGGCGAGAGAGTGTGAGAGAACTGGACATGCATAGCAACC | 2028 |
| Db | 2097 | CTGCGTGTGTCAGCTGGCTTACAGAGCGGAGCACTGCGAAGAGTGGATTTGCTTTGATTC | 2156 |
| QY | 2029 | CACATTTTCAGCCCGGGGTGTCTCGTGTAGAGGCGAATGCCATTTGCTTTTGTGGATGGGG | 2088 |
| Db | 2157 | AACCTGTCTCAAGCCATGGTGTCTGTGTAAACGGAGAGTGTCTATGCAAGCCCCGGCTGGGG | 2216 |
| QY | 2089 | AGGCACCAACTCGCAGACCCCCAGGCGCCACATGCTTAGACAGTGTTCAGGCCACACGGAAC | 2148 |
| Db | 2217 | CGGCTCNACTGCGAGCTGGCGGAGGTCAGTGCACAGACAGTGTAGTGGGATATGGCAC | 2276 |
| QY | 2149 | CTTCTCCCGAACCGGGCTTTTGCAGCTGTGACCCAAAGCTGGACTGGACACAGCTGTTC | 2208 |
| Db | 2277 | TTAGCTCCCTGACTCTGGCTCTGCAACTGTGTATCCGAATTTGATGGTCCCGACTGCTC | 2336 |
| QY | 2209 | TATCGAGATCTGTGCTCCGACTGTGTGTGGCCATTGGCGTGTGCTAGGGGGACCTGCCG | 2268 |
| Db | 2337 | TGTTGAAGTGTGCTCAGTAGACTGTGGCACTCACGGCGTCTGCATCGGGGGAGCCTGCCG | 2396 |
| QY | 2269 | CTCGAGGATGGCTGGATGGGGGAGCGCTTCGACACAGCGGGCTTGCACCCGGCTGTGC | 2328 |
| Db | 2397 | CTGTGAAGAGGGCTGGACAGCGCGGCTTTGTACCAGCGCTGTGCCACCCCGCTGCAT | 2456 |
| QY | 2329 | CGAGATGGGACCTGCCCGACGCAAGTGGAGTGCAGCCCTGGCTGGAAATGGCGAACA | 2388 |
| Db | 2457 | TGAGCAGGGACCTGTAAAGATGGCAAAATGTAAATCCGAGAGGGCTGGAAATGGTGAACA | 2516 |
| QY | 2389 | CTGCACCATCGCTCACTATCTGGATAGGGTAGTTTAAAGAGGGTTGGCCCTGGGTGTGCAA | 2448 |
| Db | 2517 | CTGCACCATTTGAT-----GGCTGCCCTGATTTGTGCAA | 2549 |
| QY | 2449 | TGGCAACGGCAGATGTACTTTAGACCTGAATTTGGCACTGCGTCTGCCAGCTGGGGCTG | 2508 |
| Db | 2550 | CGGTAAACGGGAGATGSCACATGGGTCCAGAACAGCTGGCAGTGTCTTGCACAGACCGGCTG | 2609 |
| QY | 2509 | GAGAGGAGCTGGCTGTGCACATTTCCATGGAGACTGCCCTGGGTGACAGCAACACAAATGA | 2568 |
| Db | 2610 | GAGAGGGCCGGATGCAAGCTTGCCATGGAAAACCTCTGCGCTGTATACAGAGATTAATGA | 2669 |
| QY | 2569 | TGGAGATGGCTGTGTGACTGTCAATGGACCTGACTGTCTGCCCTCAGCCCTGTGCCATAT | 2628 |
| Db | 2670 | GGGAGATGGCTGTGTGACTGTGCTGGACCTGACTGTCTGCCCTCCAGTCAAGCTGTTCAGAA | 2729 |
| QY | 2629 | CAACCCGCTGTGCTTGGCTTCCCTAACCTCTGGACATCATCCAGAGACACAGTGTCCC | 2688 |
| Db | 2730 | CAGCTCTGTCTGGGGGTCTCTGGGACCCCTTGGACATCATTCAGCAAGGCCCAGACAGA | 2789 |
| QY | 2689 | TGTTGTCAAGCAGAACCTACACTCTTTCTATGACCGCATCAAGTTCTCTGTGGCGAGGA | 2748 |
| Db | 2790 | CTGSCCTGCGGTGA-----AGTCTTCTATGATCGTATCAAGCTCTTGGCAGGCAAGGA | 2843 |
| QY | 2749 | CAGCAGCAGCAATAATCCCCGGGAGAACCCCTTTGATGGAGGCGATGCTTTGTATTTCG | 2808 |
| Db | 2844 | CAGCACCCACATCATCTCTGGAGACAACCCCTTTCAATAGACGCTGGTGTCTCTGATCCG | 2903 |
| QY | 2809 | TGGCCAAAGTATGACATCAGATGGAACCCCGCTGGTTGGTGTGAAACATCAGTTTCTCAA | 2868 |

[illegible]

| | | | | | | |
|----|------|-------------|---------------|------------|--|------|
| Db | 3984 | GGACCCGTGTA | CGCTCTATGTC | CTGACACCA | CAGTCGCGGATCTACCGAGT | 4043 |
| Qy | 3949 | CAAGTCCACTG | TGGTGAAGACCTT | GCAGAACTCT | GAGTGGTTCGGGGACAG | 4008 |
| Db | 4044 | CAAGTCTTAAG | CGGAGCCAAACCT | TGGTGGAAAT | TGGGAGTGTGGCCGGGACTGG | 4103 |
| Qy | 4009 | TGACCAAGTG | CTCCCTTTGATG | ACACTCTGCT | CGGGGATGGTGGGAAGCCACAGAAGC | 4068 |
| Db | 4104 | CGAACAAATG | CTCTACCTTTG | ATGAAGCCG | CTGTGGGATGGCGAAGGCTGTGGATGC | 4163 |
| Qy | 4069 | CACACTCAC | CAATCCCGAGGG | GTATTACAG | TGGGCAAGTGTGGGCTGATCTCTCTGGGA | 4128 |
| Db | 4164 | CACCTTGAT | GAGCCCTAGAG | GTATTGCA | GTAGAACAGACGGCTTATGTATTGTTTGA | 4223 |
| Qy | 4129 | TGGACCAAT | GATCAGACG | ATCCATCAG | ATGGGATCATCTCCACCTGCTCGGCTCTAA | 4188 |
| Db | 4224 | TGCCACCAAT | GATCCGGAAG | TCACCAAAAT | GGAATCATCTCCACCTGCTGGGCTCCAA | 4283 |
| Qy | 4189 | TGATCTCAC | ATCAGCCCGCA | CTCAGCTGT | GAATTTCTGTCAATGGATATTTCCAGGTTAAG | 4248 |
| Db | 4284 | TGACCTCAC | AGCTGTCCGAC | CACTGAGCT | GTGACTAGCATGGACGTGGCCACAGTCCG | 4343 |
| Qy | 4249 | ACTGGAGTG | CCCAAGACTT | AGCCATCA | ACCAATGGACAACTCACTTTATGTCTCTGGA | 4308 |
| Db | 4344 | TCTAGAATG | CCGACAGAC | CTTGGGTCA | ACCCATGGACAAATTCCTGTGTACGTCTCTGGA | 4403 |
| Qy | 4309 | CAACAAATG | TGCTGCAAT | CTTGAAAC | CAACCAAGGTGCGCATTTGTCGCCGGGAGGCC | 4368 |
| Db | 4404 | GAACAAAGT | CTCTGCGGAT | CAACCGAG | AAATCACCAGGTGAGCATCATCGCGGAGCGGCC | 4463 |
| Qy | 4369 | CATGCACTG | CGAGTCCCTG | GCATTTG | CACTTGAAGCAAGGTGGCCATCCACGC | 4428 |
| Db | 4464 | CATGCACTG | CGAGTTCCTG | CGCATG | CACTACT---CGCTCAGCAAGCTCGCCATCCACTC | 4520 |
| Qy | 4429 | AACCTGGAG | TGACCCAG | CTTTGGCTG | TTTCAACAATGGGGTCTGTATATGTGCTGA | 4488 |
| Db | 4521 | TGCTCTGG | AGTGACG | CGCCATCG | CCATTCTCACACCGGGGTGCTCTACATCACCGA | 4580 |
| Qy | 4489 | GACTGATGA | AAAGATCA | ACCGCAT | CAGGCATCACCACCTAGTGGAGAGATCTCACT | 4548 |
| Db | 4581 | GACGGACGA | AGAAAGAT | CAACCGCT | ACCGCAGGTCAACCAACGGAGAGATCTGCGCT | 4640 |
| Qy | 4549 | CGTTGCTGG | GGGCCCCC | AGTGGCTG | TGTAATAATGATGCCAACTGTGATTTGTTTTTC | 4608 |
| Db | 4641 | CTTAGCCGG | GGGAGCCT | CAACTGTG | ACTGCAAAAATGACGTCAACTGCTGCTATTTC | 4700 |
| Qy | 4609 | TGGAGACGA | TGGTTATG | CCAAAGGAT | GCAAGTTAAATACCCCATCTTTGCTGGCTGTGTG | 4668 |
| Db | 4701 | GGGAGATGA | CGCATACG | CCACGGAT | GCCATCTTGMACTCCCGCTCTCTTAGCTGTGC | 4760 |
| Qy | 4669 | TGCTGATGG | GGGAGCTCT | ACGTGGCG | ACCTTGGGAACATCCGAATTCGGTTTATCCGGA | 4728 |
| Db | 4761 | TCCGGATGG | CAACCATCT | ACATCGCA | CCCTCGGGAATATCCGGATCAGGGCGGTTCAGCA | 4820 |
| Qy | 4729 | GAACAAGCT | TTTCTCAAC | CCCAAGAT | GTATGAGCTGTCTTCAACAATTGACACAGGA | 4788 |
| Db | 4821 | AAACAACCT | TGTTCTTAA | CGGTTTCA | ACCAAGTATGAGCGTCTCCGGGAGNACAGGA | 4880 |
| Qy | 4789 | GCTCTATCT | GTGTTGAT | ACCACCG | CAAGCACTGTATACACCCAAAGCTGCCCAAGGAGA | 4848 |
| Db | 4881 | ACTGTACGT | GTTCACCC | CGATGGT | ATCCATCAGTACACCGTGTGAGCTGACCCGGGA | 4940 |
| Qy | 4849 | CTACCTGT | AACATCTT | ACACTG | GGGAGCGGCGACATCACACTCATCAAGACACAA | 4908 |
| Db | 4941 | GTACTTATA | CAAAATTT | CACTAC | AGCGTGAATGATGTCAACCGAGTTGATTGACAA | 5000 |
| Qy | 4909 | TGGCAACAT | GTGTAATG | TGCGCCG | AGACTCTACTTGGGATGCCCTCTGCTGGTGGTCCC | 4968 |
| Db | 5001 | CGGGAAT | TTCCCTAA | AGATCC | CCGGGACAGAGTGGCATGCCCGCACCTGCTCATGCC | 5060 |
| Qy | 4969 | AGATGGC | AGGTGTACT | GTGGGTG | ACCATGGGCAACCAAGTGCATCAAGAGTGTGACCA | 5028 |
| Db | 5061 | TGATAATC | AGATCAT | CACTTAC | CGGTGGGCAACCAAGGCGCTCAAGCCGTGTCAAC | 5120 |
| Qy | 5029 | ACAAGGACA | CGAGTTGG | CCATGAT | GACATACCATGSCAAATTCGGGCTTTCTGGCAACCAA | 5088 |
| Db | 5121 | CGAGAACCT | GTGAGCTGG | GCCTCAT | GACTTATGATGGGAACACTGGACTCTTAGCCACCAA | 5180 |
| Qy | 5089 | AAGCAATGA | AAAAAGAT | TGGAACA | ATTATGATGATGACAGCTTTGGCGGCTGTGACAA | 5148 |
| Db | 5181 | GAGCGATGA | AAACCGG | ATGGACA | ACTTTTATGACTATGATGACCGAGGGCGCTTAGCCAA | 5240 |
| Qy | 5149 | TGTGACCTT | CCCTACT | TGGCCAG | TGTGAGCTTTCCGAAGTGATACAGACAGTTTCAGTGCA | 5208 |
| Db | 5241 | TGTGACTCG | CCCCAC | CGGGGTGT | GACAGCTGCAACCGGGAATGAGAAATCCATCAC | 5300 |
| Qy | 5209 | TGTCCAGGT | AGAGACCT | CCAGCAAG | AT---GATGTCAACATAACCAACCAACTGTCTGC | 5265 |
| Db | 5301 | CGTGTGAC | ATTGAGAA | CTCCAA | CGTGTATAACGATGTCACTGTGATTACCAACCTCTCTTC | 5360 |
| Qy | 5266 | CTCAGCGCT | TTTACACT | GTGCAAG | ACCAAGTCCCGAACAGTACTACTATCGGGGC | 5325 |
| Db | 5361 | AGTGGAGG | CTCTCTCA | CCGTTGTA | CAAGATCAAGTGCAGACAGCTACAGCTTCGAG | 5420 |
| Qy | 5326 | CGATGGCT | CTTGGCG | CTGCTG | SCCAACGCGATGGAGGTGGCGCTGCAGACTGAGCC | 5385 |
| Db | 5421 | CAACGGGA | CCCTGCG | GGTCAT | GTACCCCAACGCGATGGCGGTGAGCTTCCACAGCGGCC | 5480 |
| Qy | 5386 | CCACTTGT | CGGTGG | CAACCG | CTCAACCGTGGGCAAGAGGAATGTCACGCTGCCCAT | 5445 |
| Db | 5481 | CAACGTCT | CGCAGG | CACTCT | CAACCGCTGTAACATCTCTCCCTGCGCCAT | 5540 |
| Qy | 5446 | CGCAACGG | CTCAAC | CTGTTGG | AGTGGCGCCAGCCAAAGAGCAGGCTCGGGGCCAGGT | 5505 |
| Db | 5541 | GGAGAACG | CGCTGAA | CTCCAT | CGAGTGGCGCTTGAGGAAGGAACAGATTTAAAGGCAAGT | 5600 |
| Qy | 5506 | CACTGTCT | TTTGGG | CGCGCT | CGCGTGCACACCGAATCTCTATCTCTGACTTTGA | 5565 |
| Db | 5601 | CACCATCT | TTTGGAG | GAAGCTT | CGGGTCCACGGAAGAACCTCTGTCCATTTGATTATGA | 5660 |
| Qy | 5566 | TGCGGTAA | CAACGCA | GAGAAAT | CTATGATGATGACCAACCGCAAGTTCAACCTTCGGATTTCT | 5625 |
| Db | 5661 | CCGAAATAT | CCGCAC | CTGAGA | AGATCTATGACGACCAACCGGAGTTCAACCTGAGGATCAT | 5720 |
| Qy | 5626 | GTACGAC | CAAGCG | GGCGCC | AGCCTCTGGTCAACCGCAGCAGGCTGAATGGTGTCAA | 5685 |
| Db | 5721 | TTATGAC | CAAGTGG | CGCCCTT | CTCTGTGGCTCCCGCAGCAGTGGACTGGCGGCCGTCAA | 5780 |
| Qy | 5686 | CGTGACAT | ACTCCCT | TGGGGT | TTACATTTGCTGCATCCAGAGGGCATCATGCTCTGAAAG | 5745 |
| Db | 5781 | TGTCCTCT | ACTCTT | TTCAAC | CGGGCGCTTGGCGGCGCTCCAGCGCGGGCCATGAGCGAGAG | 5840 |
| Qy | 5746 | AATGGAA | TACGAC | CAAGCG | CGCGCATCATCCAGGATCTTCGCTGATGGGAAGACATG | 5805 |
| Db | 5841 | GACAGAC | ATTGACA | AGCAAG | CGCGGATTTGTGTCGGAATGTTCCGCGAGGGAAGCTGTG | 5900 |
| Qy | 5806 | GAGCTACA | ATCTTAG | AAAGTCC | ATGTTGCTGTGCTATACACAGCAGAGGAGGATATAT | 5865 |
| Db | 5901 | GAGCTAT | TTCTCA | CTTTGAC | AAAGTCCATGCTCTCTGCTGCAGAGCAGCGTCAGTACAT | 5960 |
| Qy | 5866 | CTTTGAG | TTGCAAG | AAATGAC | CGCCTCTTTCTGTGAGATGCCCAACCGTGGCGCGGCA | 5925 |
| Db | 5961 | ATTTGAAT | ATGACT | CTCTG | ACCGCTCCACGAGTCACCATGCCAGTGTGCGCCCGGCA | 6020 |
| Qy | 5926 | GACACTAG | AGACCAT | CCGCTC | AGTGGCTACTACAGAAACATCTATCAGCCCCCTCGAGGG | 5985 |
| Db | 6021 | CAGCATGT | CCACGCA | CACCTCC | ATTGGCTACATCCCGGAACATTTACAAACCCACCGGAAG | 6080 |
| Qy | 5986 | CAATGCT | CTCAGT | CATACAG | ACTTCACTGAGGATGGGCACTCTCTTCCACACCTTTTACCT | 6045 |
| Db | 6081 | CAACGCT | CTCGT | TCATCTT | TGACTACAGTATGACGCGCGCATCTCTGAAGACGCTTTTCT | 6140 |
| Qy | 6046 | GGGCACT | GGCGC | AGGTTG | ATATACAAATGSCAACTGTCTCAAGCTGCGCAGAGCGCT | 6105 |
| Db | 6141 | GGGCACT | GGCGC | AGGTTG | TTCTATTAAGTACGGAACCTGTCTCAAGTTATCGGAGATCGT | 6200 |

QY 6106 CTATGACACCAAGGTCAGTTTACCTATGACGAGCGGACGAGCTGCTGAAGACCAT 6165
DB 6201 CTACGACACACTGCGCTCACCTTGGCTATGACGAGACCACTGGCTCCTAGATGGT 6260
QY 6166 CAACCTACAGAAATGAGGGCTTACCTGCAACCATCCGCTACCGTTCAGATTGGGCCCTCGAT 6225
DB 6261 GAATCTCCAAAGCGGGGCTTCTCCTGTACCATCATAGGTACCGAAAGGTGCGGCCCTCGT 6320
QY 6226 TGACCGACAGATCTTCGGCTTCACTGAGGAAGCATGGTCAACGCCGCTGTTTGTACTACA- 6284
DB 6321 GGACAGACAGATTTACAGGTTCTCTGAGGAAGCATGATCAACGCCGAGTTCGATTACAC 6380
QY 6285 --ACTATGACAAACAGCTTCGGGTGACACAGCATGACGAGTGTGATCAACGAGACCCCACT 6342
DB 6381 CTACACGACACAGCTTCGGCATCGCCAGCATCAAGCCCGTCATCATGTGAGACTCCCT 6440
QY 6343 GCCCATGTATCTCTATCGCTATGATGTGTGAGCAAGACAGCAGTGTGGGAAGTT 6402
DB 6441 TCCCGTTGACCTTACCGCTACGATGAGATTTCTGGCAAGGTGGAACACTTCGGCAAGTT 6500
QY 6403 TGGTGTCAATTTACTATGACATTAACAGATCATCAACACAGCTGTCAAGCCACACAA 6462
DB 6501 CGGGGTCACTTACTACGACATCAACACAGATCATCAACCTGCCGTCAAGACACTCAGCAA 6560
QY 6463 GCATTTTGATGATATGGCAGGATGAAGAAAGTGCAGTATGAGATCTTCCGCTCGCTCAT 6522
DB 6561 GCATTTTGACCCATGGCGCATCAAGGAAGTGCAGTATGAGATGTTCCGCTCGCTCAT 6620
QY 6523 GTACTGGATGACCGTCCAGTATGATAAATGCGGCGAGTGTGAAGAAAGGAGCTGAAGGT 6582
DB 6621 GTACTGGATGACCGTGCAATATGACAGTATGGCGAGGTTCATCAAGAGGAACTGAAACT 6680
QY 6583 AGGACCTTACGCAATACCACTCGCTACTCTCTATGATGATGATGCTGAGCGCACTGCA 6642
DB 6681 GGGGGCTTATGCAACACCAAAAGTACACCTATGACTACGACGGGACGGCAGCTCCA 6740
QY 6643 GACAGTCTCCATCAATGACAAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCT 6702
DB 6741 GAGTGTGGCGTCAATGACCGGCTTACCTGGGCTTATAGCTATGACCTCAATGGGAACCT 6800
QY 6703 GCACTTACGAGCCCTGGGAAACAGTGCAAGCTGCTACACACATACCGGTATGACATCCGGA 6762
DB 6801 GCACCTGTCTAAACCCAGGAAACAGTGTCTCGCTCATGCGGTTACGCTATGACCTCGTGA 6860
QY 6763 CGGCATCACTCGGCTGGGTGAGTGCATACAAAGATGATGAGTGGCTTCTTGAGCA 6822
DB 6861 CCGGATAACCGAGTAGGGGACGTGCAGTACAAATCGATGATGATGCTATTTATGCCA 6920
QY 6823 GCGGGCGGTGATATCTTTGAGTACAACTCAGCTGGCCTGCTCATCAAGGCCCTACAAACCG 6882
DB 6921 GAGAGGATCTGACATCTTTGATACAACTTCCAAAGGCGCTTCTAACGAGAGCGTACAAAC 6980
QY 6883 GCGTGCAGCTGAGTGTGAGTACCGCTACGATCGATCGCTGGGCGGCGGTGTTCAGCAA 6942
DB 6981 GGCACGCGGTGGAGTGTGCAGTACCGCTATGATGGCGTGAGCCGCGGCTTCTTACAA 7040
QY 6943 GAGCAGCCACACGCCACCTTCCAGTCTTCTATGACAGCTGACCAACCCACCAAGGT 7002
DB 7041 GACCAACCTTGGGCGACCACTACAGTACTTCTATTCGACCTTCCACCCACACAGTAT 7100
QY 7003 CACCCACCTGTACAAACCACTCCAGCTTGAGATCACTCCCTCTACTACGACTTGCAGAG 7062
DB 7101 CACCCATGTTTACAAACCACTCCAGTCTGAGATCACTCACTTACTTACTATGACCTCCAGG 7160
QY 7063 ACACCTTGTGCAATGGAGCTGAGCAGTGGTGTGATGAGTTTATAGCTTGTGACAAAT 7122
DB 7161 CCACCTCTTGGCATGGAGAGCAGTAGTGGGAAGAGTACTATGTTGCTTCAGATAAAC 7220
QY 7123 CGGGAACCCCTTGTGTCTTTAGTGGAAACAGGTTTGTATGATCAAGCAAAATCTCTGTAC 7182
DB 7221 CGGGAACCTCTGTGGCTGTTTTAGTATCAATGGCCCTCATGATCAAGCAAACTCCAAATAC 7280
QY 7183 AGCCTATGGGAGATCTTACATGGATACCAACCCCAACTTTTCAGATCATATAGGCTACCA 7242

DB 7281 AGCCTATGGGAGATTACTATGACTCAATCCAGACTTTTCAGATGGTTCATCGGCTCCA 7340
QY 7243 TGGTGGCTCTATGATCACTCACCAAGTTTGTCCATATGGGCGGCGAGATTATGATGT 7302
DB 7341 CGGAGGCTCTTACGACCCCTTACCAAGCTCGTTCACTTTACGCAAGCTGATTATGACGT 7400
QY 7303 GCTGGCGGAGCTGGGACTAGCCAGACCAAGCTGTGGAGACACCTTAGTAGACGAA 7362
DB 7401 GCTGGCAGGACGGTGGACGCTCCCGCATACCATGTGGAGAA---TGTGGGCAAGGA 7457
QY 7363 CGTCATGCTTTTAAATCTCTATATGTTCAAAAAACAACCCCATCAGCAACTCCAGGA 7422
DB 7458 GCCAGCCCTTCAACCTGTATGTTCAAGAACAAATCCACTCAGTATAGCTGGA 7517
QY 7423 CATCAAGTGTTCATGACAGATGTTAAACAGCTGCTGCTCACCTTTGGATTCCAGCTTACA 7482
DB 7518 TTTAAGAACTTACGTGACAGACGTGAAGAGCTGCTCGTGTGATGTTGGATTTCAGCTCAG 7577
QY 7483 CAACGTGATCCCTGGTTATCCCAACACAGACATGATGCCATGGAAACCTCCTACGAGCT 7542
DB 7578 CAACATCATCTCTGGATTCCCAAGGCCAAATGTATTTGTGCTCCCCCTATGA--- 7634
QY 7543 CATCCACACAGATGAAAAACGACGAGTGGGCAACACAGCAAGTCTATCTCTCGGGTACA 7602
DB 7635 -----ACTGTACAGAGCCAAAGTGAAGATGGACAGCTCATTTACAGGTGTCCA 7685
QY 7603 GTGTGAAGTACAGAGCAGCTCAAGGCTTTTGTCACTTGAACGGTTTGAACAGCTCTA 7662
DB 7686 GCAGACAACAGAGAGGATTAACAGGCTTTTCTGGCTCTAGAAGGACAGGTCACTCTAA 7745
QY 7663 TGGCTCCACAATCACAGCTGCCAGCAGGCTCCAAAGACCAAGAGTTTGCATCCAGCG 7722
DB 7746 AAAGCTCCATGAGGCATCCGAGAAAGC-----AGGCCACTGGTTTGTACGACAC 7799
QY 7723 CTCAAGTCTTTGGCAAGGGGCTCAAGTTTGGCTTTGAAGATGGCGAGTGACCAACAGAT 7782
DB 7800 GCCCATCATCGGCAAGGCGCATGTTTCGCCATCAAGAAAGGCGGCTGACCAAGCGGT 7859
QY 7783 CATCAGTGTGCCCATGAGATGGGCGAAGGTTGTGCCATCTTGAACCATGTCCTCACTA 7842
DB 7860 GTCTAGCATCGCCAGTGAAGACAGCCGCAAGGTAGCATTCGCTGTGAACACGCTTACTA 7919
QY 7843 CCTAGAAACCTGCATCTTCAACCTTGTGGTGTGATACCATTACTTTGTGAAACACAGG 7902
DB 7920 CTTGGAACAAGTGCATCTACAGCATCGAGGCAAGGACACACATCTTCTGTGAAGATCGG 7979
QY 7903 ACCTTCAGAAAGTGAACCTGGCCATCTTGGCCCTCAGTGGGGGCGGCGAACCCTTGGAGAA 7962
DB 7980 TGCAGCGGACGGTGAACCTGGTTACGCTGGGACCCACCATTTGGGCGCAAGGTGTGGAGAG 8039
QY 7963 TGGGGTCAACGTCACTGTGTCCAGATCAACACAGTACTTAATGGCAGGACTAGACCTA 8022
DB 8040 CGGGGTGAACGTGACCGCTGTCAACGCCACGCTGCTGGTGAACGCGAGGACTCGAAGGTT 8099
QY 8023 CACAGACATCCAGCTCCAGTACCGGCGCATGTGCTTGAACAACACGCTACCG----- 8073
DB 8100 CACCAAACTTGAATTCAGTACTCCAGCTGTGCTCAGCATAGCTACGCTCACCC 8159
QY 8074 GACAACTTTGGATGAGGAGAAAGCAGCGGTCTTGGAGCTGGCCCGGAGAGCCGTGCG 8133
DB 8160 CGACACACTGGATGAAGAGAAAGCCCGCTCTTGGACCAAGCGCGACAGAGGGCCCTGGG 8219
QY 8134 CCAAGCTTGGCCCGCGCAGCAGCAGAGACTTGGCGGAAGGAGGAGGCGCTGCGGGCTG 8193
DB 8220 TACTGCTGGGCCAAGAGCAGCAAGAACCGCAGGACGGGAGAGAGGAGGCGCTCTGTG 8279
QY 8194 GACAGCGGCGAGAAAGCAGCAGGTTGTGAGCAGAGGCGGGTGAAGGCTACGACGGCTT 8253
DB 8280 GACGAGGCGGAGAAAGCAGCAACTCTCTGAGCAACGGGACGGGTGCAAGGTTATGAGGCTA 8339
QY 8254 TTTGCTGATCTCTGTGAGCAGGTACCCAGAACTGTCTAGACAGCGGCCAAACATCCACTT 8313

Db 8340 TTACGTGCTTCCGGTGGAAAGTACCCAGAGCTGGCAGACAGTAGCAGCAACATCCAGTT 8399
Qy 8314 CATGAGACAGCGAGATGGCCGCGAGGTGACAGA 8348
Db 8400 CTTAAGACAGATGAGATGGAAAGAGGTAAACAA 8434

RESULT 14

US-09-800-198-66
; Sequence 66, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Cornie AM
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrmann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 66
; LENGTH: 8689
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-800-198-66

Query Match 40.7%; Score 3397.8; DB 3; Length 8689;
Best Local Similarity 64.8%; Pred. No. 0;
Matches 5469; Conservative 0; Mismatches 2712; Indels 254; Gaps 19;

Qy 35 ATGACGTGAAGGAGAGAGCTTACCGTCTGCTGACCCGCGCGCGCGAGCGCGC 94
Db 133 ATGGATGAAGGATCGCGACATCGCTCTTTGACAGGGGACGGTGTGCAAGGAGTGT 192
Qy 95 CGCTACACACAGCTCGTCCGGGACAGCGAGAGGGGCAAG---CCCCGCGAGAAATCGTAC 151
Db 193 CGCTACACACAGCTCTCTTGACAGTGAAGAGTGGCGTGGCCAGCGAGAGTCTCTAC 252
Qy 152 AGCTCCAGCGAGACCTGAAAGGCTACGACAGGACGCCCGCTAGCCTATGGCAGCGC 211
Db 253 AGTTCCAGTGAGACCTGAAAGGCTTATGACCATGACAGCAGATGCACTATGGAACCGA 312
Qy 212 GTCAGGACATTTGCGCGAGGAGGCGGAGGAATTTGCGCGACAGGTGCGCACTTCAAC 271
Db 313 GTCACAGACCTGTGTGACCGGGAGTCCGATGAGTTTCTAGACAAGGGGCTAATTTCAAC 372
Qy 272 CTGCGGAGCTGGGGCTGGAAGAGTAAGCGCCCTTCAAGGACCTGTATACCGGACAGAC 331
Db 373 CTGCGAGATTTGGAAATCTGGAG---CCCTCCCAACACCGAGTGTACTGTTCGAC 429
Qy 332 ATTGGCTGCCCAATCGGCTACTCCATGGGGCTGGCTCTGATGCCGACATGGAGGCT 391
Db 430 ATGGGGATCTCCACACGGGCTACTCCCTGAGCAGTGGGTCTGATGGGACTCGGACAC 489
Qy 392 GACAGGTGTCTCCCTGAGCAGCCCGTGGGTCTGTGGGCGGGGACACAGGTGAGG 451
Db 490 GAGGGAGGATGTCTCCAGAACATGSCCATCAGACTGTGGGACGAGGGATAAATTCGAG 549
Qy 452 CGCAGCTCTGCTGTGCGCGGGCCAAATTCCAATCTCACACTCACCGACACCGAGCAT 511
Db 550 CGCAGCTCTGCTGTGACCGCGGAGAACTCAGCCCTTACTCTGACTGATTTCTGACAA 609
Qy 512 GAAACACTGAGACTGATCATTCGGGGGGCC---TGCAGAACACCGCGGCTCCGGAC 567
Db 610 GAAATAAATCGGATGACGACAAATGGTTCGAGCCCATTCACCTACCTCTCTAGCCTC 669

Qy 568 GCGCGCGCGCGCTCTCGCACGCCACACACCCCAACACAGCACCGCGGCTCCCAATA 627
Db 670 CTCCCATCTGCTCAGCTGCTAGTCTCCATAATCTCTCCACAGTTAGTGC---AGATGCC 728
Qy 628 CTCCTTGAAACCGGGGCAACTTTCACGCGCGAGGAGCAACCCGAGCCCGG----- 674
Db 729 ATTGCTAGACAGCAACACCTCTCCATCAGATCATGAGACACCAACCCCGATGAGGAATTC 788
Qy 675 -----CCCCCAGGACCACTCGCTCTCCGAGAGCCCTGCGCGGGCGGCC 722
Db 789 CCTAATTATACCTCTCAGAGCATGCTCAGGGCCCCAGCAAGCTTCCAGTAGTGGCCC 848
Qy 723 AGGAGCTTGCCACGCGCCAGGAGAACTGGCTGTCAACAGCAACATCCCCCTCGAGACCA 782
Db 849 TCCGNAACCAACACAGCCAGTCAACGCTGAGGGCCCCCTCTGSCACCTCTCATAAACAC 908
Qy 783 GGAACCTAGGCAAGAGCCATTCCTAGGAGACATTGAGAGCAACCTCATTTGAGATGAGACA 842
Db 909 CTGTGCCACCACTCTCTGCAACTCTGCAACTCCCTCAACAGAAACTCACTGACCAATCGGCG 968
Qy 843 TTCTCGGCGCTCCCGCCA----- 861
Db 969 GAGTCAAAATCCACGCCCCAGCTCTGCAACCAATGACCTGGCCACACGCGCGAGTCCGT 1028
Qy 862 -----TGATGGGGCTTACAGTGACGCGGCGGCACTTCTCT 891
Db 1029 TCAGCTCCAGGACAGCTGGGTGCTGAACAGTAAGTGCCTGGAGACGCGGCACTTCTCT 1088
Qy 892 CTTTCAA---GCCTGGAGGACCTTCCCGCTCTTTGCAACCATCAGCGGTACCCACT 948
Db 1089 CTTTCAAGAGCTCTCCGGAAGCACACCCCTGTTTTCAGCAGCTCTTCTCCAGGATACCCCT 1148
Qy 949 GAGCTCCAGACAGTGTACTCTCTCGGCCCCGACCCCTGCGCGGAGCACTTTCGCCG 1008
Db 1149 GACCTCAGGAGCGTTTATACACACACCCCGCTGCTGCCAGGAATACATTTCTCTAG 1208
Qy 1009 GCGCGCTTTAACTCAAGAGCCCTCCAAGTACTGTAACTGGAAGTGCAGCGGCTTGAG 1068
Db 1209 GAAGGCTTCAAGCTGAGNAACCCCTCCAATACTGCAGTTGGAATGCGCGGCTGTC 1268
Qy 1069 CGCATCTGTCATCTCAGCCACTCTGTCTATCTGCTGGGCACTTTGTGTGCGCATGCACT 1128
Db 1269 TGCATTTGCGCTGCTCTCTCTGCGCAATTTTGTGGCTATTTTCATAGCAATGCATCT 1328
Qy 1129 GTTTGGCTTAACTGCACTGCGACCTGCGAGCGGAGGCGAGATGTATGAGATCAGGAGGA 1188
Db 1329 GCTCGGACTCAATTTGGCAACTCCAGCGCGGAGATGACACACCTTTTAAACA-----ATGG 1382
Qy 1189 CACAGCCAGCAGTTGGCTGTGCAACCGGACGTCTCCCTATACCCCTCAGGGGCGACTGG 1248
Db 1383 CGTAAGGACCGGCTTACAGGAAACGATGATGTGGCAACAGTGCCTCTCGGAGGCAAGT 1442
Qy 1249 CTTAGAGACCCCTGACAGGAAAGCAAGAACCAAGAAAGGAAAGCCCAAGTATGTTCTT 1308
Db 1443 GCGCTGTCTGTTCAAAA----- 1459
Qy 1309 TCCAGAGGACAGTTTATAGATTTCTGGAGAAATTTGATGTGGAGGCGGAGCCCTCCCAAG 1368
Db 1460 -----ACAGCAGCATAGACAGCGCGGAGGAGGAGTCCGTCGAGCGGCTGACACAGGA 1511
Qy 1369 GATTCTCTCTGCGCACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTCTGTGCACTGAA 1428
Db 1512 AGTCCACACAGGGGTGTTTGGAGTCCAGATTCACNTCAGTCAGCTCAGTCTTCTTAA 1571
Qy 1429 ATTCAATGTGTCTCTGGAAAGGACGCTCTGGTGGCATTTATGGCAAGAAAGGCTCC 1488
Db 1572 GTTCAACATCTCCTGGGAGGATGCGCTCTTCGGGCTCTACATAAGAGAGGACTGCC 1631
Qy 1489 TCCTTCACATACACAGTTTTCAGTTTGGAGCTGCTGGATGGCAGGAGGCTCTCTAACCCA 1548
Db 1632 ACCATCTGACAGTATGACTTTCATGGAAACGCTGAGCGAA-----A 1676

QY 1549 GGAGGCGGAGCGCTAGAGGGACCCGCGCCAGTCTCGGGAACTGTGCCCCCTCCAG 1608
DB 1677 GGAGAAAGTGGATGTGGTCACTACCCAGGGAACCGCGAGCATCCAGACCCCTGGTCA 1736
QY 1609 CCATGAGACAGCGCTTATCCAGTATTTGGATTTCAGGAATCTGGCACTTTGGCTTTTACAA 1668
DB 1737 GAACGAGGCTGTGTTCTGTCAGTACTTGGATGTGGGCTGTGGCACCTCGCCCTTCAAA 1796
QY 1669 TGACGGAAGAGAGTCAGAAAGTGGTTCTTTCTCAACCACTGCCATTGAGTCGGTGATAA 1728
DB 1797 TGACGGCAAGGACAAGGAGATGGTCTCTTCAATACGGTGTGTAGATTTCAGTCAGGA 1856
QY 1729 CTGCCCCAGCAACTGCTATGSCAAATGGTCACTGCACTCTCTGGGACCTGCACTGCTTCT 1788
DB 1857 CTGTCCACGAAACTGCGACGGGAACGGCGAATGCGTGTCTGCACTGTGTCACTGTTTCCC 1916
QY 1789 GGGTTTCTTGGGCCCCGACTGTGGCAGAGCCCTCTGCCCCGTGCTCTGTAGCGGAATGG 1848
DB 1917 AGGATTCTAGGTGCAGACTGCGCTAAAGCTGCGCTGCCCTGTCTGTGCAGTGGGAATGG 1976
QY 1849 CCAATACATGAAGGAGATGCTTGTGCCACAGTGGCTGGAAAGGCGCTGAGTCGATGT 1908
DB 1977 ACAGTATTCAAAGGACATGCCAGTGTCTACAGTGGCTGGAAAGGAGCAGAAATGCGATGT 2036
QY 1909 GCCCAACCAACAGTGTATCGATGTGGCTGCGCAAGCAACCATGGCACCTGCATCACGGGCAC 1968
DB 2037 GCCCATGAACCAAGTGCATCGATCTCTTCTGTGGGGGCCACGGCTCTGTGCAATTGATGGGA 2096
QY 1969 CTGCACTCTGCAACCCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTGGACTGCATGGACCC 2028
DB 2097 CTGCGTGTGTGCACTGGCTACAAGGCGGAGCACTCGGAAGAAGTGGATTGCTTGGATCC 2156
QY 2029 CACATGTTTCAGGCGGGGTGTCTGGTGAGAGCGCAATGCCATGTCTTGTGGGATGGGG 2088
DB 2157 AACCTGCTCCAGCCATGTGTGTGTGAACGGAGAGTGTCTATGCAAGCCCGCGTGGGG 2216
QY 2089 AGGCACCAACTCGAGAGCCCCAGGGCCACATGCTTTAGACCACTGTTCAGGCCACCGAAC 2148
DB 2217 CGGGCTCAACTCGAGCTGGCAGGGTCCAGTGTCCACAGCCAGTGTAGTGGGCATGGCAC 2276
QY 2149 CTTCCTCCGCGACACCGGCTTTGCACTGTGACCCAAAGCTGGACTGGACACAGCTGTTC 2208
DB 2277 TTACCTCCCTGACTCTGGCTCTGCAACTGTGATCCGAATTGGATGGGTCCGACTGTCTC 2336
QY 2209 TATCGAGATCTGTGCTGCCACTGTGTGGCCATGSGCTGTGCTGTAGGGGCACTTGGCG 2268
DB 2337 TGTGAAGTGTGCTCAGTAGACTGTGGCACTCACGGCGTCTGCAATCGGGGAGCGCTGCG 2396
QY 2269 CTGCGAGGATGGCTGGATGGGGGACGCTGCGACAGCGGGCTGCGACCCGCGCTGTGC 2328
DB 2397 CTGTGAAGAGGCTGGACAGGCGCGCTTGTGACACAGCGCTGTGCGACCCCGCTGCAT 2456
QY 2329 CGAGCATGGGACCTGCGCGACGGCAAGTGGAGTGGAGCTGCAAGCCCTGGCTGGAATGGCGAACA 2388
DB 2457 TGAGCAGCGGACCTGTAAAGATGGCAAAATGTGAATGCCAGAGGGCTGGAATGGTGAACA 2516
QY 2389 CTGCAACCATCGCTCACTACTCTGGATAGGGTAGTTAAAGAGGGTTGCGCTGGGTTGTGCAA 2448
DB 2517 CTGCACCATTTGAT-----GGCTGCCCTGATTTGTGCAA 2549
QY 2449 TGGCAACGCGAGATGTACCTTAGAAGTGGTGGCACTGCGTCTGCGAGCTGGGCTG 2508
DB 2550 CGGTAAACGGGAGATGCACACTGGGTGAGAAAGCTGGCAGTGTGTCTGCGACAGCCGGCTG 2609
QY 2509 GAGAGAGCTGGCTGTGACACTTCCATGGAGACTGCTTGGGTGAGCAGCAAGACAATGA 2568
DB 2610 GAGAGGCGCGGATGCAAGTGTGCCATGGAACCTCTCTGCGCTGATAAACAAGGATAATGA 2669
QY 2569 TGGAGATGGCCCTGGTGGACTGCATGGACCTGATGCACTGCTGCCCTCCAGCCCTGTGCCATAT 2628
DB 2670 GGGAGATGGCCCTGGTGGACTGCGCTGGACCTGACTGCTGCTCCAGTCCAGCTGTGAGAA 2729
QY 2629 CAACCGGCTGTGCTTGGCTCCCTTAAACCTCTGAGACATCATCCAGGAGACACAGGTCCC 2688

DB 2730 CAGCCTGCTGTCTGTGGGGTCTCGGGACCCCTTGGACATCATTTCAAGAAAGCCAGACAGA 2789
QY 2689 TGTGTACAGAGAACCTACACTCTTCTATGACCGCATCAAGTTCCTCGTGGCGAGGA 2748
DB 2790 CTGSCCTTCGGGTGA-----AGTCTTCTATGATCGTATCAAGCTCTTGGCAGGCAAGGA 2843
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DB 2844 CAGCACCCACATCATTTCTGGAGCAACCCCTTCAATAGCAGCTGTGTCTCTGATCCG 2903
QY 2809 TGGCCAAAGTGAATGATCATCAGATGGAAACCCCTCGTGTGTGAAACATCAAGTTTGTCAA 2868
DB 2904 AGGCCAAAGTAGTAACACGAGTGGGACCCCTCGTGTGGTGTGAATGTGTCTTTGTCAA 2963
QY 2869 TAACCCCTCTCTTTGGATATACATCAGCAGCAAGATGGCAGCTTTGACTTGGTGACAAA 2928
DB 2964 GTACCCAAAATATGGCTTACACCATCACTCGCCAGGACGCGATTTGACCTGATTTGCCAA 3023
QY 2929 TGGCGGCATCTCCATCATCTCGGTTTCGAGCGGGCACCTTTTCATCACACAGGAGCACAC 2988
DB 3024 TGGGGGCTCTGCTTGTGACTCTTCACTTTGAGCGAGCCCTTTTCATGAGCCGGAGCGCAC 3083
QY 2989 CCTGTGCTGCGCATGGGATCGCTTCTTGTTCATGGAACCAATCATCATGAGACATGAGGA 3048
DB 3084 AGTATGCGCGCGTGGAAACAGCTTCTATGCCATGGACACACCTGGTAAATGAAGACGGAGGA 3143
QY 3049 GAATGAGATTTCCAGCTGTGACCTGAGCAATTTTGGCCGCCCAACCCAGCTCGTCTCTCC 3108
DB 3144 GAACTCCATCCCCAGCTGTGACCTTCTGAGTGGCTTTTGTCCGGCTCATCCGATCATCATCTC 3203
QY 3109 ATCCCCCACTGACGTCTTTCGCGAGCTCTGTGACAGAAAGGCGCCCATTTGCGCGGAAT 3168
DB 3204 CTCTCTCTGTGCACTTCTTTCAGCGCTTCCCTTGGCGACCAACCGTGAAGCTCCGTTACCTCAG 3263
QY 3169 TCAGGCTTTGAGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGTGAGCTACCTTGAG 3228
DB 3264 CCAGGTTCTTCATGAGGAGATCGAGCTCCCTGGCACCAACCGTGAAGCTCCGTTACCTCAG 3323
QY 3229 CAGCGGACCCCTGGCTACAAATCTGTCTGAGGATCAGCTCACCCACCGACCATCCC 3288
DB 3324 CTCCAGAACAGCAGGATACAGTCACTGCTGAAGATCACCATGACCCAGTCCACGGTGCC 3383
QY 3289 CTTCAACTCATGAAGGTGCACTCATGTAGCGGTGGAGGCGCGCTCTTCAGGAAGTG 3348
DB 3384 CTGGAACCTCATCGGGTTCATTTGATGGTGTGCGTGGAGGGGCGATCTCTTCCAGAAAGTC 3443
QY 3349 GTTCGCTGCAAGCCCCAGACCTGTCTTATTTTCATTTGGGAACAAGACAGACGCTTACAA 3408
DB 3444 GTTCCAGGCTTCTCCCAACCTGGCTTACATTCATCTGGGACAAGACAGACGCTTATGG 3503
QY 3409 CCAGAAAGTGTTTGGGCTTTTCAGAAAGCTTTGTTTCGTGGGTTATGAATATGAATCCTG 3468
DB 3504 CCAAGGGGTTTATGGCTTATCGGATGCTGTGTGTCTGTGGATTTGAATATGAGACCTG 3563
QY 3469 CCCAGATCTAATCTGTGGGAAAAAGAAACAACAGTGTCTGACGGCTATGAAATTTGACGC 3528
DB 3564 CCCAGCTCATCTCTGTGGGAAAAAGAGACAGCCCTACTTTCAGGATTCGAGCTGGACCC 3623
QY 3529 GTCCAAGCTTGGAGGATGGAGCCCTAGACAAACATCATGTCCTTCAACATTCAAAGTGGTAT 3588
DB 3624 TTCCAACTTGTGTGCTGCTCCCTGGATAGCACCAACACCCCTCAATGTGAAAAAGCGGAAT 3683
QY 3589 CTTGCACAAAGGGAATGGGAGAACCAAGTTTGTGTCTCAGCAGCCCTCTGTCAATTTGGAG 3648
DB 3684 ACTACTCAAAGGCAACAGGGGAGAACCAAGTTTCTGACCCAGCAGCCCGCCATCATCACAG 3743
QY 3649 CATCATGGGCAATGGCGCGGAGAGACATCTCTGCCCCCAGCTGCAACGGCCCTTGCTGA 3708
DB 3744 CATATGGGTAAACGTCGCCGACAGACATCTCTGTCCCAGCTGCAATGGCCCTTGCTGA 3803
QY 3709 CGGCAACAAGCTCTCGGCCCGCAGTGGCCCTCACCTGTGGCTCTGACCGGAGCCCTCTATGT 3768

3804 AGGCAACAACTGTGGCCCGGTGGCTGTGGGATCGATGGAGCCTCTTTGT 3863
3769 GGGTGAATTAACATACATTAAGAGATCTCCCTCTGGAAATGTCAACCAATCTTGA 3828
3864 CGGTGACTTCAATTAATATATCGCGCGCATCTTCCCTCTCGAAACGTGACCAAGTATCTTGG 3923
3829 GCTGAGGAATAAAGATTTAGACATAGTCAAGTCCAGCACACAAATACTACCTGGCCAC 3888
3924 GTTACGAAATAAAGATTTAAACATAGCAACAGCCAGGACACAAGTACTACTTTGGCTGT 3983
3889 AGACCCCATGAGTGGGCGGTCTTCTTTCTGACAGCAACAGCCGCGGTCTTTAAAT 3948
3984 GGACCTGTGACTGGCTCGCTCTATGTCTGACACCAACAGTCCGCGATCTACCGAGT 4043
3949 CAGTCCACTGTGTGTGAGGAGCTTGTCAAGAACTCTGAGTGTGTGGGGGACAGG 4008
4044 CAAGTCTCTAAGCGGAGCCAAAGACCTGGCTGGGAAATTCGGAAGTTGTGGCGGAGCTGG 4103
4009 TGACCACTGCTCCCTCTTGTATGACACTCGCTGGGGATGGTGGGAAGGCCACAGAAAGC 4068
4104 CGAACATGTCTACCTTTGATGAAGCCCGCTGTGGGATGGCGGAAGGCTGTGATGC 4163
4069 CACACTCAACCAATCCCAGGGGTATTAAGTGGACAAAGTTTGGGCTGATCTACTTTCGTGA 4128
4164 CACCTGATGAGCCTTAGAGGTAATGCAGTAGACAAAGAACGGGCTTATGATTTTGTGA 4223
4129 TGGCACCATGATCAGACGATCGATCAGATGGGATCATCTCCACCCTGCTCGCTCTAA 4188
4224 TGGCACCATGATCCGGAAGGTGCGAAATATGGAATCATCTCCACCCTGCTGGGCTCCAA 4283
4189 TGATCTCACATCAGCCCGGCACCTCAGCTGTGATTTCTGATGATATTTCCCAAGTAAAG 4248
4284 TGACCTCACAGTCTCGACACACTGAGCTGTGATCTAGCATGACGTGGCCAGGTCCG 4343
4249 ACTGGAGTGGCCACAGACTTAGCCATCAACCCAAATGGACAACTCACTTTATGTCCTGA 4308
4344 TCTAGATGGCCGACAGACCTTGGGTCAACCCCATGGACAAATTCCTGTACGTCCTGGA 4403
4309 CAACAATGTGGTCTCTGAATCTCTGAACACACAGGTGGGCAATTTGCGCGGAGGCC 4368
4404 GAACAACGTCTATCTCGGGATCACCGGAAATCACCGGTGAGCATCATCGCGGAGCGCC 4463
4369 CATGCATGCCAGGTCCCTGGCATGTGACCACTTCTGTAAGCAAGGTGGCCATCCACGC 4428
4464 CATGCATGCCAGGTTCGCGCATGCACTACT---CGCTCAGCAAGCTCGCCATCCACTC 4520
4429 AACCTTGGAGTCAGCCACCGCTTTGGCTGTTTCAACAATGGGGTCTGTATATGTGA 4488
4521 TGCTCTGGAGTCAGCCAGCGCATCGCCATTTCTCACACCGGGGTGCTCTACATCACCGA 4580
4489 GACTGATGAGAAAGATCAACCCGATCAGCAGGTCAACNCTAGTGGAGAGATCTCACT 4548
4581 GACGACGAGAAGAAGATCAACCGCTACGCGAGGTCAACCAACGAGAGATCTCGCT 4640
4549 GCTTGTGGGCGCCCGAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATGTTTTC 4608
4641 CTTAGCCGGGCGAGCTCAGACTGTGACTGCAAAAATGACGTCAACTGCACTGCTGCTATTC 4700
4609 TGGAGACGATGGTTATGCAAGGATGCAAAAGTTAAATACCCCATCTTCTTGGCTGTGTG 4668
4701 GGGAGATGACGCATACGCCACCGATGCCATCTTGAATCCCGCTCTCTTAGCTGTGGC 4760
4669 TGCTGATGGGAGCTCTACGTGGCGGACCTTGGGAACATCCGAATTCGGTTTATCCGGAA 4728
4761 TCCGGATGGCAACCATCTACATCGGAGACCTCGGGAATATCCGATCAGGCGGTGACCAA 4820
4729 GAACAAGCTTTCTCAACACCCAGAACATGATGAGTGTCTTCAACCAATTTGACCAAGGA 4788
4821 AACAACAACCTGTTCTTAACGGGTTCAACCAAGTATGAGGCTGCTCTCGGGAGAACAGGA 4880
4789 GCTCTATCTGTTGATACCAACCGGACAGCACTGTATACACCAAGCTTCCGACCAAGGAGA 4848
4881 ACTGTACGTGTTCAACCGCGATGGTATCCATCAGTACACCGTGTGGTGTGGTACCGGGGA 4940

4849 CTACCTGTACAACCTTCACTTACCTTACCTGAGGACGCGACATCACACTCATCACAGACAA 4908
4941 GTACTTATACAAATTTACCTTACAGCGCTGACATGATGTACCGAGTTGATTGACAACAA 5000
4909 TGGCAACATGGTAAATGTTCGCGGAGACTCTACTGGATGCCCTCTGGGCTGTGTGTCCTC 4968
5001 CGGGAATTCCTTAAAGATTCGCGGGACAGCAGTGGCATGCCCGACACACTGTCTCATGCC 5060
4969 AGATGCCAGGTCTACTGGGTGACCATGGSCACCAACAGTGCACTCAAGAGTGTGACCA 5028
5061 TGAATATCAGATCATCACCTTACCGTGGGCAACAACGGAGGCTTCAAGCGGTGTCAAC 5120
5029 ACAAGCACACGAGTGTGGCCATGATGACATACCATGCAATTCGCGGCTTCTTGGCAACAA 5088
5121 GCAGAACCTGGAGCTGGGCTCATGACTTATGATGGGAACACTGGACTCTCTAGCCACAA 5180
5089 AAGCAATGAACACGGATGGACAAATTTATGATGACAGAGCTTTTGGCGGCTGTGACAA 5148
5181 GAGCGATGAACCGGATGGACAACTTTTATGATGATGACAGAGGCGGTCTGACCAA 5240
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5241 TGTGACTTCGCCCCCAGCGGGGTGTGACCGACCTGCAACCGGAAATGGAGAAATCCATCAC 5300
5209 TGTCCAGGTAGACACCTCCAGCAAGGAT---GATGTCAACATAACCAACCAACCTGTCTGC 5265
5301 CGTTGACATTTGAGAACCTCCAAACCGTATACGATGTCTGTGATTTACCAACCTCTCTTC 5360
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5361 AGTGGAGGCTCTCTACACCGTGTACAAAGTCAAGTCAAGTCCGGAACAGCTTACAGCTCTCAG 5420
5326 CGATGGCTCTTTCGGGCTGTCTGCGCAACGCGATGGAGGTGGCGCTGAGACTGAGCC 5385
5421 CAACGGGACCTTCGCGTCTATGTACGCAACCGCATGGGCTCAGCTTCCACAGCGAGCC 5480
5386 CCACTTGTGGCTGGCACCGTCAACCCACCGTGGGCAAGAGAAATGTCACTGCTGCGCCAT 5445
5481 CCAGTCTCTCGAGGACACCTCTCACCCACCATCGGGGCTGTAAATCTCTCTGCGCCAT 5540
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5541 GGAGAACGGCTTGAATCTCCATCGAGTGGCGCTGAGGAAGAAACAGATTAAAGGCAAGT 5600
5506 CACTGTCTTTGGGCGCGGCTGCGGTGCAACCCGAAATCTCTATCTCTGGACTTTGA 5565
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5721 TTATGACCAAGTGGCGCGCCCTTCTGTGGCTCCCCCAGCAGTGGACTGGCGGCGGTCAA 5780
5686 CGTGACATACTCCCTGGGGGTTACATTGTGTGCAATCCAGGGGCACTGCTGTAAG 5745
5781 TGTCTCTACTTCTTCAACGGGCGCTTGGCGGCGCTCAGCGGGGCGCATGAGCGAGAG 5840
5746 AATGGAATACGACAGCGGCGCGCATCATATCCAGGATCTTCGCTCATGGGAAGACATG 5805
5841 GACAGCATTTGACAGCAAGCGGATGTGTGTCCGNAATGTTCCCGACCGGAAAGTCTG 5900
5806 GAGCTACACATCTTAGAGAAAGTCCATGGTGTCTACTACACAGCAGAGGCGAGTATAT 5865
5901 GAGCTATTCCTACTTGTGACAAGTCCATGGTCTCTCTGCTCAGAGCGCAGGTCTAGTACAT 5960
5866 CTTTGTGATTCGACAGAAATGACCGCTCTCTTCTGTGACCATGCCCAACGTGGCGCGGCA 5925
5961 ATTTGAATATGACTCTCTCTGACCGCTCCACGCAAGTCAACCATGCCAGTGTGCGCGCGCA 6020

| | | | | | | | |
|----|------|--|------|----|------|--|------|
| QY | 5926 | GACACTAGAGACCAATCCGCTCAGTGGGCTACTACAGAAAACATCTATCAGCCCCCTGAGGG | 5985 | Db | 7101 | CACCCATGTTTACAACCACTCCAACTCTGAGATCACCTCACTCTACTATGACCTCCAGGG | 7160 |
| Db | 6021 | CAGCATGTCACGACACCTCCATGGCTATACCGGAACATTTTACAAACCCACCGGAAG | 6080 | QY | 7063 | ACACTCTTTTGCCATGGAGCTGAGCTGCTGATGAGTTTATACATAGCTTGTGACAACAT | 7122 |
| QY | 5986 | CAATGCCCTCAGTCTACAGGACTTCACTGAGATGGGCACCTCTCTTACACCTTCTACCT | 6045 | Db | 7161 | CCACTCTTTTGCCATGGAGCAGTAGTGGGAAGAGTACTATGTTGCCCTCAGATAAAC | 7220 |
| Db | 6081 | CAAGCCCTCGGTCACTTTTGACTACAGTGTGACGGCCGCACTCTGAAGAGCTCTTTCCT | 6140 | QY | 7123 | CGGACCCCTCTTGTCTTTTATAGTGAACAGGTTTATGATCAAGCAAAATCCCTGTATCAC | 7182 |
| QY | 6046 | GGGCACTGGCCGCGAGGGTGATATACAGTATGGCAAACTGTCAAAGCTGGCAGAGCGCT | 6105 | Db | 7221 | CGGACTCTCTCGCTGTTTATAGTATCAATGSCCTCATGATCAAGCAATCCCAATACAC | 7280 |
| Db | 6141 | GGGCAACGGGCGCAGGTTCTATAAGTACGGAATACTGTCCAAGTTATCGGAGATCGT | 6200 | QY | 7183 | AGCCTATGGGAGATCTACATGATACCAACCCCACTTTTCAAGATCATATAGGCTACCA | 7242 |
| QY | 6106 | CTATGACACACCAAGGTCAGTTTACCTATGACGAGACGGCAGCATGCTGGAAGACCAT | 6165 | Db | 7281 | AGCCTATGGGAGATTTACTATGACTCCAATCCAGACTTTTTCAGATGGTCTATCGGCTTCCA | 7340 |
| Db | 6201 | CTACGACAGCACTGCGCTCACCTTCGGCTATGAOGAGACCACTGCGCTCTTGAAGATGGT | 6260 | QY | 7243 | TGGTGGCTCTATGATCCACTCACCAGCTTGTCCACATGGCCGGCGAGATTATGATGT | 7302 |
| QY | 6166 | CAACCTACAGAAATGAGGCTTCACTCGACCAATCCGCTACCGTCAAGTGGGCCCCCTGAT | 6225 | Db | 7341 | CGGAGGCTCTACGACCCCTCACCAAGCTGTTTCACTTTTACGGCAGGTGATGACGT | 7400 |
| Db | 6261 | GAACTCTCAAGCGGGGCTTCTCTGTACCATCAGGTACCGAAAGGTCGGGCCCTCGT | 6320 | QY | 7303 | GCTGGCCGAGCGCTGGACTAGCCACGACGAGCTGTGGAAGCACCTTAGTAGCAGCAA | 7362 |
| QY | 6226 | TGACCGACAGATCTTCCGCTTCACTGAGGAAGGCATGTCAAGCCCGTTTTGTACTACA- | 6284 | Db | 7401 | GCTGGCAGGACGGTGGAGCTCCCCGACTACACCATGTGGAGGAA---TGTGGGCAAGGA | 7457 |
| Db | 6321 | GGCAAGCAGATTTTACAGTTCTCTGAGGAAGGCATGATCAACGCGAGGTTTCTGATACAC | 6380 | QY | 7363 | CGTCATGCCCTTTAATCTCTATATGTTTCAAAAACAAACCCCATCAGCAACTCCCAGGA | 7422 |
| QY | 6285 | --ACTATGACACAGCTTCCGGTGACAGCATGCGGCTGTGATCAACGAGACCCCACT | 6342 | Db | 7458 | GCCAGCCCCCTTCAACCTGTACATGTTTCAAGAACAAACATCCACTCAGTATAGAGCTGGA | 7517 |
| Db | 6381 | CTTACACGCAACACAGCTTCCGCATCGCCAGCATCAAGCCCGTCACTCAGTGAGACTCCCT | 6440 | QY | 7423 | CATCAAGTGTTCATGACAGATGTTAACAGCTGGCTGCTCACCTTTTGGATTTCCAGCTACA | 7482 |
| QY | 6343 | GCCCATTTGATCTCTATCGCTATGATGTGTGAGGCAAGACAGACGAGTTTGGGAAGTT | 6402 | Db | 7518 | TTTAAAGAACTACGTGACAGACGTGAAGAGCTGGCTGCTGATGTTTGGATTTTCACTCAG | 7577 |
| Db | 6441 | TCCCGTTGACCTTACCGCTACGATGAGATTTCTGGCAAGGTGGAACACTTCGGCAAGTT | 6500 | QY | 7483 | CAACGTGATCCCTGGTTATCCCAAACGACAGCATGGATGCCATGGAACCCCTCTACGAGCT | 7542 |
| QY | 6403 | TGGTGTCAATTTACTATGACATTAACAGATATACACAGCTGTCTATGACCCACACCA | 6462 | Db | 7578 | CAACATCATTTCTGATTTCCCAAGAGCCAAATGTAATTTGTGGCTCCCCCTATGA--- | 7634 |
| Db | 6501 | CGGGTCACTACTACGACATCAACCCAGATCATCACTGCGCTCATGACACTCAGCAA | 6560 | QY | 7543 | CATCCACACACAGATGAAACCGCAGGAGTGGGAACAAGCAAGTCTATCCCTCGGGGTACA | 7602 |
| QY | 6463 | GCATTTGATGATATGGCAGATGAAGAACTGAGTATGATGATCTTCCGCTCCGCTCAT | 6522 | Db | 7635 | -----ACTGTCCAGAGAGCCAAAGTGAATGGAAGTCAATCAGGTGTCTCA | 7685 |
| Db | 6561 | GCATTTTGAACCCATGGCGCATCAAGGAAGTGCAATGAGATGTTCCGGTCCCTCAT | 6620 | QY | 7603 | GTGTGAGTACAGAAAGCAGCTCAAGGCTTTTGTCACTTTAGAACGGTTTGACCAAGCTCTA | 7662 |
| QY | 6523 | GTACTGGATGACCGTCCAGTATGATAACATGGGGCGAGTAGTGAAGAAAGGAGCTGAAAGT | 6582 | Db | 7686 | GCAGAACACAGAGAGGCATTAACAGGCTTTTCTGGCTCTAGAGGACAGGTCATCTCTAA | 7745 |
| Db | 6621 | GTACTGGATGACCGTGCAATATGACAGTATGGCAGGTCATCAAGAGGGAACCTGAACCT | 6680 | QY | 7663 | TGGCTCCACAATCACCAGCTGCCAGAGGCTCCAAAGACCAAGAAAGTTTGTATCCAGCGG | 7722 |
| QY | 6583 | AGGACCTTAGCCCAATACCACTCGCTACTCTCTATGATGATGATGCTGAGCGGCAGCTGCA | 6642 | Db | 7746 | AAAGTCCATCGAGCATCCGAGAGAAAGC-----AGGCCACTGGTTTGTACACCAC | 7799 |
| Db | 6681 | GGGGCCCTATGCCAACACCAACAAAGTACACCTATGACTACGACGGGGAGCGGCAGCTCCA | 6740 | QY | 7723 | CTCAGTCTTTTGGCAAGGGGTCAAGTTTGCCTTGAAGGATGCGGAGTGACCAACAGACAT | 7782 |
| QY | 6643 | GACAGTCTCCATCAATGACAAAGCCACTCTGGGCTACAGCTACGACCTCAATGGGAACCT | 6702 | Db | 7800 | GCCCATCATCGGCAAAAGGCATCATGTTCCGCTCAAGAAAGGGCGGTGACCAAGGCGT | 7859 |
| Db | 6741 | GAGTGTGGCCGTCAATGACGGCTTACCTGGGTTATAGCTATGACCTCAATGGGACCT | 6800 | QY | 7783 | CATCAGTGTGGCCATGAGGATGGCGAAGGGTTGCTGCCATCTTTGAACCATTGCCCACTA | 7842 |
| QY | 6703 | GCATTTACTGAGCCCTGGGAACAGTGCACGGCTCACCACTACCGGTATGACATCCGCGA | 6762 | Db | 7860 | GTCTAGCATCGCAGTGAAGACGCGCAAGGTAGCATCCGTGTTTGAACAACGCGCTACTA | 7919 |
| Db | 6801 | GCACCTGCTAAACCCAGGAAACAGTCTCGCTCATGCTGCGGTTACGCTATGACCTCCGTCG | 6860 | QY | 7843 | CCTAGAGAACCTGCACTTTCACATTTGATGGGTGATACCCATTTACTTTTGTGAACACGAG | 7902 |
| QY | 6763 | CGGCATCACTCGGCTGGGTGACGTGCAATACAAGATGGATGAGGATGGCTTCTGAGGCA | 6822 | Db | 7920 | CTTGACACAAGATGCACTACAGCATCGAGGGCAAGGACACACACTACTTCTGTAAGATCGG | 7979 |
| Db | 6861 | CCGGATAAACAGGCTAGGGAGCGTGCAGTACAAATCGATGATGATGGGTATTTATGCCA | 6920 | QY | 7903 | ACCTTCAGAAAGGTGACCTGGCCATCTCGGCTCAGTGGGGGGCGGCGAAACCTCGAGAA | 7962 |
| QY | 6823 | GCGGGCGGTGATATCTTTGAGTACAACTCAGCTGGCTGCTCATCAAGGCCCTTACAACCG | 6882 | Db | 7980 | TGCAGCGAGCGGTGACCTGGTTTACGCTGGGGAACCACTTGGGCGCAAGGTCCTGGAGAG | 8039 |
| Db | 6921 | GAGAGGATCTGACATCTTTGAATACAACTTCAAGGGCTTCTTAAACGAGAGCGTACAACAA | 6980 | QY | 7963 | TGGGGTCAACGTCACCTGTGTCCAGATCAACACAGTACTTAAATGSCAGGACTAGACGCTA | 8022 |
| QY | 6883 | GGCTGGCAGTGGAGTGTCAAGTACCGCTACGATGGCTGGGGCGGCGGTGTCAGAGCAA | 6942 | Db | 8040 | CGGGGTGAACGTGACCGTGTACACCCCAACGCTGCTGGTGAACGCGCAGGACTCGAAGGTT | 8099 |
| Db | 6981 | GGCCAGCGGTGGAGTGTGCAGTACCGCTATGATGGCTGAGCGCGCGGCTTCTTACAA | 7040 | QY | 8023 | CAACAGATCCAGCTCCAGTACGGGGCTACTGTGCTTGAACACACACGCTACGG----- | 8073 |
| QY | 6943 | GAGCAGCCACAGCCACCACTGAGTCTTCTATGACAGACCTGACCAACCCCAACCAAGT | 7002 | Db | 8100 | CACCAACATTTGAATTTCCAGTACTCCACGCTGCTGCTCAGCATACGCTACGGCTCACCCC | 8159 |
| Db | 7041 | GACCAACCTGGGGCCACCACTACAGTACTTCTATTCGACCTCCACACCCCAACACGTTAT | 7100 | QY | 8074 | GACACGTTGGATGAGGAGAGGCAACGGTCTCTGAGCTGGGCCCGCAGAGAGCGGTGG | 8133 |
| QY | 7003 | CACCCACCTGTACAAACCACTCCAGCTCTGAGATCACTCCCTCTCTACTACGACTTGCAAGG | 7062 | | | | |

Db 8160 CGACACACTGGATGAAGAGAGGCCCGCGCTCTGAGCAACAGCGGACAGAGAGGCCCTGGG 8219
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Db 8220 TACTGCTGGCCCAAGAGCAGCAGAAAGCCAGGAGCGGAGAGAGGCGTAGCGTCTGTG 8279
Qy 8194 GACAGAGGGGGAAGCAGCAGGTGTGTGAGCAGAGCGCGGTGCAAGGCTTACGACGGCTT 8253
Db 8280 GACGGAGGGGAGAGCAGCACTCTCTGAGCAGCGGACGGGTGCAAGGTTATGAGGGCTA 8339
Qy 8254 TTTCGTGATCTGTGTCAGCAGTACCCAGAACTGTGACAGCGGCCCAACAACTCACTT 8313
Db 8340 TTACGTGCTTCCGCTGGAACAGTACCAGAGCTGGCAGACAGTAGCAGCAACATCCAGTT 8399
Qy 8314 CATGACAGCAGCAGGATGGCCGGAGGTGACAGA 8348
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RESULT 15

US-09-808-602-7
; Sequence 7, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US20020155115A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 9826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (280)..(8478)
US-09-808-602-7

Query Match 40.5%; Score 3385; DB 3; Length 9826;
Best Local Similarity 64.7%; Pred. No. 0;
Matches 5393; Conservative 0; Mismatches 2790; Indels 154; Gaps 18;
Qy 35 ATGACCTGAGAGAGAGCCTTACCGTCTGCTGACCCCGCGCGCCGCGAGCGCGC 94
Db 280 ATGGATGAAGGACCGCGACACCGCTCTTTGACCAGAGACGCTGTGGCAAGAGTGT 339
Qy 95 CGCTACACCAAGCTCGTCCGCGGACGAGGAGGGCAAG---CCCCCGAGAAATCGTAC 151
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Qy 152 AGCTCCAGCAGACCTCTGAAGGCTACGACAGGACCGCCCTAGCTATGGCAGCGCC 211
Db 400 AGCTCCAGTGAGACTCTGAAGGCTATGACCATGACAGCAGGATGCACTATGGAACCGA 459
Qy 212 GTCAGACATTTGCGCGCAGGAGCGCAGGAATTTGCCGACAGGTGCCAACTTCAAC 271
Db 460 GTACAGACCTCATCCACCGGAGTCAGATGAGTTTCTTAGAAGGAACCAACTTCACC 519
Qy 272 CTGCGGAGCTGGGCTGGGAAGAGTAACGCCCTTCAACGGGAGCCCTGTACCGGACAGAC 331

Db 520 CTTGGCCGAACCTGGGCATCTGTGA---GCCCTCCCCACACCGAAGCGGCTACTGCTCCGAC 576
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Qy 392 GACACGGTCTGTCCCTTAGCACCCTGTCGCTCTGTGGGCGCGAGACACACGGTCAGGG 451
Db 637 GAGGGAGGATGTCTCCAGAACACGCCATCAGACTGTGGGCGAGAGGATAAATCCAGG 696
Qy 452 CGCAGCTCTGCTGTGTCAGCGGGCCAAATTCCAATCTCACAATCTCACCACACCGAGCAT 511
Db 697 CGCAGTTCCGGCTGTGTCAGTCTGGAATACTCGGCCCTTACCCCTGACTGACTCTGAACA 756
Qy 512 GAAACACTGAGACTGATCATCCGGCGGCC---TGCAAGAACACCGCGGCTCCGGAC 567
Db 757 GAAACAAATCAGATGATGAAACGGTCTGCCATTCACCTACATCTCTCGCTAGTCTC 816
Qy 568 GCGCGCGCCGCTCTCGCAGCGCCACACCCCAACAGCAACACGCGGCTCTCCATTA 627
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Qy 628 CTCCTGTAACCGGGCACTTACGCGGAGGAGCAACCCAGCCGCGCCGCCCGCCAGGACCA 687
Db 876 ATTGCTAGACAGCAACACCTCCCATCAAAATCATGGACACCAACCCGTGATGAGAAATTCTC 935
Qy 688 CTCGCTCTCCGGAGAGCCCTCTGCGCGCGCGCCAGGAGCCTGCCACGCCCAGAGAA 747
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Qy 748 CTGGCTGTCTCAACAGCAACATCCCTCTGGAGACCAAGAACCTTAGGCAAGCAGCAATTCCT 807
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Qy 808 AGGGAATTTGAGGACAACTCATTTAGATGAGCAATTTCTGGGCGCTCTCCGCGCATATGG 867
Db 1038 ACCCTCTCAACACACACGCTGTCCCATCACCCTCTGCGGCACTCTCCCTCAACAGGAA 1097
Qy 868 GCGTTACAGTGAGCGGCACTTCTCTTCAAGCTGGAGGACCTCCCGCTCTCTGTCAC 927
Db 1098 CTCCTGACCAATCGGCGGAGTCAGATCCACGCCCGCGCCAGCGCCCAATGACCTGGC 1157
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Qy 1227 TATACCCCTCAGGGGCACTGGCTTAGAGACCCCTGACAGGAAGGCAAGGCAAGGACACAG 1286
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QY 1407 TAGACCATCTCTGTGCATCTGAAATTCATATGTGTCTCTGGGAAAGGAGCCCTGTTGGCA 1466
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QY 1527 ATGGCAGGAGGCTCTTAACCCAGGAGCGCGAGCCTAGAGGGACCCCGCGCAGTCTC 1586
Db 1694 ACGGA-----AGGAGAGTGGAGTGTGGTTGAGTCTCCAGGGAACGCC 1738
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Db 1799 TGTGGCATCTGGCCCTTCTACAAATGATGGAAGAAGACAAAGAGATGGTTTCTTCAATCTG 1858
QY 1707 CTGCCATTGAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGGTGACTGCACT 1766
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QY 1767 CTGGGACCTGCCACTGCTTCTCGGGTTTCTGGGCCCCGACTGTGGCAGAGCCTCTGCC 1826
Db 1919 CCGGGGTGTGTCACTGTGTTTCCAGGATTTCTAGGAGCAGACTGTGCTAAAGCTGCCCTGCC 1978
QY 1827 CCGTCTCTGTAGCGGAATGCCAATACATGAAAGGCGAGATGCTGTGTGCCACAGTGGCT 1886
Db 1979 CTGTCTGTGCAATGGGAATGGAACAATTTCTAAGGGACGTGCCAGTGTCTACAGCGCT 2038
QY 1887 GGAAAGGCGCTGAGTCGATGTGCCCAACCAACAGTGTATCGATGTGGCTGTGCAGCAACC 1946
Db 2039 GGAAGGTGCAGAGTCGACGTGCCCATGAATCAGTGCATCGATCCTCTCTCGGGGGCC 2098
QY 1947 ATGGCACTGTGATCAGCGGCACCTGATCTGCAACCTCGCTACAGGGCGAGAGCTGTG 2006
Db 2099 ACGGCTCTCTGCAATGATGGGAATCTGTCTGTCTGTGGCTACAAAGCGCGAGCACTGTG 2159
QY 2007 AGGAAGTGACTGTGATGGACCCACATGTTCAAGCGCGGGTGTCTGCGTGAGAGCGAAT 2066
Db 2159 AGGAAGTTGATTTGCTTGGATCCCACTGTCTCAGCCACGAGTCTGTGTGAATGGAGAT 2218
QY 2067 GCCATTGCTTTGTGGATGGGAGGCAACCACTGGGAGACCCCGAGGCGCACATGCTTAG 2126
Db 2219 GCCTGTGCAGCCCTGGCTGGGGTGGTCTGAATGTGAGCTGGCGAGGGTCCAGTGCCTCAG 2278
QY 2127 ACCAGTGTTCAGGCCACGGACCTTCTCCCGGACACCGGGCTTTGACGCTGTGACCCAA 2186
Db 2279 ACCAGTGCAGTGGGCATGGCAGTACTGCTGTGACACGGGCTCTGACGCTCGATCCCA 2338
QY 2187 GCTGGACTGGACACGACTGTCTTATCGAGATCTGTGCTGCCGACTGTGTGGCCATGGCG 2246
Db 2339 ACTGGATGGGTCCGACTGCTCTGTTGAGTGTGCTCAGTACAGTGTGGCACTCAGCGCG 2398
QY 2247 TGTGCTAGGGGCACTCTGCGCTGTGAGGATGGCTGGATGGGGGAGCCTGGACCAGC 2306
Db 2399 TCTGCATCGGGGAGCCTGCGCTGTGGAAGAGGGCTGGACAGGCGAGGCTGTGACCAGC 2458
QY 2307 GGGCCTGCCACCGCGCTGTCCGAGCATGGGACCTGCCCGGACGGAAGTGGAGTGCA 2366
Db 2459 GCGTGTGCCACCCCGCTGATTTGAGCAGCGGACCTGTAAAGTGGCAATGTGAATGCC 2518
QY 2367 GCCCTGGCTGGAATGGCGAACACTGCACCATCGCTCACTATCTGGATAGGGTATGTTAAG 2426
Db 2519 GAGAGGGCTGGAATGGTGAACACTGCACCATTTGTAGGCAAAACGCGAGGCAACGAAACAG 2578
QY 2427 AGGGTTGCCCTGGGTTGTGAATGGCAACGCGAGATGTACTTTAGACCTGGAATGGTTGCC 2486
Db 2579 ATGGCTGCCCTGACTTGTGCAACGGTAAACGGGAGATGCACACTGGGTTCAGAACAGCTGGC 2638

QY 2487 ACTGCGTCTGCCAGCTGGGCTGGAGGAGCTGGCTGTGTGACACTTCCATGGAGACTGCCT 2546
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QY 2547 GCGGTGACAGCAAAAGACAATGATGGAGATGGCCTGTGTGGACTGCATGGAGCCCTGACTGCT 2606
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QY 2607 GCCTCAGGCCCTGTGCCATATCAACCCGCTGTGTGCTTGGCTCCCTTAAACCCCTCTGGACA 2666
Db 2759 GCCTGCACTGAGCCTGTGCAACAGCCTGTCTGCCGGGGTCCCGGAGCCCACTGGACA 2818
QY 2667 TCATCCAGGAGACACAGGTCCTGTGTACAGCAGAACTACACTCTCTTCTATGACCGCA 2726
Db 2819 TCATTGAG-----CAGGGCCAGAGGATTTGGCCGAGTGAAGTCTCTTATGACCGTA 2872
QY 2727 TCAAGTTCTCTGTGGGAGGAGCAGCAGCACATAATCCCGGGGAGAACCCCTTTTCATG 2786
Db 2873 TCAAGCTCTTTGGCAGGCAAGGATAGCACCCACATCATTTCTTGGAGAGAACCCCTTTCAACA 2932
QY 2787 GAGGCATGCTTGTGTTATTTCGTGGCCAGTGTGATGACATCAGATGGGAACCCCTCGTGTG 2846
Db 2933 GCAGCTTGGTTTCTCTCATCCGAGGCCAGTAGTACTACAGATGGAACTCCCTGCTGTCG 2992
QY 2847 GTGTGAACATCAGTGTTCATAAACCTCTCTTTGGATATACAATCAGCAGGCAAGATG 2906
Db 2993 GTGTGAACGCTGCTTTTGTCAAGTACCCAAAATACGGCTACACCATCACCCGCCAGGATG 3052
QY 2907 GCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCTCGGTTTCAGCGGGCAC 2966
Db 3053 GCAGCTTCGACCTGATCGCAAAATGGAGGTGCTTCTTGACTCTTACACTTTGAGGAGGCC 3112
QY 2967 CTTTTCATCACACAGGAGCACACCTGTGTGGCTGCCATGGGATCGCTTCTTTGTCTATGGAAA 3026
Db 3113 CGTTTCATGAGCCAGAGGCGACTGTGTGGCTGCCGTGGACAGCTTTTACGCCATGGACA 3172
QY 3027 CCATCATCATGAGACATGAGGAGAAATGAGATTTCCAGCTGTGACTGAGCAATTTTGCCC 3086
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QY 3087 GCGCCAACCCAGTCTCTCTCCATCCCACTGAGCTCTCTCGCCAGCTCTCTGTGCAGAGA 3146
Db 3233 GGCCTGATTCCAATCATCATCTCTCCCACTGTCACTTCTTTAGTGTGCCCTTGGGC 3292
QY 3147 AAGGCCCATTTGTGCCGAAATTCAGGCTTTGCAAGGAGAAATCTCTATCTCTGTGCTGCA 3206
Db 3293 AGAATCCCATCGTGCCTGAGACCCAGGTTCTTCATGAAGAAATCGAGCTCCCTGGTTCCA 3352
QY 3207 AGATGAGCTGAGCTACCTGAGCAGCCGAGCCCTGGCTACAAATCTGTCTCTGAGGATCA 3266
Db 3353 ATGTGAACCTTCGCTATCTGAGCTCTAGAACTGAGGGTACAAGTCACTGCTGAAGATCA 3412
QY 3267 GCCTCACCCACCGACCATCCCTTCAACCTCATGAAGTGCACCTCATGTGTAGCGGTGG 3326
Db 3413 CCATGACCCAGTCCACAGTGCCCTGAAACCTCATTTAGGGTTTCACCTGATGGTGTGTCG 3472
QY 3327 AGGGCGGCTCTTTCAGGAAAGTGGTTGCTGAGCAGCCCAAGCTGCTTATTTATTTTCATTT 3386
Db 3473 AGGGGCACTCTTCCAGAAGTCAATTCAGGCTTCTCCCAACCTGCGCTCCACCTTCATCT 3532
QY 3387 GGGCAAGACAGACGCTCTACAAACGAAAGTGTGTGGGCTTTTCAGAACCTTTGTTTCG 3446
Db 3533 GGGCAAGACAGATGCGTATGGCCAAAGGGTGTATGGACTCTCAGATGCTGTGTGTCTG 3592
QY 3447 TGGGTTATGAATATGAATCTCTGCCAGATCTAATCTCTGGGAAAAAGAAACAACAGTGC 3506
Db 3593 TCGGGTTTGAATATGAGACCTGTCCAGTCTAATTTCTCTGGGAGAAAGGACAGCCCTCC 3652
QY 3507 TGCAGGGCTATGAAATTGACCGGCTCCAGCTTGGAGGATGGAGCCTAGACAAACATCATG 3566
Db 3653 TTCAGGGATTCGAGCTGGACCCCTCAAACCTCGTGGTGTGCTCCCTAGACAAACCAACA 3712
QY 3567 CCCTCAACATTCAAAGTGGTATCTCTGCACAAAGGGAATGGGGAGAACCAAGTTTGTGTCTC 3626

| | | | |
|----|------|---|------|
| QY | 5784 | TCTTTCGCTGATGGGAAGACATGGAGCTACACATACTTAGAGAAAGTCCATGGTCTCTACT | 5843 |
| DB | 5930 | TGTTTCGCTGACGGGAAGTGTGGAGCTACTCTTACCTTGACAAGTCCATGGTCTCTCTGC | 5989 |
| QY | 5844 | TACACAGCCAGAGCGCAGTATATCTTTGAGTTGCACAAGAAATGACCGCCTCTCTTCTGTGA | 5903 |
| DB | 5990 | TTCAGAGCCAAACGTCAGTATATATTTTGGATGATGACTCTCTGACCGCCTCTTTGCCGTCA | 6049 |
| QY | 5904 | CGATGCCAAACGTTGGCGGCAGACACTAGAGACCATCGCTCAGTGGGGCTACTACAGAA | 5963 |
| DB | 6050 | CCATGCCACGCTGGCCCCGGCACAAGATGTCACAACACCTCCATTCGGCTACATCCGTA | 6109 |
| QY | 5964 | ACATCTATACGCCCCCTGAGGGCAATGCCCTCAGTCATACAGGACTTCACTGAGGATGGGC | 6023 |
| DB | 6110 | ATATTTTACAACCGCCTGAAAGCAATGCTTCGGTCACTCTTTTGACTACAGTGATGACGGC | 6169 |
| QY | 6024 | ACTCTCTTACACCTTCTACTCGGCNACTGGCGCAGGGTGATATACAGTATGGCAAAAC | 6083 |
| DB | 6170 | GCATCTCTGAAGACCTCTCTTTTGGGACCGGACGCCAGGTGTTCTCAAAGTATGGGAAC | 6229 |
| QY | 6084 | TGTCAAAGCTGGCAGAGACGCTCTATGACACCAACGAGGTCAGTTTTCACTATGACGAGA | 6143 |
| DB | 6230 | TCTCCAGTTTATCAGAGATTGTTCTACGACAGTACCGCCGTCACCTTCGGGTATGACGAGA | 6289 |
| QY | 6144 | CGGCAGGCATGCTGAAGACCATGAACTTACAGAAATGAGGGCTTCACTGCACCATCGCT | 6203 |
| DB | 6290 | CCACTGGTGTCTTGAAGATGGTCAACCTCCAAAGTGGGGCTTCTCTCGCACCATCAGGT | 6349 |
| QY | 6204 | ACCGTCAGATTGGSCCCTGATTGACCGACAGATCTTCGCTTCACTGAGGAAGGCATGG | 6263 |
| DB | 6350 | ACCGAAGATTGGCCCCCTGGTGAAGAAGCAGATCTACAGGTTCTCCGAGAAGGCATGG | 6409 |
| QY | 6264 | TCAACGCCCTTTTGACTACAACCT--ATGACAACAGCTTTCGGGTGACGAGCATGAGG | 6320 |
| DB | 6410 | TCAAATGCCAGTTTGACTACACCTTATCATGACAACAGCTTTCGCGATCGCAAGCATCAAGC | 6469 |
| QY | 6321 | CTGTGATCAAGGAGACCCCACTGCCAATTCATCTCTATCGCTATGATGATGTCTCAGGCA | 6380 |
| DB | 6470 | CCGTCAATAGTGAGACTTCCCTCCCGGTGACCTCTACCGCTATGATGAGATTTCTGGCA | 6529 |
| QY | 6381 | AGACAGACGAGTTTGGGAAGTTTGGTGTCATTTATATGACATTAACCCAGATCATCACCA | 6440 |
| DB | 6530 | AGGTGGAACACTTTTGGTAAGTTTGGAGTCACTATTATGACATCAACCCAGATCATCACCA | 6589 |
| QY | 6441 | CAGCTGTCTGACCCACCAACCAAGCATTTTGAATGCATATGCCAGATGAAGGAAGTCAGT | 6500 |
| DB | 6590 | CTGCGGTGATGACCTCAGCAAAACACTTCGACACCCATGGCGCGATCAAGGAGGTCAGT | 6649 |
| QY | 6501 | ATGAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCAGTATGATAACATGGGCGCAG | 6560 |
| DB | 6650 | ATGAGATGTTCCGCTCCCTCATGTACTGGATGACGGTGCAATATGACAGCATGGCAGGG | 6709 |
| QY | 6561 | TAGTGAAGAAGGAGCTGAAGGTAGGACCCCTACGCGCAATAACAATCGCTACTCTATGAGT | 6620 |
| DB | 6710 | TGATCAAGAGGAGCTAAACCTGGGGCCCTATGCGCAATAGCACGAAGTACACCTATGACT | 6769 |
| QY | 6621 | ATGATGCTGACGGCCAGCTCGACAGCTCCCATCAATGACAAGCCACTCTGGCGCTACA | 6680 |
| DB | 6770 | ACGATGGGACGGGCAGCTCCAGAGCGTGGCCGTCGAATGACCGCCGACCTGGCGCTACA | 6829 |
| QY | 6681 | GCTACGACCTCAATGGGAAACCTGCATTTACTGAGCCCTGGGAAACAGTGCACGGCTCACAC | 6740 |
| DB | 6830 | GCTATGACCTTAAATGGGAACTCTCCACTTACTGAAACCCAGGCAACAGTGTGGCGCTCATGC | 6889 |
| QY | 6741 | CACTACGGTATGACATTCGGGACCGCATCACTCGGCTGGGTGAGCTGCAATACAAGATGG | 6800 |
| DB | 6890 | CTTTGCGCTATGACCTCCGGATCCGATAACCAAGACTCGGGGATGTGCAGTACAAATTTG | 6949 |
| QY | 6801 | ATGAGGATGGCTTCTCTGAGGCAGCGGGCGGTGATATCTTTTGAGTACAACTCAGCTGGCC | 6860 |
| DB | 6950 | ACGACGATGACTATCTGTGCCAGAGAGGGTCTGCATCTTCGAATACAAATCCAAAGGCC | 7009 |

| | | | |
|----|------|---|------|
| Qy | 6861 | TGCTCATCAAGGCGCTTAAACACGGGCTGGCAGCTGGAGTGTCAAGTACCCGTACGATGSGCC | 6922 |
| Db | 7010 | TCCTAAACAAGAGCTTAAACAAGGCCACGGGGTGGAGTGTCCAGTACCCGTATGATGGCG | 7069 |
| Qy | 6921 | TGGGGCGGCGGTGTCACGACAGAGCAGCAGACAGCCACCACTGCAAGTTCTTCTATGCGAG | 6980 |
| Db | 7070 | TAGGACGGCGGGCTTCTTCAAGACCACTGGGCCACCACTGCGAGTACTTCTACTCTG | 7129 |
| Qy | 6981 | ACCTGACCAACCCCAACAAGGTCAACCACTGTACAACCACTCCAGCTCTGAGATCACCT | 7040 |
| Db | 7130 | ACCTCCACAACCGACGCGCATCAACCATGTCTACAATCACTCCAACCTCGAGATTACCT | 7189 |
| Qy | 7041 | CCCTCTATACGACTTGGAAAGACACTCTTTGGCAATGGAGCTGAGCAGTGGTGATGAGT | 7100 |
| Db | 7190 | CACGTACTACGACCTCCAGGGCCACTCTTTGGCATGGAGACAGCAGTGGGGAGGAGT | 7249 |
| Qy | 7101 | TTTACATAGCTTGTGACACATCGGACCCCTCTTCTGTCTTTAGTGGAAACAGGTTTGA | 7160 |
| Db | 7250 | ACTATGTTGGCTCTGTATAACAGGACTCTCTGGCTGTGTTTCAGATCAACGGCTCA | 7309 |
| Qy | 7161 | TGATCAAGCAAAATCCTGTACACAGCCTATGGGAGATCTACATGATACCAACCCCAACT | 7220 |
| Db | 7310 | TGATCAACAGCTGAGTACACGGCCTATGGGAGATTATTATGACTCCAACCCCGACT | 7369 |
| Qy | 7221 | TTCAGATCATATGAGTACCATGTGTGGCTCTATGATCACTCACAAGACTTGTCCACA | 7280 |
| Db | 7370 | TCCAGATGGTCAATTGGCTTCCATGGGGCACTCTATGACCCCTTGACCAAGCTGGTCCACT | 7429 |
| Qy | 7281 | TGGGCGGCGAGATTATGATGTCTGGCGGACGCTGGACTAGCCAGACCAAGACTGT | 7340 |
| Db | 7430 | TCACTCAGCGTGATATGATGTGCTGGCAGGAGATGGACCTCCCCAGACTATACCATGT | 7489 |
| Qy | 7341 | GGAAAGCACTTGTAGCAGCAAGCTCATGCTCTTTTAATCTCTATATGTTCAAAAAACA | 7400 |
| Db | 7490 | GGAAAAACGT---GGCAGGAGCGCGCCCTTTAACTGTATATGTTCAAGAGCAACA | 7546 |
| Qy | 7401 | ACCCATCAGCAACTCCCAAGACATCAAGTGTCTCATGACAGATGTTTAAACAGCTGCTGC | 7460 |
| Db | 7547 | ATCCTCTCAGCAGTGAGCTAGATTGTTGAAGAACTACCTGACAGATGTGAAAGCTGGCTTG | 7606 |
| Qy | 7461 | TCACCTTTGATTTCCAGCTACACAACGTGATCCCTGGTTATCCCAACCAAGACATGGATG | 7520 |
| Db | 7607 | TGATGTTTGGATTTCAGCTTAGCAACATCAATCCTGGCTTCCCGAGAGCCAAATGTATT | 7666 |
| Qy | 7521 | CCATGGAAACCTCTCTACGAGCTCATCCACACAGATGAAACCGCAGGAGTGGGCAACA | 7580 |
| Db | 7667 | TCGTGCTCTCCTCTATGA-----ATTGTACAGAGTCAAGCAAGTGAGATG | 7714 |
| Qy | 7581 | GCAAGTCTATCTCGGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGGCCCTTTGTCAACCT | 7640 |
| Db | 7715 | GACAGCTCATTTACAGGTGTCCAACAGACACAGAGAGACATAACAGGCCCTTCACTGGCTC | 7774 |
| Qy | 7641 | TAGAACGTTTGACAGCTCTATGGTCCACATCAACAGCTGCCAGCAGGCTCCAAAGA | 7700 |
| Db | 7775 | TGGAA-----GGACAGAGTCAATTACTAAAAAGCTCCACGCCAGCATCCGAGAGAAAGCAG | 7828 |
| Qy | 7701 | CCAAGAGTTTGGATCCAGCGGCTCAGTCTTTGGCAAGGGGGTCAAGTTTGGCTTCAAGG | 7760 |
| Db | 7829 | GTCACTGTTTGGCAACCAACGCCCATCATTTGGCAAGGCATCATGTTTGGCCATCAAAG | 7888 |
| Qy | 7761 | ATGGCCGAGTGACCAACAGACATCATCAGTGTGGCCAAATGAGGATGGCGGAAGGGTTGCTG | 7820 |
| Db | 7889 | AAGGGCGGTGACCAACGGCGGTGTCCAGCATCCGACGGAAGATAGCCGCAAGGTGGCAT | 7948 |
| Qy | 7821 | CCATCTTGAACCATGCCCCTACTCTAGAGAACCTGCATCTCACCATGTATGGGGTGGATA | 7880 |
| Db | 7949 | CTGTGCTGAAACAACGCCCTACTACTCTGACAAAGATGCACATACAGCATCGAGGGCAAGACA | 8008 |
| Qy | 7881 | CCCAATTACTTTGTAAACACAGGACCTTTCAGAAGTGACCTGGGCCATCCTCGGCTCTCAGTG | 7940 |
| Db | 8009 | CCCACTACTTTGTGAAGATTGGCTCAGCCGATGGCGACCTGGTTCACACTAGGCAACCA | 8068 |
| Qy | 7941 | GGGGCGCGCAACCCCTGGGAATGGGGTCAACGTCACTGTGTCCAGATCAACACAGTAC | 8000 |

| | | | |
|----|------|--|------|
| Db | 8069 | TCGGCCGCAAGGTGCTAGAGCGGGTGAACGTGACCGTGTCCAGCCACGCTGCTGG | 8128 |
| Qy | 8001 | TTAATGCGAGGACTAGACGCTACACAGACATCCAGTCCAGTACGGGGCACTGTGCTTGA | 8060 |
| Db | 8129 | TCAACGGCAGGACTCGAAGGTTCCAGAACATTGAGTCCAGTACTCCACGCTGCTCTCA | 8188 |
| Qy | 8061 | ACACAGCTACGG-----GACAACTGTGGATGAGGAGAAAGGCACGGGTCTCTGGAGC | 8111 |
| Db | 8189 | GCATCGCTATGSCCTCACCCCGACACCCCTGACGAGAGAAAGGCCCGCTCTGGACC | 8248 |
| Qy | 8112 | TGCCCCGGCAGAGCCGTGCGCAAGCGTGGGCCCGCGAGCAGCAGACTGCGGGAAG | 8171 |
| Db | 8249 | AGCGGAGACAGAGGGCCCTGGGCACGGCTGGGCCAAGGAGCAGCAGAAAGCCAGGGACG | 8308 |
| Qy | 8172 | GGGAGNAGCCCTGCGGGCCTGGACAGAGGGGGAGAGCAGAGTCTGTGAGCACAGGGC | 8231 |
| Db | 8309 | GGAGAGGGGGAGCCGCTGTGACTGAGGGCGAGAAGCAGAGCTTCTGAGCACCGGGC | 8368 |
| Qy | 8232 | GGGTGCAAGGCTACGAGCGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAACTGTCTAG | 8291 |
| Db | 8369 | CGGTGCNAGGTTACGAGGATATTACGTCTTCCCGTGGAGCAATACCCAGAGCTTGCAG | 8428 |
| Qy | 8292 | ACAGCGCCAAACATCCACTTTCATGAGACAGCGAGATGGCCCGAGGTTGACAGA | 8348 |
| Db | 8429 | ACAGTAGCAGCAACATCCAGTTTTTAAAGCAGAAATGAGATGGGAAAGAGGTAACAAA | 8485 |

Search completed: December 10, 2005, 17:30:32
 Job time : 5963 secs

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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 19:05:23 ; Search time 1303 Seconds
(without alignments)
11396.585 Million cell updates/sec

Title: US-10-029-020-13
Perfect score: 8354
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
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- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
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- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|----------------------|
| 1 | 1708.8 | 20.5 | 3111 | 3 | US-08-891-845-1 |
| 2 | 1708.8 | 20.5 | 3111 | 3 | US-09-514-573-1 |
| 3 | 1708.8 | 20.5 | 3111 | 3 | US-10-290-578-1 |
| 4 | 1673.6 | 20.0 | 1680 | 3 | US-08-891-845-3 |
| 5 | 1673.6 | 20.0 | 1680 | 3 | US-09-514-573-3 |
| 6 | 1673.6 | 20.0 | 1680 | 3 | US-10-290-578-3 |
| 7 | 1185.6 | 14.2 | 2387 | 3 | US-08-891-845-11 |
| 8 | 1185.6 | 14.2 | 2387 | 3 | US-09-514-573-11 |
| 9 | 1185.6 | 14.2 | 2387 | 3 | US-10-290-578-11 |
| 10 | 108.6 | 2.5 | 2007 | 3 | US-09-976-594-407 |
| 11 | 109 | 1.3 | 6763 | 3 | US-09-949-016-3399 |
| 12 | 109 | 1.3 | 13857 | 3 | US-09-620-312D-75 |
| 13 | 109 | 1.3 | 34534 | 3 | US-09-949-016-15141 |
| 14 | 96.4 | 1.2 | 399 | 3 | US-08-861-893-29 |
| 15 | 93.2 | 1.1 | 601 | 3 | US-09-949-016-121669 |
| 16 | 92.2 | 1.1 | 6049 | 3 | US-08-793-273C-3 |
| 17 | 92.2 | 1.1 | 6049 | 6 | PCT-US95-11684-3 |
| 18 | 84 | 1.0 | 7286 | 3 | US-08-793-273C-1 |
| 19 | 84 | 1.0 | 7286 | 6 | PCT-US95-11684-1 |
| 20 | 84 | 1.0 | 7346 | 3 | US-09-554-267-1 |
| 21 | 82.8 | 1.0 | 601 | 3 | US-09-949-016-121670 |
| 22 | 65.8 | 0.8 | 601 | 3 | US-09-949-016-121671 |
| 23 | 64.4 | 0.8 | 601 | 3 | US-09-949-016-121668 |
| 24 | 58.4 | 0.7 | 7218 | 2 | US-08-232-463-14 |

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|------|------|-----|---------|---|---------------------|-------------------|
| 25 | 57 | 0.7 | 4716 | 3 | US-09-949-002-67 | Sequence 67, Appl |
| 26 | 57 | 0.7 | 4716 | 3 | US-09-949-002-145 | Sequence 145, App |
| 27 | 57 | 0.7 | 4724 | 2 | US-08-404-665-3 | Sequence 3, Appli |
| 28 | 57 | 0.7 | 4724 | 2 | US-08-404-671-3 | Sequence 3, Appli |
| 29 | 57 | 0.7 | 4724 | 2 | US-08-404-781-3 | Sequence 3, Appli |
| 30 | 57 | 0.7 | 88002 | 3 | US-09-949-002-639 | Sequence 639, App |
| 31 | 57 | 0.7 | 88002 | 3 | US-09-949-002-717 | Sequence 717, App |
| C 32 | 56 | 0.7 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appli |
| C 33 | 56 | 0.7 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appli |
| C 34 | 54.2 | 0.6 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appli |
| C 35 | 52.6 | 0.6 | 2183 | 3 | US-10-104-047-1064 | Sequence 1064, Ap |
| 36 | 52.6 | 0.6 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appli |
| 37 | 51.4 | 0.6 | 324 | 3 | US-09-902-540-4979 | Sequence 4979, Ap |
| C 38 | 51.4 | 0.6 | 23951 | 3 | US-09-902-540-1245 | Sequence 1245, Ap |
| C 39 | 49.8 | 0.6 | 690 | 3 | US-09-252-991A-3288 | Sequence 3288, Ap |
| C 40 | 49.8 | 0.6 | 1173 | 3 | US-09-252-991A-3422 | Sequence 3422, Ap |
| C 41 | 49.8 | 0.6 | 1434 | 3 | US-09-252-991A-3260 | Sequence 3260, Ap |
| C 42 | 49.6 | 0.6 | 293 | 3 | US-09-313-294A-6760 | Sequence 6760, Ap |
| C 43 | 49.6 | 0.6 | 3489 | 2 | US-08-728-323A-1 | Sequence 1, Appli |
| C 44 | 49.6 | 0.6 | 3489 | 3 | US-09-298-568-1 | Sequence 1, Appli |
| C 45 | 49.6 | 0.6 | 3489 | 3 | US-09-410-399-1 | Sequence 1, Appli |

ALIGNMENTS

RESULT 1
US-08-891-845-1
; Sequence 1, Application US/08891845
; Patent No. 6096873
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Sliwowski, Mark
; TITLE OF INVENTION: Gamma-Herregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: 60/021640
; APPLICATION NUMBER: 07/12/96
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3111 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-891-845-1

Query Match 20.5%; Score 1708.8; DB 3; Length 3111;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 300 GTTGTGGATGTGAGGAGCGGGCCGAGGCGCATGGACGTGAAGAGAGGAAGCCTTA 359
QY 61 CGGCTCGCTGACCCGGCGCGGAGCGCGGCTACACGAGCTGTCGCGGGACAG 120
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QY 121 CGAGGAGGCAAGCCCGCCGAGAAATCGTACAGCTCCAGCGGAGACCTTGAAGCCCTACGA 180
Db 420 CGAGGAGGCAAGCCCGCCGAGAAATCGTACAGCTCCAGCGGAGACCTTGAAGCCCTACGA 479
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Db 480 CCAGAGCGCCCGCTAGCTATGAGCAGCGCGCTCAAGACATGTCGCGCAGAGGCGGA 539
QY 241 GGAATTTCTGCCGACAGGTGCCAACTTCAACCTCGCGGAGCTGGGGCTGGAAGAAGTAAC 300
Db 540 GGAATTTCTGCCGACAGGTGCCAACTTCAACCTCGCGGAGCTGGGGCTGGAAGAAGTAAC 599
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QY 481 TTCCAAATCTACACTACCGACACCGAGCATGAAACACTGAGACTGATCTATCGGGCGG 540
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Db 1080 CAGGAACCTTAGCAAGACGCAATCTTAGGACATTTGAGGACACCTCTATTGAGATGA 1139
QY 841 CATTTCTGGCGCTCCCGCATGATGGGGCTTAAGTGAAGGCGCATCTTCTTCAAGCC 900
Db 1140 CATTTCTGGCGCTCCCGCATGATGGGGCTTAAGTGAAGGCGCATCTTCTTCAAGCC 1199
QY 901 TGGAGGCACTTCCCGCTCTTCTGACCAACATCAACAGGGTACCACCTGAGCTCCAGCAC 960
Db 1200 TGGAGGCACTTCCCGCTCTTCTGACCAACATCAACAGGGTACCACCTGAGCTCCAGCAC 1259
QY 961 AGTGACTCTCTCCGCCCCGACCCCTGCCCCGAGCACCTTTCGCCCCGGCGGCTTTAA 1020
Db 1260 AGTGACTCTCTCCGCCCCGACCCCTGCCCCGAGCACCTTTCGCCCCGGCGGCTTTAA 1319
QY 1021 CCTCAAGAGCCCTCAAGTACTGTAACTGGAAGTGGCAGCCCTGAGCGGCATCTGTCAT 1080
Db 1320 CCTCAAGAGCCCTCAAGTACTGTAACTGGAAGTGGCAGCCCTGAGCGGCATCTGTCAT 1379

QY 1081 CTCAGCACCTCTGCTCATCTGCTGGCATACTTTTGGCCCATGACACCTGTTGGCCTAAA 1140
Db 1380 CTCAGCACCTCTGCTCATCTGCTGGCATACTTTTGGCCCATGACACCTGTTGGCCTAAA 1439
QY 1141 CTGSCACCTCTCAGCCGATGGAGGGCGAGATGTATGAGATCACGGAGGACACAGCCAGCAG 1200
Db 1440 CTGSCACCTCTCAGCCGATGGAGGGCGAGATGTATGAGATCACGGAGGACACAGCCAGCAG 1499
QY 1201 TTGGCCTGTGCCAAACCGACGTCTCCCTATATACCCCTCAGGGGGGCACTGGCTTAGAGACCC 1260
Db 1500 TTGGCCTGTGCCAAACCGACGTCTCCCTATATACCCCTCAGGGGGGCACTGGCTTAGAGACCC 1559
QY 1261 TGACAGAAAGGCAAGGAACACAGAAAGAAAGCCAGTAGTTTCTTTTCCAGAGGACAG 1320
Db 1560 TGACAGAAAGGCAAGGAACACAGAAAGAAAGCCAGTAGTTTCTTTTCCAGAGGACAG 1619
QY 1321 TTTTCATAGATTCTGGAGAAATTTGATGTGGAAAGCGAGCCTCCAGAAAGATTCTCTCTGG 1380
Db 1620 TTTTCATAGATTCTGGAGAAATTTGATGTGGAAAGCGAGCTTCCAGAAAGATTCTCTCTGG 1679
QY 1381 CACTTTCTGAGATCTCAAGTGTTCATAGACCATCTGTCGATCTGAAATTCATGTGTC 1440
Db 1680 CACTTTCTGAGATCTCAAGTGTTCATAGACCATCTGTCGATCTGAAATTCATGTGTC 1739
QY 1441 TCTGGAAAGCGACCCCTGTTGGCATTTATGGCAGAAAGGCTCCTCCTTCCACATAC 1500
Db 1740 TCTGGAAAGCGACCCCTGTTGGCATTTATGGCAGAAAGGCTCCTCCTTCCACATAC 1799
QY 1501 ACAGTTTGACTTTTGTGAGCTGTGATGGCAGGAGCTCTTAACCCAGAGGCGCGAG 1560
Db 1800 ACAGTTTGACTTTTGTGAGCTGTGATGGCAGGAGCTCTTAACCCAGAGGCGCGAG 1859
QY 1561 CTTAGAGGAGACCCCGCGCCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAGACAG 1620
Db 1860 CTTAGAGGAGACCCCGCGCCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAGACAG 1919
QY 1621 CTTTCATCCAGTATTGGATTTCAGGAATCTGGCATTTTACAAATCAGCGAAAGGA 1680
Db 1920 CTTTCATCCAGTATTGGATTTCAGGAATCTGGCATTTTACAAATCAGCGAAAGGA 1979
QY 1681 GTCAGAGTGGTTTCTTCTCACCACCTGCTTGAAGTCG 1720
Db 1980 GTCAGAGTGGTTTCTTCTCACCACCTGCTTGAAGTCG 2019

RESULT 2
US-09-514-573-1
; Sequence 1, Application US/09514573
; Patent No. 6500941
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Sliwowski, Mark
; TITLE OF INVENTION: Gamma-Herregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/514,573
; FILING DATE: 28 FEB 2000
; CLASSIFICATION:
; PRIORITY DATA:
; APPLICATION NUMBER: 08/891845
; FILING DATE: 10 JULY 1997

```

, APPLICATION NUMBER: 60/021640
, FILING DATE: 07/12/96
, ATTORNEY/AGENT INFORMATION:
, NAME: Lee, Wendy M.
, REGISTRATION NUMBER: 40,378
, REFERENCE/DOCKET NUMBER: P1043
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 415/225-1994
, TELEFAX: 415/952-9881
, TELEX: 910/371-7168
, INFORMATION FOR SEQ ID NO: 1:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 3111 base pairs
, TYPE: Nucleic Acid
, STRANDEDNESS: Single
, TOPOLOGY: Linear
, US-09-514-573-1

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| Query Match | 20.5% | Score 1708.8 | DB 3 | Length 3111 |
|-----------------------|----------------|--|----------|-------------|
| Best Local Similarity | 99.6% | Pred. No. 0 | | |
| Matches 1713 | Conservative 0 | Mismatches 7 | Indels 0 | Gaps 0 |
| QY | 1 | GTTTTGTGGATGTGGAGGAGCGCGGGCCGGAGGCCATGCAGCTGTGAAGAGAGGAAAGCCTTA | 60 | |
| DB | 300 | GTTTTGTGGATGTGGAGGAGCGCGGCCCGHAGCCATGAGCTGTGAAGAGAGGAAAGCCTTA | 359 | |
| QY | 61 | CCGCTCGCTGACCCCGCGCCGCAACCGCAGCGCCGCTACACCAAGTCTGTCGCGGAGACAG | 120 | |
| DB | 360 | CCGCTCGCTGACCCCGCGCCGCAACCGCAGCGCCGCTACACCAAGTCTGTCGCGGAGACAG | 419 | |
| QY | 121 | CGAGGAGGGCAAAAGCCCCCGCAGAAATCGTACAGCTCCAGCGAGACCCTGAAGGCCTACGA | 180 | |
| DB | 420 | CGAGGAGGGCAAAAGCCCCCGCAGAAATCGTACAGCTCCAGCGAGACCCTGAAGGCCTACGA | 479 | |
| QY | 181 | CCAGGAGCGCCCGCTAGCCTATGCGACGCCGTCGTCGAAGGACATTTGTGCCGCGAGAGGCCGA | 240 | |
| DB | 480 | CCAGGAGCGCCCGCTAGCCTATGCGACGCCGTCGTCGAAGGACATTTGTGCCGCGAGAGGCCGA | 539 | |
| QY | 241 | GGAAATTCGTGCGCACAGGTGCCAACTTTCACCTCGCGGAGCTGGGGCTGGAAGAAGTAAC | 300 | |
| DB | 540 | GGAAATTCGTGCGCACAGGTGCCAACTTTCACCTCGCGGAGCTGGGGCTGGAAGAAGTAAC | 599 | |
| QY | 301 | GCCCCCTCACGGGACCCCTGTACCGGACAGACATTTGGCTGCTCCCAATTCGCGCTACTCCAT | 360 | |
| DB | 600 | GCCCCCTCACGGGACCCCTGTACCGGACAGACATTTGGCTGCTCCCAATTCGCGCTACTCCAT | 659 | |
| QY | 361 | GGGGGCTGGCTCTGATGCCGACATGAGGGCTGACACGGTGTGTGTCCCTCGAGCACCCCGT | 420 | |
| DB | 660 | GGGGGCTGGCTCTGATGCCGACATGAGGGCTGACACGGTGTGTGTCCCTCGAGCACCCCGT | 719 | |
| QY | 421 | GCCTCTGTGGGCCGAGACACACGGTCAGGGCGAGCTCTGCTGTCTCGACCGGGCCAA | 480 | |
| DB | 720 | GCCTCTGTGGGCCGAGACACACGGTCAGGGCGAGCTCTGCTGTCTCGACCGGGCCAA | 779 | |
| QY | 481 | TTCCAAATCTCACACTCACCGCACACCGAGCATGAAAACACTTGAGACTGATCATTCGGCGGG | 540 | |
| DB | 780 | TTCCAAATCTCACACTCACCGCACACCGAGCATGAAAACACTTGAGACTGATCATTCGGCGGG | 839 | |
| QY | 541 | CCTGCGAAGACACGCGCGGCTCCGGAGCCGCGCCGCTCTCGCACGCCCAACACCCC | 600 | |
| DB | 840 | CCTGCGAAGACACGCGCGGCTCCGGAGCCGCGCCGCTCTCGCACGCCCAACACCCC | 899 | |
| QY | 601 | CAACGAGCACACGCGGCTCCATTACTCCCTGAAACGGGGGCAACTTTCAGCCGAGGAG | 660 | |
| DB | 900 | CAACGAGCACACGCGGCTCCATTACTCCCTGAAACGGGGGCAACTTTCAGCCGAGGAG | 959 | |
| QY | 661 | CAACCCGAGCCCGGCCCCCGACCGACACTCGCTCTCCGGAGAGCCCTGCGCGGCGGC | 720 | |
| DB | 960 | CAACCCGAGCCCGGCCCCCGACCGACACTCGCTCTCCGGAGAGCCCTGCGCGGCGGC | 1019 | |
| QY | 721 | CCAGGAGCTGCCCAACGCCCCAGGAGAACTGGCTGCTCAACAGCAACAATCCCTCTGGAGAC | 780 | |
| DB | 1020 | CCAGGAGCTGCCCAACGCCCCAGGAGAACTGGCTGCTCAACAGCAACAATCCCTCTGGAGAC | 1079 | |

| | | | | |
|----|------|----------|--|------|
| Qy | 781 | CAGGAA | CCTTAGGCAAGGAGCCATTCCTTAGGGACATTTGCAGGACAACTCATTCAGATGGA | 840 |
| Db | 1080 | CAGAAA | CCTTAGGCNAGCAGCCATTCCTTAGGGACATTTGCAGGACAACTCATTCAGATGGA | 1139 |
| Qy | 841 | CATTCT | CGGCGCTCCCGGCATGATCGGGCTTACAGTGCAGGGACATTCCTCTCTTCAAGCC | 900 |
| Db | 1140 | CATTCT | CGGCGCTCCCGGCATGATGGGCTTACAGTGCAGGGACATTCCTCTTCAAGCC | 1199 |
| Qy | 901 | TGGAGG | CACTCCCTCCCGCTCTTCTTGACCAATCACCAGGGTACCCACTGACGCTCCAGCAC | 960 |
| Db | 1200 | TGGAGG | CACTCCCTCCCGCTCTTCTTGACCAATCACCAGGGTACCCACTGACGCTCCAGCAC | 1259 |
| Qy | 961 | AGTGTA | CTCTCTCGGCGGACCCCTGCCCCGACAGCACTTCGCCCGGGCCGGCCTTTAA | 1020 |
| Db | 1260 | AGTGTA | CTCTCTCGGCGGACCCCTGCCCCGACAGCACTTCGCCCGGGCCGGCCTTTAA | 1319 |
| Qy | 1021 | CCTCAAGA | AGCCCTCCAAGTACTGTAACCTGGAAGTCGCAGCCCTGAGCGCCATCGTCAT | 1080 |
| Db | 1320 | CCTCAAGA | AGCCCTCCAAGTACTGTAACCTGGAAGTCGCAGCCCTGAGCGCCATCGTCAT | 1379 |
| Qy | 1081 | CTCAGC | CACTCTCGTGCATCCTCTGCTGGCATACTTTTGTGGCCATGCACCTGTTGGCCCTAAA | 1140 |
| Db | 1380 | CTCAGC | CACTCTCGTGCATCCTCTGCTGGCATACTTTTGTGGCCATGCACCTGTTGGCCCTAAA | 1439 |
| Qy | 1141 | CTGGCA | CACTGACCGCATGAGGGGCGAGATGTAATAGATACAGGAGGACACAGCCAGCAG | 1200 |
| Db | 1440 | CTGGCA | CACTGACCGCATGAGGGGCGAGATGTAATAGATACAGGAGGACACAGCCAGCAG | 1499 |
| Qy | 1201 | TTGGCCT | GTGCCAAACCGACGTCTCCCTATACCCCTCAGGGGGACATGGCTTTAGAGACCCC | 1260 |
| Db | 1500 | TTGGCCT | GTGCCAAACCGACGTCTCCCTATACCCCTCAGGGGGACATGGCTTTAGAGACCCC | 1559 |
| Qy | 1261 | TGACAGA | AAAGGCAAAAGGAACCAAGAGGAAAGCCAGTAGTTCTTTCCAGAGGACAG | 1320 |
| Db | 1560 | TGACAGA | AAAGGCAAAAGGAACCAAGAGGAAAGCCAGTAGTTCTTTCCAGAGGACAG | 1619 |
| Qy | 1321 | TTTTCAT | ATAGATTCCTGGAGAAATTTGATGTGGGAAGCGAGCCCTCCAGAGAGATTCTCTCTGG | 1380 |
| Db | 1620 | TTTTCAT | ATAGATTCCTGGAGAAATTTGATGTGGGAAGCGAGCTTCCAGAGAGATTCTCTCTGG | 1679 |
| Qy | 1381 | CACCTT | CTGGAGATCTCAAGTGTTTCATAGACCACTCTGTGCATCTGAAATTCATATGTGTC | 1440 |
| Db | 1680 | CACCTT | CTGGAGATCTCAAGTGTTTCATAGACCACTCTGTGCATCTGAAATTCATATGTGTC | 1739 |
| Qy | 1441 | TCCTGG | AAAGGCAAGCCCTGGTTGGCATTTATGCGAGAAAGGCGCTCCCTCTTTCACATAC | 1500 |
| Db | 1740 | TCCTGG | AAAGGCAAGCCCTGGTTGGCATTTATGCGAGAAAGGCGCTCCCTCTTTCACATAC | 1799 |
| Qy | 1501 | ACAGTT | TTGACTTTGTGAGCTGCTGGATGCGAGAGGCTCTTAACCCAGAGAGCGCGGAG | 1560 |
| Db | 1800 | ACAGTT | TTGACTTTGTGAGCTGCTGGATGCGAGAGGCTCTTAACCCAGAGAGCGCGGAG | 1859 |
| Qy | 1561 | CCTTAG | AGGGGACCCCGCGCAGTCTCGGGAACTGTGCCCCCTCCAGCCCATGAGACAGG | 1620 |
| Db | 1860 | CCTTAG | AGGGGACCCCGCGCAGTCTCGGGAACTGTGCCCCCTCCAGCCCATGAGACAGG | 1919 |
| Qy | 1621 | CTTTCAT | CCAGTATTTGGATTCAGGAATCTGGCACTTTGGCTTTTTTACAATGACGGAAAGGA | 1680 |
| Db | 1920 | CTTTCAT | CCAGTATTTGGATTCAGGAATCTGGCACTTTGGCTTTTTTACAATGACGGAAAGGA | 1979 |
| Qy | 1681 | GTCAGA | AGTGGGTTTCTTTCTCAACCATGCGCATTGAGTCG | 1720 |
| Db | 1980 | GTCAGA | AGTGGGTTTCTTTCTCAACCATGCGCATTGCGCTTG | 2019 |

RESULT 3
US-10-230-578-1
; Sequence 1, Application US/10290578
; Patent No. 6916624
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; Slivkowski, Mark
;

;;
; TITLE OF INVENTION: Gamma-Herregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/290,578
; FILING DATE: 08-No. 6916624-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/021640
; FILING DATE: 12-Jul-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3111 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-290-578-1

Query Match 20.5%; Score 1708.8; DB 3; Length 3111;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GTTTGTGGATGTGGAGGACGGCGCGGAGGCCATGACGTGAAGGAGAGGAAGCCTTA 60
DB 300 GTTTGTGGATGTGGAGGACGGCGCGGAGGCCATGACGTGAAGGAGAGGAAGCCTTA 359
QY 61 CCGCTCGCTGACCCGCGCGCGGACGCGGAGCGGCTACACGCTCGTCCGCGGACAG 120
DB 360 CCGCTCGCTGACCCGCGCGCGGACGCGGAGCGGCTACACGCTCGTCCGCGGACAG 419
QY 121 CGAGGAGGCAAAAGCCCGCAGAAATCGTACAGCTCCAGCGAGACCCCTGAAGGCCCTACGA 180
DB 420 CGAGGAGGCAAAAGCCCGCAGAAATCGTACAGCTCCAGCGAGACCCCTGAAGGCCCTACGA 479
QY 181 CGAGAGCGCCCGCTAGCCTATGGACGCGCGGTCAAGACATTTGTCCGCGAGGCGCGA 240
DB 480 CCAGAGCGCCCGCTAGCCTATGGACGCGCGGTCAAGACATTTGTCCGCGAGGCGCGA 539
QY 241 GGAATTTCTGCCGACAGGTGCCAACTTCAACCTCGCGGAGCTGGGGCTGGGAAGATAAC 300
DB 540 GGAATTTCTGCCGACAGGTGCCAACTTCAACCTCGCGGAGCTGGGGCTGGGAAGATAAC 599
QY 301 GCCCCCTCACGGACCCCTGTACCGGACAGACATTTGGCCTGCCCGCCCAATCGGCTACTCCAT 360
DB 600 GCCCCCTCACGGACCCCTGTACCGGACAGACATTTGGCCTGCCCGCCCACTCGGCGCTACTCCAT 659
QY 361 GGGGGCTGGCTGTATGCCGACATGGAGGCTGACCGGTGTGTCTCCCTGAGCACCCCGT 420
DB 660 GGGGGCTGGCTGTATGCCGACATGGAGGCTGACCGGTGTGTCTCCCTGAGCACCCCGT 719
QY 421 GCGTCTGTGGGCGGAGCACACGGTCCAGGGCGGACGCTCCTGCCTGTCCAGCGCGGCCAA 480

DB 720 GCGTCTGTGGGCGGAGCACACGGTCAAGCGCGAGCTCCTGCTGTCCAGCGCGGCCAA 779
QY 481 TTCCAATCTCACACTCACCGACACCGAGCATGAAAAACACTGAGACTGATCATCCGGGGCGG 540
DB 780 TTCCAATCTCACACTCACCGACACCGAGCATGAAAAACACTGAGACTGATCATCCGGGGCGG 839
QY 541 CTTGCGAAGCACGCGGGCTCCGGAGCGCGCGCGCTCTCGACGCCACACACCCC 600
DB 840 CTTGCGAAGCACGCGGGCTCCGGAGCGCGCGCGCTCTCGACGCCACACACCCC 899
QY 601 CAACCCAGCACGCGGGCTCCATTAACCTCCCTGAACCGGGGCAACTTTCACGCCGAGGAG 660
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QY 661 CAACCCAGCGCGGGCTCCCGACGACACTCGCTCTCCGGAGAGCGCCCTCGCGGGCGGCG 720
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DB 1080 CAGGAACCTAGGCAAGCAGGCATTTCTTAGGACATTTGCAGGACAAACCTCATTTGAGATGGA 1139
QY 841 CATTTCTCGGGCTCTCCCGCATGATGGGGCTTACAGTGAAGGGGCACTTCTCTTCAAGCC 900
DB 1140 CATTTCTCGGGCTCTCCCGCATGATGGGGCTTACAGTGAAGGGGCACTTCTCTTCAAGCC 1199
QY 901 TGGAGGACCTCCCGCTCTTCTGCACACATCACCAGGGGTACCCACTGAGCTCCAGCAC 960
DB 1200 TGGAGGACCTCCCGCTCTTCTGCACACATCACCAGGGGTACCCACTGAGCTCCAGCAC 1259
QY 961 AGTGTACTCTCTCCCGCGGACCCCTCGCCCGCAGCACCTTTCGCCCGCGCGGCTTTAA 1020
DB 1260 AGTGTACTCTCTCCCGCGGACCCCTCGCCCGCAGCACCTTTCGCCCGCGGCTTTAA 1319
QY 1021 CTTCAAGAAGCCCTCCAAAGTACTGTAACTGGAAGTGGCGAGCCCTGAGCGGCATCTGTCAT 1080
DB 1320 CTTCAAGAAGCCCTCCAAAGTACTGTAACTGGAAGTGGCGAGCCCTGAGCGGCATCTGTCAT 1379
QY 1081 CTAGCCCACTCTGTCATCTGTCGATCTTTTGGCCCATGACCTGTTTGGCCCTAAA 1140
DB 1380 CTAGCCCACTCTGTCATCTGTCGATCTTTTGGCCCATGACCTGTTTGGCCCTAAA 1439
QY 1141 CTGSCACTCTGAGCCGATGGAGGGGCGAGATGTTATGAGATCACGGAGGACACAGCCAGCAG 1200
DB 1440 CTGSCACTCTGAGCCGATGGAGGGGCGAGATGTTATGAGATCACGGAGGACACAGCCAGCAG 1499
QY 1201 TTGGCTGTGCGCAACCGACGCTCTCCCTATACCTCTAGGGGGGACCTGGCTTAGAGACCCC 1260
DB 1500 TTGGCTGTGCGCAACCGACGCTCTCCCTATACCTCTAGGGGGGACCTGGCTTAGAGACCCC 1559
QY 1261 TGACAGAAAGGCAAGGAAACCAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 1320
DB 1560 TGACAGAAAGGCAAGGAAACCAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 1619
QY 1321 TTTTCATAGATTCTCGGAAATTTGATGTGGGAAGCGAGCCCTCCAGAGAGATTTCTCTCTGG 1380
DB 1620 TTTTCATAGATTCTCGGAAATTTGATGTGGGAAGCGAGCTTCCAGAGAGATTTCTCTCTGG 1679
QY 1381 CACTTTCTGAGATCTCAAGTGTTCATAGACCATCTCTGTGTCATCTGAAATTCATGTGTC 1440
DB 1680 CACTTTCTGAGATCTCAAGTGTTCATAGACCATCTCTGTGTCATCTGAAATTCATGTGTC 1739
QY 1441 TCTGGGAAAGCGAGCCCTGTTGGCATTATGCGAGAAAGGCGCTCCCTCTTCCACATAC 1500
DB 1740 TCTGGGAAAGCGAGCCCTGTTGGCATTATGCGAGAAAGGCGCTCCCTCTTCCACATAC 1799
QY 1501 ACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGAGGCTCCTAACCCAGAGGCGCGGAG 1560

Db 1800 ACAGTTTGACTTTTGTGAGCTGTGATGACGAGGAGCTCTTAACCCAGGAGCGCGGAG 1859
Qy 1561 CCTAGAGGGACCCCGCCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAGACAGG 1620
Db 1860 CCTAGAGGGACCCCGCCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAGACAGG 1919
Qy 1621 CTTTCATCCAGTATTTGGATTTCAGAAATCTGGCACTTGGCTTTTACAAATGACGGAAGGA 1680
Db 1920 CTTTCATCCAGTATTTGGATTTCAGAAATCTGGCACTTGGCTTTTACAAATGACGGAAGGA 1979
Qy 1681 GTCAGAAAGTGGTTTCCTTTCTCAACCACTGCCATGAGTGG 1720
Db 1980 GTCAGAAAGTGGTTTCCTTTCTCAACCACTGCCATGAGTGG 2019

RESULT 4

US-08-891-845-3
; Sequence 3, Application US/08891845
; Patent No. 6096873
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Sliwowski, Mark
; TITLE OF INVENTION: Gamma-Herregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1680 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-891-845-3

Query Match 20.0%; Score 1673.6; DB 3; Length 1680;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1676; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 35 ATGGACGTGAAGGAGAGAGAGCCCTTACCGTCTCGTGAACCGGCGCCGCGAGCGC 94
Db 1 ATGGACGTGAAGGAGAGAGAGCCCTTACCGTCTCGTGAACCGGCGCCGCGAGCGC 60
Qy 95 CGCTACACCAAGCTCGTCCGGGACAGCGAGAGGGGCAAGCCCGGAGAAATCGTACAGC 154
Db 61 CGCTACACCAAGCTCGTCCGGGACAGCGAGAGGGGCAAGCCCGGAGAAATCGTACAGC 120
Qy 155 TCCAGCGAGACCCCTGAAGGCGCTACGACGAGCGCCCGCTTAGCCTATGGCAGCGCGTC 214

Db 121 TCCAGCGAGACCCCTGAAGGCTTACGACACGAGGACGCCCGCTAGCCCTATGGCAGCCGCTC 180
Qy 215 AAGGACATTTGTCCGCGAGAGCCGAGGAAATTTCTGCCGCACAGGTGCCAACTTCACCCCTG 274
Db 181 AAGGACATTTGTCCGCGAGAGCCGAGGAAATTTCTGCCGCACAGGTGCCAACTTCACCCCTG 240
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Db 241 CGGAGCTGGGGCTGGAAGAAGTAACGCCCTCTCAACGGAACCTGTATCCGGACAGACATTT 300
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Db 301 GGCCTGCCCCAATGCGGCTACTCCATGGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 360
Qy 395 ACGGTGCTGTCCCTTGAGCACCCCGTGTGTGGGGCGCGAGACACAGCTCAGGCGC 454
Db 361 ACGGTGCTGTCCCTTGAGCACCCCGTGTGTGGGGCGCGAGACACAGCTCAGGCGC 420
Qy 455 AGCTCCTGCTGTTCACAGCGGGCCAAATTCCAATCTCACACTCACCGACACCGAGCATGAA 514
Db 421 AGCTCCTGCTGTTCACAGCGGGCCAAATTCCAATCTCACACTCACCGACACCGAGCATGAA 480
Qy 515 AACACTGAGACTGATCATCCGGGCGGCTGAGAACACAGCGGCTCCGGACCGCCCG 574
Db 481 AACACTGAGACTGATCATCCGGGCGGCTGAGAACACAGCGGCTCCGGACCGCCCG 540
Qy 575 CGGCGCTCTCGACGCGCCACACCCCAACAGCACACCGGCTCCATTAACCTCCCTG 634
Db 541 CGGCGCTCTCGACGCGCCACACCCCAACAGCACACCGGCTCCATTAACCTCCCTG 600
Qy 635 AACCGGGGCAACTTTCACGCGGAGGAGCAACCCCGAGCCCGCCCAACGACCACTCGCTC 694
Db 601 AACCGGGGCAACTTTCACGCGGAGGAGCAACCCCGAGCCCGCCCAACGACCACTCGCTC 660
Qy 695 TCCGAGAGCCCTCTCGCGGCGGCTGAGAGGCTTCCCAACGCGGCTCCGGACGAGAACTGGCTG 754
Db 661 TCCGAGAGCCCTCTCGCGGCGGCTGAGAGGCTTCCCAACGCGGCTCCGGACGAGAACTGGCTG 720
Qy 755 CTCAACAGCAACATCCCTCTGGAGACAGGAACTTAGGCAAGCAGCATTTCTTAGGAGACA 814
Db 721 CTCAACAGCAACATCCCTCTGGAGACAGGAACTTAGGCAAGCAGCATTTCTTAGGAGACA 780
Qy 815 TTGACGAGCAACCTCATTTGAGATGGACATTTCTCGGCGCTTCCGCCCATGATGGGCTTAC 874
Db 781 TTGACGAGCAACCTCATTTGAGATGGACATTTCTCGGCGCTTCCGCCCATGATGGGCTTAC 840
Qy 875 AGTACGCGGCACTTCTCTTCAAGCCTGGAGGACCTCCCGCTCTTTCGACACATCA 934
Db 841 AGTACGCGGCACTTCTCTTCAAGCCTGGAGGACCTCCCGCTCTTTCGACACATCA 900
Qy 935 CCAGGGTACCCACTGACGTCCAGCACAGTGTACTCTCCCGCCCGAGCCCTGCCCGC 994
Db 901 CCAGGGTACCCACTGACGTCCAGCACAGTGTACTCTCTCCCGCCCGAGCCCTGCCCGC 960
Qy 995 AGCACCTTCCCGCGCGGCTTTAACTCAAGAGCCCTTCAAGAGCCCTTCAAGTACTGTAAG 1054
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Qy 1235 TCAGGGGCACTGGCTTTAGAGACCCCTGACAGAAAGGCAAGGAAACCAAGAGGAAG 1294
Db 1201 TCAGGGGCACTGGCTTTAGAGACCCCTGACAGAAAGGCAAGGAAACCAAGAGGAAG 1260

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| 961 | AGCAC | TTGGCCCGCGCGCTTTAA | CCTCAAGAAAGCCCTCAAGTACTGTA | CTA | CTGAAG | 1020 |
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| 1055 | TGCGC | AGCCCTGAGCGCCATCGT | CAATCTCAGCCACTCTGGT | CACTCCTGCTGGC | ATACTTT | 1114 |
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| 1115 | GTGGC | CAATGACACTGTTTGGCCT | TAAACTGSCACCTG | CAGCGGATGGAGGGC | AGTGTAT | 1174 |
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| 1081 | GTGGC | CAATGACACTGTTTGGCCT | TAAACTGSCACCTG | CAGCGGATGGAGGGC | AGTGTAT | 1140 |
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| 1235 | TCAGG | GGGCGACTGTGCTTAGA | AGCCCTGACAGGAAGG | CAAAAGCAACACAGAA | AGGAAG | 1294 |
| | | | | | | |
| 1201 | TCAGG | GGGCGACTGTGCTTAGA | AGCCCTGACAGGAAGG | CAAAAGCAACACAGAA | AGGAAG | 1260 |
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| 1295 | CCCA | GTAAGTTCTTTCCAGAGG | ACAGTTTCA | TAGATTCGAGAAAT | TGATGTGGGAAGG | 1354 |
| | | | | | | |
| 1261 | CCCA | GTAAGTTCTTTCCAGAGG | ACAGTTTCA | TAGATTCGAGAAAT | TGATGTGGGAAGG | 1320 |
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| 1355 | CGAGC | CTCCCAAGAGATTCTCT | TGGCACTTTCTGGAGAT | CTCAAGTGTTCATAGAC | CCAT | 1414 |
| | | | | | | |
| 1321 | CGAGC | CTCCCAAGAGATTCTCT | TGGCACTTTCTGGAGAT | CTCAAGTGTTCATAGAC | CCAT | 1380 |
| | | | | | | |
| 1415 | CCTGT | GCATCTGAATTCATATG | CTCTCTGGAAAGCAGC | CCCTGTTGGCATTTATGC | | 1474 |
| | | | | | | |
| 1381 | CCTGT | GCATCTGAATTCATATG | CTCTCTGGAAAGCAGC | CCCTGTTGGCATTTATGC | | 1440 |
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| 1441 | AGAAA | GGCCTCCCTCTTACAT | CACACAGTTTGACTTTG | TGGAGCTGCTGGATGGC | CAGG | 1500 |
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| 1535 | AGGT | CTCTAAACCAAGAGG | CGCGAGCTTAGAGGGG | ACCCCGCCAGTCTCGGGG | AACT | 1594 |
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| 1501 | AGGT | CTCTAAACCAAGAGG | CGCGAGCTTAGAGGGG | ACCCCGCCAGTCTCGGGG | AACT | 1560 |
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| 1595 | GTG | CCCCCTCCAGCCAT | GAGACAGGCTTCAT | TCCAGTATTTGGATT | CAGGAATCTGGCAC | 1654 |
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| 1655 | TTG | CTTTTTTACAATG | ACGGAAGGAGT | CTAGAACTGTTTCTCTT | CTCAACACTGCCATT | 1714 |
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RESULT 6

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RESULT 7

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US-08-891-845-11
; Sequence 11, Application US/08891845
; Patent No. 6096873
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Sliwkowski, Mark
; TITLE OF INVENTION: Gamma-Herregulin
```

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; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2387 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-891-845-11
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Query Match 14.2%; Score 1185.6; DB 3; Length 2387;
Best Local Similarity 98.8%; Pred. No. 2.1e-279;
Matches 1194; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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QY 1310 CCAGAGGACAGTTTCATGATTTCTGGAGAAATGTAGTGGGAAGCGAGCCTCCAGAA 1369
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RESULT 9

US-10-290-578-11
; Sequence 11, Application US/10290578
; Patent No. 6916624
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; Sliwowski, Mark
; TITLE OF INVENTION: Gamma-Herregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/290,578
; FILING DATE: 08-No. 6916624-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/021640
; FILING DATE: 12-Jul-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2387 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-290-578-11
Query Match 14.2%; Score 1185.6; DB 3; Length 2387;
Best Local Similarity 98.8%; Pred. No. 2.1e-279;
Matches 1194; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 530 CATCCGGCGGCTGCGAACCACGCGCGCTCCGGACGCGCGCGCGCTCGCAC 589
Db 1 CATCCGGCGGCTGCGAACCACGCGCGCTCCGGACGCGCGCGCGCTCGCAC 60
QY 590 GCCCACACCCCCCAACACGACACACGCGGCTCCATTAACTCCCTGAAACCGGGCAACTTC 649
Db 61 GCCCACACCCCCCAACACGACACACGCGGCTCCATTAACTCCCTGAAACCGGGCAACTTC 120
QY 650 ACGCCGAGGAGCAACCCCGCGGCCCCACGACACCTCGCTCTCCGGAGAGCCCT 709
Db 121 ACGCCGAGGAGCAACCCCGCGGCCCCACGACACCTCGCTCTCCGGAGAGCCCT 180
QY 710 GCGGCGGCGCCGAGGAGCTGCCAGCCGAGGAACTGGCTCTCAACAGCAATC 769
Db 181 GCGGCGGCGCCGAGGAGCTGCCAGCCGAGGAACTGGCTCTCAACAGCAATC 240
QY 770 CCGCTGAGACACGAGAACCTAGCAAGCAGCCATTCTAGGAGACATTCAGTGACGGCACTTC 829
Db 241 CCGCTGAGACACGAGAACCTAGCAAGCAGCCATTCTAGGAGACATTCAGTGACGGCACTTC 300
QY 830 ATTGAGATGACATTTCTCGGCGCTTCCGCGCATGATGGGCTTTACAGTGACGGCACTTC 889
Db 301 ATTGAGATGACATTTCTCGGCGCTTCCGCGCATGATGGGCTTTACAGTGACGGCACTTC 360
QY 890 CTCTTCAAGCCTGGAGGACCTCCCGCTTCTTGACACACATCACCAGGATACCCACTG 949
Db 361 CTCTTCAAGCCTGGAGGACCTCCCGCTTCTTGACACACATCACCAGGATACCCACTG 420
QY 950 ACGTCCAGCACAGTGTACTCTCTCCGCGCCGACCCCTGCGCGGAGCAGCCTTTGCGCCGG 1009
Db 421 ACGTCCAGCACAGTGTACTCTCTCCGCGCCGACCCCTGCGCGGAGCAGCCTTTGCGCCGG 480
QY 1010 CCGGCTTTAACTCAAGAGCCCTCCAGTACTGTAACTGGAGATGGGAGCGCTGAGC 1069
Db 481 CCGGCTTTAACTCAAGAGCCCTCCAGTACTGTAACTGGAGATGGGAGCGCTGAGC 540
QY 1070 GCCATCGTCATCTCAGCCACTCTGTCATCTCTGTCATCTTTTGGGCGCATGCACTG 1129
Db 541 GCCATCGTCATCTCAGCCACTCTGTCATCTCTGTCATCTTTTGGGCGCATGCACTG 600
QY 1130 TTTGGCCTAAACTGGCACCTTCAGCGGATGGAGGGGAGATGTATGAGATCAGGAGGAC 1189
Db 601 TTTGGCCTAAACTGGCACCTTCAGCGGATGGAGGGGAGATGTATGAGATCAGGAGGAC 660
QY 1190 ACAGCCAGCAGTTGGCTGTGGCAACCGAGCTCTCCCTATACCCCTCAGGGGCACTGGC 1249
Db 661 ACAGCCAGCAGTTGGCTGTGGCAACCGAGCTCTCCCTATACCCCTCAGGGGCACTGGC 720
QY 1250 TTAGAGACCCCTGACAGGAAAGGCAAGAACCCAGAGGAAAGCCAGTAGTTTCTTT 1309
Db 721 TTAGAGACCCCTGACAGGAAAGGCAAGAACCCAGAGGAAAGCCAGTAGTTTCTTT 780
QY 1310 CCAGAGGACAGTTTCATGATTTCTGGAGAAATGTAGTGGGAAGCGAGCCTCCAGAA 1369

Db 781 CCAGAGACAGTTTCATAGATTCTGGAGAAATGATGTGGAAAGGCGAGCTTCCCAAG 840
QY 1370 ATTCTCTCGGCACTTTCTGGAGATCTCAAGTCTTCATAGACCATCCTGTGATCTGA 1429
Db 841 ATTCTCTCGGCACTTTCTGGAGATCTCAAGTCTTCATAGACCATCCTGTGATCTGA 900
QY 1430 TTCAATGTGTCTCTGGAAAGGAGCCCTGGTTGGCAATTTATGGCAGAAAAGGCTCCCT 1489
Db 901 TTCAATGTGTCTCTGGAAAGGAGCCCTGGTTGGCAATTTATGGCAGAAAAGGCTCCCT 960
QY 1490 CTTTCACATACAGATTTGATTTTGGAGCTCTCTGATGGCAGAGGCTCTTAACCCAG 1549
Db 961 CTTTCACATACAGATTTGATTTTGGAGCTCTCTGATGGCAGAGGCTCTTAACCCAG 1020
QY 1550 GAGCGCGGAGCTAGAGGAGCCCGCGCCAGCTCTCGGGAACTGTGCCCTCCAGC 1609
Db 1021 GAGCGCGGAGCTAGAGGAGCCCGCGCCAGCTCTCGGGAACTGTGCCCTCCAGC 1080
QY 1610 CATGAGACAGCTTCATCCAGTATTTGGATTCAAGGAATCTGGCACTTTGGCTTTTACAAT 1669
Db 1081 CATGAGACAGCTTCATCCAGTATTTGGATTCAAGGAATCTGGCACTTTGGCTTTTACAAT 1140
QY 1670 GACGGAAGAGTCAAGAGTGGTTTCTCTTCTCACCAGTCCATGAGTGGTGGATAAC 1729
Db 1141 GACGGAAGAGTCAAGAGTGGTTTCTCTTCTCACCAGTCCATGAGTGGTGGATAAC 1200
QY 1730 TGCCCCAG 1737
Db 1201 GGACAGAG 1208

RESULT 10

US-09-976-594-407/c
; Sequence 407, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 407
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 474200.1
US-09-976-594-407

Query Match 2.58; Score 208.6; DB 3; Length 2007;
Best Local Similarity 72.74; Pred. No. 1.7e-40;
Matches 296; Conservative 0; Mismatches 109; Indels 2; Gaps 2;
QY 7941 GGGGGCGGGAACCTCGAGAAATGGGGTCAACGTCACCTGTGTCCAGATCAACACAGTAC 8000
Db 2007 GGGGCCCAAGGCGCTGGAGAACGGGATCAACGTCAGCGTGTGCGATCCACACGCTGG 1948
QY 8001 TTAATGCGAGACTAGACGCTACACAGATCCAGTCCAGTACGCGGCACT-GTGCTTG 8059
Db 1947 TGATCGCAGGACGCGCAGGTTTCGGAGCTGGAGATGCAAGTTCGGCGCGCTGCGCTGC 1888
QY 8060 AACACAGCTACGGGACAACTTTGGATG-AGGAGAGCGACGGTCTCTGAGCTGGCCG 8118
Db 1887 CACGTGCGCTACGCGCATGACCTTGACAGAGGAGGCGCGCATCTCTGGAGCAGGCGCG 1828
QY 8119 GCAGAGAGCGGTGCGCAAGCGTGGGCGCCGAGCAGCAGAGACTGCGGGAAGGGAGGA 8178

Db 1827 GCAGAGCGCGCTCGCCCCGGCGCTGGGCGCGAGCAGCAGCGCGTGGCGACGCGGAGGA 1768
QY 8179 AGGCTCTGGGGCTTGACAGAGGCGGAGAGCAGCAGAGTGTCTGAGCACAGGCGGCTGCA 8238
Db 1767 GGGCGGCGCTCTTGACGAGGCGGAGAGCGGAGCTGTCTGAGCGCGGCAAGGTGCA 1708
QY 8239 AGGCTACGACGCGCTTTTCTGTGATCTCTGTCGAGCAGTACCAGAACTCTGACAGCGC 8298
Db 1707 GGGCTACGACGCGGTACTACGTACTCTCGGTGAGCAGTACCCCGAGCTGGCGACAGCGC 1648
QY 8299 CAACAACATCCACTTCATGACAGACGAGGATGGCCGAGGTGAC 8345
Db 1647 CAACAACATCCAGTTCTTGGCGCAGAGCGAGATCGGCGAGGATAC 1601

RESULT 11

US-09-949-016-3399
; Sequence 3399, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3399
; LENGTH: 6763
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3399

Query Match 1.38; Score 109; DB 3; Length 6763;
Best Local Similarity 52.38; Pred. No. 7.1e-16;
Matches 350; Conservative 0; Mismatches 295; Indels 24; Gaps 4;
QY 1729 CTGCCCCAGCAACTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCGCACCTGCTTCC 1788
Db 411 CTGCCCCAGATGACTGCAATGATCAGGTCGTCGTGTCGTCGTGTCGTGTCGTGTCGTGTC 470
QY 1789 GGGTTTCTCTGGGCCCCGACTGTGGCAGAGCCTCTGCCCCCGTCTCTGTAGCGGAATGG 1848
Db 471 GGGCTACACTGGCCCCCAGCTGTGGCTGGCCATCTCTGCCGGGACTGCCAAGGCGGTGG 530
QY 1849 CCAATACATGAAGGAGATGCTTGTGCCACAGTGTGTCAGAGTGGAAAGGCGCTGAGTGCATGT 1908
Db 531 GGGCTGCTGCAGGGCGTGTGTGTGCGGGCAGGCTTCTCAGGCCCCGACTGCCAGCCA 590
QY 1909 GCCCACCACCAAGTGTATCGATGTGCTGCTGCACCAACCATGGCACCTGTCATCAGGSCAC 1968
Db 591 GGGCTCTCTGCC-----CTCAGGTTGCACCCAGAGGGGAGCGTGTGAGGGTGGCG 641
QY 1969 CTGCATCTGCAACCTCTGGCTTACAAAGGCGGAGAGCTGTGAGGAAAGTGCATGAGACCC 2028
Db 642 CTGCGTGTGTGACCCAGGCTACACTGTTGACGACTGTGGCATGAGGAGCTGC-----CCT 696
QY 2029 CACATGTTGAGGCGGGGTGTCTGCGTGTGAGAGCGGAATGCCATGCTTTGTGSGATGGGG 2088
Db 697 CGCGTGTGAGTCAGAGGGGGCGCTGTGTGAGAAATGGGC-----GCTGCGTGTGTAAACC 749
QY 2089 AGGCACCAACTGCGAGACCCCGAGGCGCATGCTTTAGACCAGTGTTCAGGCGCACCGAAC 2148
Db 750 CGGCTACACTGGCGAGGACTGTGGGTGAGGAGCTGCCCTCGGGGTGTCAGCAGCGGGG 809
QY 2149 CTTTCTCCGGACACCGGGGCTTTTGCAGCTGTGTGACCAAGCTGTGACTGGACACGACTGTT 2208

Db 810 ACCTGCAAGGA--CGGGCGCTGCTGTGTGACCCCGGCTACACTGGGAGGACTGTGG 866
QY 2209 TATGAGATCTGTGTGCGCACTGTGGTGGCCATGGCGTGTGCGTAGGGGGCACTGTGCG 2268
Db 867 TAGCGGAGCTCCCTGGGACTGTGGCGAGGGCGGGCGCTGCTGGAGCGGCGCTGGCT 926
QY 2269 CTGCGAGGATGCTGATGGGGGCGAGCTGCGACCGAGGGGCTGCCACCGCGCTGTGC 2328
Db 927 GTGTGGCCGGGTACACAGGCGAGACTGCGAGCAGCGGACATGTCCGAGGAGACTGCGG 986
QY 2329 CGAGCATGGGACCTGTGCGCGAGCGCAAGTGTGCGAGTGCAGCCCTGTGCTGGAATGGCGAACA 2388
Db 987 GGGCGCGGCGCTGCGAGGACGGCGAATGCAATTTGCGACACGGGCTACAGCGGGGACGA 1046
QY 2389 CTGCACCAT 2397
Db 1047 CTGCGGCGT 1055

RESULT 12

US-09-620-312D-75

; Sequence 75, Application US/09620312D

; Patent No. 6569662

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Adundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyang

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aifeng J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yuning

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhiwei

; APPLICANT: John Tillinghast

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6569662el Nucleic Acids and

; FILE REFERENCE: 784CIP2B

; CURRENT APPLICATION NUMBER: US/09/620,312D

; PRIOR FILING DATE: 2000-07-19

; PRIOR FILING DATE: 2000-04-25

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 1105

; SOFTWARE: pt_fl_genes Version 1.0

; SEQ ID NO 75

; LENGTH: 13857

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(13857)

US-09-620-312D-75

Query Match 1.3%; Score 109; DB 3; Length 13857;
Best Local Similarity 52.3%; Pred. No. 1e-15;
Matches 350; Conservative 0; Mismatches 295; Indels 24; Gaps 4;
QY 1729 CTGCCCCAGCACTGCTATGGCAATGGTACTGTCATCTCTGGGACCTGCCACTGCTTCCT 1788
Db 555 CTGCCCCAGTACTGCAATGATGATGAGGTGCTGTGCTGCTGCTGCTGCTGCTGCTTCC 614
QY 1789 GGGTTCTTGGCCCCGAGCTGCGAGAGCCCTCTGCCCGCTGCTGTACCGGAATGG 1848
Db 615 CGGCTACACTGGCCCCCAGCTGTGGTGGCCATCTCTGCTCCCGGGACTGCCAAGGCCGTGG 674

QY 1849 CCATACATGAAGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGCCCTGAGTGGCATGT 1908
Db 675 GCGTGTGTCAGGGCGCTGTGTGTGTCGGGAGGCTTCTCAGGCCCCGAGCTCAGGCCA 734
QY 1909 GCCCACCACAAACAGTGTATCGATGTGGCTGCGAGCAACATGGCACCTGCGATCAGGGGCAC 1968
Db 735 GCGTCTCTGCC-----CTCGAGGTTCAGCCAGAGGGGACGCTGTGAGGGTGGCG 785
QY 1969 CTGCAATCTGCAACCTTGCTGTACAAAGGCGAGAGCTGTGAGGAAGTGCATGTGACGCC 2028
Db 786 CTGCGTGTGTGACCCAGGCTACACTGTGTGACGACTGTGTGCAATGAGGAGCTGC-----CCT 840
QY 2029 CACATGTTCAAGCGGGGTGCTGCGGTGAGAGGCGAATGCCATTTGCTTTGGGATGGG 2088
Db 841 CGCGTTTCAGTTCAGAGGGGGCGCTGTGAGAAATGGGC-----GCTGCGTGTGTAAACC 893
QY 2089 AGGCACCAACTGGGAGACCCCGGCGCCACATGCTTAGACAGTGTTCAGGCCACCGGAAC 2148
Db 894 CGGCTACACTGGCGAGGACTGTGGGTGAGAGCTGCCCTCGGGCTGCAGCCAGCGGG 953
QY 2149 CTTCTCCCGGACACCGGGCTTTGAGCTGTGACCCAAAGCTGAGCTGGACAGCACTGTTTC 2208
Db 954 ACGTGTCAAGGA---CGGGCGCTGCGTGTGTGACCCCGGCTACACTGGCGAGGACTGTGG 1010
QY 2209 TATCGAGATCTGTGCTGCCGACTGTGTGTGCGCATGGCGTGTGGTAGGGGCGACCTGCCCG 2268
Db 1011 TAGCGGAGCTGCCCTGCGGACTGTGTGAGGGGGCGGCTGTGTGACGCGCGCTGCT 1070
QY 2269 CTGCGAGGATGGCTGGATGGGGGCGAGCTCGACACGCGGGCTGCCACCGCGCTGTGC 2328
Db 1071 GTGCTGCCCGGTACACAGCGAGGACTGCGACGCGGACATGTCCGAGGAGCTGCCCG 1130
QY 2329 CGAGCATGGACCTGCCCGACCGCAAGTGCAGATGCGAGCCCTGCTGGATGGCGAACA 2388
Db 1131 GGGCGCGGGCGCTGCGAGGACGCGCAATCATTTGCGACACGCGGCTACACGCGGGACGA 1190
QY 2389 CTGCACCAT 2397
Db 1191 CTGCGGCGT 1199

RESULT 13

US-09-949-016-15141

; Sequence 15141, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15141

; LENGTH: 34534

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-15141

Query Match 1.3%; Score 109; DB 3; Length 34534;
Best Local Similarity 52.3%; Pred. No. 1.6e-15;
Matches 350; Conservative 0; Mismatches 295; Indels 24; Gaps 4;
QY 1729 CTGCCCCAGCACTGCTATGGCAATGGTACTGTCATCTCTGGGACCTGCCACTGCTTCCT 1788

Db 2901 CTGCCAGATGACTGCAATGATCAGGGTCGTGTGTCCTGGTGTGCTGTGCTTTCC 2960
Qy 1789 GGGTTTCTGGGCGCCGACTGTGGCAGAGCTCTGCGCGGTCTCTGTAGCGGAATGG 1848
Db 2961 CGGCTACACTGGGCGCCGAGCTGTGGCTGCGCATCTGTCCGGGACTGCCAAGCCCGTGG 3020
Qy 1849 CCAATACATGAAGGAGATGCTTTGTGCCACAGTGTGGAAAGGGCGCTGAGTGCATGT 1908
Db 3021 GCGCTGGTGCAGGGCGTGTGTGTGCGCGGAGGCTTCTCAGGCGCCGACTGCAGCCA 3080
Qy 1909 GCCCAACAACTAGTGTATGATGTGGCTGTGCAGCAACCAATGAGCACTGTGATCACGGGAC 1968
Db 3081 GCGCTCTGCC-----CTCAGGTTTCAGCCAGAGGGGACGCTGTGAGGGTGGGG 3131
Qy 1969 CTGCATCTGCAACCTGGCTTACAGGCGGAGAGCTGTGAGGAAGTGCATGATGACACC 2028
Db 3132 CTGCGTGTGTGACCCAGGCTTACACTGGTGACGACTGTGGCATGAGGAGCTGC-----CCT 3186
Qy 2029 CACATGTTCAGGCGGGGTCTCTGCGTGTAGAGCGGAATGCCATTGCTTTGTGGGATGGG 2088
Db 3187 CGCGTTGCACTGAGAGGGGCGCTGTGAGATGGGC-----GCTGCGTGTGAACCC 3239
Qy 2089 AGCACAACACTGCGAGACCCCGAGGCCACATGCTTAGACCACTGTTCAGGCGCACCGAAC 2148
Db 3240 CGGCTACACTGGCGAGACTGTGGGTGAGGAGCTGCCCTCGGGGCTGCAGCCAGCGGGG 3299
Qy 2149 CTTCTCCCGGACACCGGGCTTTGACAGCTGTGACCCAGCTGAGCTGGACACGACTGTT 2208
Db 3300 ACGCTGCAAGGA---CGGGCGCTGCCTGTGTGACCCCGGCTACACTGGCGAGGACTGTGG 3356
Qy 2209 TATCGAGATCTGTGTCGCCACTGTGTGGTCCCATGGCTGTGCTAGGGGGCACTTGGCCG 2268
Db 3357 TAGCGGAGTGCCTTGGGACTGTGTGGAGGGCGGCGTGTGGACGGCGCTGCGT 3416
Qy 2269 CTGCGAGATGCTGTGATGGGGGAGCCTTCGACACAGCGGCTGCCACCGCGCTGTGTC 2328
Db 3417 GTGCTGCCCGGTGTACACAGCGGAGGACTGCAGCAGCGGACATGTCCGAGGAGCTGCCG 3476
Qy 2329 CGAGCTGGACCTGCGCGACGCGAGTGCAGTGCAGCTGCGAGCTGGCTGGATGGCGACA 2388
Db 3477 GGGCGCGGGCGCTGCGAGGACGCGGAATGCAATTTGCGACACGGGCTTACAGCGGGACGA 3536
Qy 2389 CTCGACAT 2397
Db 3537 CTGCGGCGT 3545

RESULT 14
; Sequence 29, Application US/09861893
; Patent No. 6960434
; GENERAL INFORMATION:
; APPLICANT: Feinberg, Andrew
; APPLICANT: Strichman-Almashanu, Liora
; APPLICANT: Jiang, Shan
; TITLE OF INVENTION: METHODS FOR ASSAYING GENE IMPRINTING AND
; FILE REFERENCE: 01107.00128
; CURRENT APPLICATION NUMBER: US/09/861,893
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/206,158
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/206,161
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-861-893-29

Query Match 1.2%; Score 96.4; DB 3; Length 399;

Best Local Similarity 56.0%; Pred. No. 2e-13;
Matches 204; Conservative 0; Mismatches 156; Indels 4; Gaps 1;
Qy 7584 AGCTTATCTCTGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGGCTTTTGTACCTTAG 7643
Db 40 AGCCCATCTTTCGGAGTCCAGCAGAGTGGCGCGGAGCCAAAGGCTTCTGTGCTGG 99
Qy 7644 AACGGTTTGACAGCTCTATGGCTCCACAATCACCAGTGCACGAGGTGCCAAGACCA 7703
Db 100 GGAAGATGSCCGAGGTGCAGGTGAGC-----CGGCGCGGGCGCGCGAGTCTCTGG 155
Qy 7704 AGAAGTTTGATCCAGCGGCTCAGTCTTTTGGCAAGGGGTCAAGTTTGCCTTGAAGGATG 7763
Db 156 CTGTGTTCGCCACGGTCAAGTCGTCATCGGAAGGGCGTCTATGTGGCGGTGAGCCAGG 215
Qy 7764 GCGGAGTGACACAGACATCATCAGTGTGGCCAAATGAGGATGGCGAAGGGTGTCTGCCA 7823
Db 216 GCGCGGTGAGACCAACAGCTGCTCAACATCGCCCAACGAGGACTGCATCAAGGTGGCGCG 275
Qy 7824 TCTTGAACCATGCCCACTACCTAGAGAACCTGCACCTTCAACCATTTGATGGGTGGATACCC 7883
Db 276 TGCTCAACAACGCTTCTACCTGGAGAACCTGCACCTTCAACATCGAGGGCAAGGACACGC 335
Qy 7884 ATTACTTTGTAAACAGGACCTTCAGAAAGGTGACCTGGCCATCTCTGGGCTCAGTGGGG 7943
Db 336 ACTACTTTCATCAAGACCAACACCGCCGAGAGGACCTGGGCGAGCTGCGTGTGACCAAGC 395
Qy 7944 GSGG 7947
Db 396 GCGG 399

RESULT 15
US-09-949-016-121669/c
; Sequence 121669, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121669
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-121669

Query Match 1.1%; Score 93.2; DB 3; Length 601;
Best Local Similarity 51.9%; Pred. No. 1.5e-12;
Matches 321; Conservative 0; Mismatches 273; Indels 24; Gaps 4;
Qy 1775 TGCCACTGCTTCTCTGGGTTTCTTGGGCGCCGAGCTGTGGGAGAGCCTCTCCCGCTGCTC 1834
Db 600 TGCAATTTGACACAGGGCTTACAGCGGGAGCACTGGCGGTGCGCAGCTGCCCTGGCGAC 541
Qy 1835 TGTAGCGGAATGGCCAATACATGAAGGAGAGATGTTGTGCCACAGTGTGCTGGAAGGC 1894
Db 540 TGCAACAAAGGGCGCTGCGAGGACGCGCGTGTGCTGTGCTGGCGGGGTACACTGGA 481
Qy 1895 GCTGAGTGGATGTGCCACCAACAGTGTATCGATGTGCGCTGCAGCAACCATGGCACC 1954
Db 480 ACCGATTGGGCTCGCGCGCTGCCACGC-----GACTGTAGAGGTGCGGGCGC 430

| | | | |
|----|------|---|------|
| Qy | 1955 | TCATCATCGGCACTGTCATCTGCAACCCCTGGCTACAGGGCGAGAGCTGTGAGGAAGTG | 2014 |
| Db | 429 | TCGAGAACGGCGTGTGTGTTTGCATGCGGCTACAGGGCGAGGACTGCGGTGTGCGC | 370 |
| Qy | 2015 | GACTGATGGACCCACATGTTTCAGGCCGGGGTGTCTGGTGAGAGGCGAATGCCATTGC | 2074 |
| Db | 369 | AGCTGTCTCTGGGGAC---TGTGCTGGCCGGGGCCGCTGTGAGAGTGGCGCTGCATGTGT | 313 |
| Qy | 2075 | TTTGTGGGATGGGAGGCACCAACTGCGAGACCCCGAGGCCACATGCTTAGACCAAGTGT | 2134 |
| Db | 312 | TGGCCGGGGTACACAGGCCGGGACTGCGGCACGCCG-----CCTGTCTGGCGACTGT | 259 |
| Qy | 2135 | TCAGGCCACGGAACTTCTCCCGGACACCGGGCTTTGCAGCTGTGACCCCAAGCTGGACT | 2194 |
| Db | 258 | CGCGGGCGCGGCGCTGCGTGGATGGCGCTGCGTGTGCA-----ACCCGGCTTCACC | 205 |
| Qy | 2195 | GGACAGGACTGTTCTATCGAGATCTGTGTGCCGACTGTGTGGCCATGGCGTGTGCGTA | 2254 |
| Db | 204 | GGTGAGGACTGTGGGAGCGCTGCTGTCCCGGGACTGCCGTGGGCACGGCCTTTGCCGAG | 145 |
| Qy | 2255 | GGGGGCACCTGCCGCTGCGAGGATGGCTGGATGGGGGCGAGCTGCGACACAGCGGCCCTGC | 2314 |
| Db | 144 | GATGGCTGTGCTGTGTGACGACGGCTACTCAGGGGAAGACTGACGACCGCGAGCTGC | 85 |
| Qy | 2315 | CACCCGCGCTGTGCCGAGCATGGGACCTGCCCGGACGGCAAGTGCAGTGCAGCCCTGGC | 2374 |
| Db | 84 | CCCGGGGGCTGCCGAGGCCGCGCCAGTGCCTAGATGGCGGTGTGTGTGCGAGGACGGC | 25 |
| Qy | 2375 | TGGATGGGGAACACTGC | 2392 |
| Db | 24 | TACTCTGGCGAGGATTGC | 7 |

Search completed: December 10, 2005, 15:51:17
Job time : 1323 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 18:38:31 ; Search time 4392 Seconds
(without alignments)
12676.877 Million cell updates/sec

Title: US-10-029-020-13
Perfect score: 8354
Sequence: 1 gtttggtgatggaggagc.....ccggagggtgacagagaggac 8354

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------------|--------------------|
| 1 | 8354 | 100.0 | 8354 | 6 ABS52100 | Abq82345 Human NOV |
| 2 | 8354 | 100.0 | 8354 | 10 Adf74829 | Adf74829 Murine NO |
| 3 | 8225 | 98.5 | 8645 | 6 ABS78652 | Abq82345 Human NOV |
| 4 | 7791.2 | 95.7 | 8355 | 10 Adf74841 | Adf74841 Murine NO |
| 5 | 7779.2 | 93.1 | 8438 | 6 ABS85378 | Abq82345 Human NOV |
| 6 | 3680.8 | 44.1 | 8624 | 12 ADQ20349 | Adq20349 Human sof |
| 7 | 3621.6 | 43.4 | 8774 | 12 ADQ24356 | Adq24356 Human sof |
| 8 | 3544.6 | 42.4 | 8964 | 12 ADH01384 | Adh01384 Teneurin |
| 9 | 3504.6 | 42.0 | 8645 | 6 ABS82344 | Abq82344 Human NOV |
| 10 | 3500.6 | 41.9 | 8645 | 12 ADH41968 | Adh41968 Novel hum |
| 11 | 3473.8 | 41.6 | 8204 | 12 ADH41972 | Adh41972 Novel hum |
| 12 | 3473.8 | 41.6 | 8657 | 12 ADH41990 | Adh41990 Novel hum |
| 13 | 3473.8 | 41.6 | 8657 | 12 ADH41932 | Adh41932 Novel hum |
| 14 | 3472.6 | 41.6 | 8675 | 6 ABS82343 | Abq82343 Human NOV |
| 15 | 3472.2 | 41.6 | 8636 | 12 ADH41998 | Adh41998 Novel hum |
| 16 | 3472.2 | 41.6 | 8657 | 12 ADH41992 | Adh41992 Novel hum |
| 17 | 3472.2 | 41.6 | 8657 | 12 ADH41994 | Adh41994 Novel hum |
| 18 | 3472.2 | 41.6 | 8657 | 12 ADH41996 | Adh41996 Novel hum |
| 19 | 3424.4 | 41.0 | 8473 | 6 ABS82345 | Abq82345 Human NOV |

| | | | | | | |
|----|--------|------|-------|----|----------|--------------------|
| 20 | 3422 | 41.0 | 8473 | 12 | ADH41948 | Adh41948 Novel hum |
| 21 | 3418.4 | 40.9 | 9852 | 12 | ADH71219 | Adh71219 Human gen |
| 22 | 3399.8 | 40.7 | 8487 | 6 | ABQ82346 | Abq82346 Human NOV |
| 23 | 3398.8 | 40.7 | 8487 | 12 | ADH41976 | Adh41976 Novel hum |
| 24 | 3385 | 40.5 | 9668 | 12 | ADH71239 | Adh71239 Human gen |
| 25 | 3385 | 40.5 | 9756 | 12 | ADH71249 | Adh71249 Human gen |
| 26 | 3385 | 40.5 | 9823 | 12 | ADH71257 | Adh71257 Human gen |
| 27 | 3385 | 40.5 | 9823 | 12 | ADH71245 | Adh71245 Human gen |
| 28 | 3385 | 40.5 | 9826 | 5 | AAS14085 | Aas14085 Human FCT |
| 29 | 3385 | 40.5 | 9826 | 12 | ADH71253 | Adh71253 Human gen |
| 30 | 3384.8 | 40.5 | 8797 | 12 | ADJ75919 | Adj75919 Marker ge |
| 31 | 3362.6 | 40.3 | 9826 | 10 | ABS32023 | Abq32023 Human FCT |
| 32 | 3351.4 | 40.1 | 9729 | 5 | AAS14089 | Aas14089 Human FCT |
| 33 | 3351.4 | 40.1 | 9729 | 10 | ABS32028 | Abq32028 Human FCT |
| 34 | 3351.4 | 40.1 | 9729 | 12 | ADH71251 | Adh71251 Human gen |
| 35 | 3335.6 | 39.9 | 6999 | 12 | ADH71273 | Adh71273 Human gen |
| 36 | 3274.2 | 39.2 | 13202 | 4 | AAS1828 | Aas1828 Human pol |
| 37 | 3258 | 39.0 | 8297 | 12 | ADQ21281 | Adq21281 Human sof |
| 38 | 3258 | 39.0 | 12879 | 6 | ABK92230 | Abk92230 Prostata |
| 39 | 3258 | 39.0 | 12880 | 11 | ADN39609 | Adn39609 Cancer/an |
| 40 | 3256.4 | 39.0 | 8297 | 13 | ADU06138 | Adu06138 Novel bro |
| 41 | 3165 | 37.9 | 9695 | 8 | ACC72052 | Acc72052 BCU0205B |
| 42 | 3158.4 | 37.8 | 8575 | 6 | ADI16807 | Adi16807 Human NOV |
| 43 | 3158.4 | 37.8 | 8575 | 12 | ADH71271 | Adh71271 Human gen |
| 44 | 3137.4 | 37.6 | 7781 | 12 | ADQ19483 | Adq19483 Human sof |
| 45 | 3068.6 | 36.7 | 9058 | 8 | ACC72051 | Acc72051 BCU0205A |

ALIGNMENTS

RESULT 1
ABS52100
ID ABS52100 standard; DNA; 8354 BP.

AC ABS52100;

DT 05-NOV-2002 (first entry)

DE Human TEN-M4-like gene.

XX Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cell signal processing; metabolic pathway modulation; metabolic disorder; obesity; diabetes; infectious disease; neurodegenerative disorder; acne; Alzheimer's disease; Parkinson's disease; immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; gastro-intestinal disease; reproductive; neurological disease; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBE1; TEN-M4; adipocyte complement-related C1q tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6/enk-2; Glucose transporter; type 1a membrane sushi-containing domain; butyrophilin; type 1a membrane-sushi domain containing; SNP; gene; ds; single nucleotide polymorphism.

Homo sapiens.

| Key | Location/Qualifiers |
|-----------|--|
| variation | /tag= a |
| variation | /standard_name= "Single nucleotide polymorphism (SNP)" |
| variation | replace(117,G) |
| variation | /tag= b |
| variation | /standard_name= "Single nucleotide polymorphism (SNP)" |
| variation | replace(260,A) |
| variation | /tag= c |
| variation | /standard_name= "Single nucleotide polymorphism (SNP)" |

WO200257453-A2.

| | | | | | | | | | |
|----|------|--|------|--|------|---|--|------|--|
| QY | 1381 | CACCTTTCTGGAGATCTCAAGTGTTCATAGACCACTCCTGTGCATCTGAAATTCATATGTGC | 1440 | | 2461 | ATGTACTTTAGACCTGAATGGTTGGCACTGCGCTCTGCCAGCTGGGCTGGAGAGGAGCTGG | 2520 | | |
| Db | 1381 | CACCTTTCTGGAGATCTCAAGTGTTCATAGACCACTCCTGTGCATCTGAAATTCATATGTGC | 1440 | | QY | 2521 | CTGTGACACTTCCATGGAGACTGCGGTGACAGAAAGACAATGATGGAGATGGCCCT | 2580 | |
| QY | 1441 | TCGTGGAAAGGCAAGCCCTGGTTGGCATTTATGGCAGAAAGGCGCTCCCTCTTCAATAC | 1500 | | Db | 2521 | CTGTGACACTTCCATGGAGACTGCGGTGACAGAAAGACAATGATGGAGATGGCCCT | 2580 | |
| Db | 1441 | TCGTGGAAAGGCAAGCCCTGGTTGGCATTTATGGCAGAAAGGCGCTCCCTCTTCAATAC | 1500 | | QY | 2581 | GGTGGACTGCATGGAGCCCTGACTGTGCTCCAGCCCTGTGCCATATCAACCCGCTGTG | 2640 | |
| QY | 1501 | ACAGTTTGAATTTGTGGAGCTGCTGGATGCGAGAGGCTCCTAACCCAGAGGCGGGAG | 1560 | | Db | 2581 | GGTGGACTGCATGGAGCCCTGACTGTGCTCCAGCCCTGTGCCATATCAACCCGCTGTG | 2640 | |
| Db | 1501 | ACAGTTTGAATTTGTGGAGCTGCTGGATGCGAGAGGCTCCTAACCCAGAGGCGGGAG | 1560 | | QY | 2641 | CCTTGGCTCCCTTAACCTCTTGACATCATCAGGAGACAAGGTCCTTGTGCAGCA | 2700 | |
| QY | 1561 | CCTAGAGGGACCCCGCGCAGTCTCGGGAACTGTGCCCTCCAGCCATGAGACAGG | 1620 | | Db | 2641 | CCTTGGCTCCCTTAACCTCTTGACATCATCAGGAGACAAGGTCCTTGTGCAGCA | 2700 | |
| Db | 1561 | CCTAGAGGGACCCCGCGCAGTCTCGGGAACTGTGCCCTCCAGCCATGAGACAGG | 1620 | | QY | 2701 | GAACCTTACACTCTTCTATGACCGCATCAAGTTCTCTGTGGCAGGAGACAGCACAT | 2760 | |
| QY | 1621 | CTTCATCCAGTATTTGGATTCAGGAATCTGGCACTTGGCTTTTAAATGACGGAAAGGA | 1680 | | Db | 2701 | GAACCTTACACTCTTCTATGACCGCATCAAGTTCTCTGTGGCAGGAGACAGCACAT | 2760 | |
| Db | 1621 | CTTCATCCAGTATTTGGATTCAGGAATCTGGCACTTGGCTTTTAAATGACGGAAAGGA | 1680 | | QY | 2761 | AATCCCGGGGAGAAACCCCTTTGATGGAGGGCATGCTTGTGTTATTCGTGGCCAAAGTAT | 2820 | |
| QY | 1681 | GTGAGAAAGTGGTTTCTTCTCAACCACTGCCATTTGATCGGTGGATAATGCCCCAGCAA | 1740 | | Db | 2761 | AATCCCGGGGAGAAACCCCTTTGATGGAGGGCATGCTTGTGTTATTCGTGGCCAAAGTAT | 2820 | |
| Db | 1681 | GTGAGAAAGTGGTTTCTTCTCAACCACTGCCATTTGATCGGTGGATAATGCCCCAGCAA | 1740 | | QY | 2821 | GACATCAGATGGAAACCCCTCTGGTTGGTGTGAACATCAGTTTGTCAATAACCTCTCTT | 2880 | |
| QY | 1741 | CTGCTATGGCAATGGTGACTGTCATCTCTGGGACCTGCCACTGCTTCTGGGTTTCTCTGG | 1800 | | Db | 2821 | GACATCAGATGGAAACCCCTCTGGTTGGTGTGAACATCAGTTTGTCAATAACCTCTCTT | 2880 | |
| Db | 1741 | CTGCTATGGCAATGGTGACTGTCATCTCTGGGACCTGCCACTGCTTCTGGGTTTCTCTGG | 1800 | | QY | 2881 | TGGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC | 2940 | |
| QY | 1801 | CCCCGACTGTGGCAGAGCCTCTGCCCCGTCTGTAGCGGAAATGGCCCAATACATGAA | 1860 | | Db | 2881 | TGGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC | 2940 | |
| Db | 1801 | CCCCGACTGTGGCAGAGCCTCTGCCCCGTCTGTAGCGGAAATGGCCCAATACATGAA | 1860 | | QY | 2941 | CATCATCTCGCGGTTCCAGCGGGCACCTTTTCATCACACAGGAGCACACCTGTGGCTGCC | 3000 | |
| QY | 1861 | AGCAGATGCTTGTGCCAGTGGCTGGAAAGGCGTGGATGGATGGCCACCAACCA | 1920 | | Db | 2941 | CATCATCTCGCGGTTCCAGCGGGCACCTTTTCATCACACAGGAGCACACCTGTGGCTGCC | 3000 | |
| Db | 1861 | AGCAGATGCTTGTGCCAGTGGCTGGAAAGGCGTGGATGGATGGCCACCAACCA | 1920 | | QY | 3001 | ATGGGATCGCTTCTTGTGTCATGGAAACCATCATCATGAGACATGAGAGNAATGAGATTCC | 3060 | |
| QY | 1921 | GTGTATCGATGTGGCTTGACAGCAACCATGGCACCTGCATCACCGGCACCTGCATCTGCAA | 1980 | | Db | 3001 | ATGGGATCGCTTCTTGTGTCATGGAAACCATCATCATGAGACATGAGAGNAATGAGATTCC | 3060 | |
| Db | 1921 | GTGTATCGATGTGGCTTGACAGCAACCATGGCACCTGCATCACCGGCACCTGCATCTGCAA | 1980 | | QY | 3061 | CAGCTGTGACCTGAGCAATTTTGGCCGCCCAACCCAGTCGTCTCTCCATCCCCACTGCAC | 3120 | |
| QY | 1981 | CCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTGGACTGTCATGGAACCCCAATGTTTCAGG | 2040 | | Db | 3061 | CAGCTGTGACCTGAGCAATTTTGGCCGCCCAACCCAGTCGTCTCTCCATCCCCACTGCAC | 3120 | |
| Db | 1981 | CCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTGGACTGTCATGGAACCCCAATGTTTCAGG | 2040 | | QY | 3121 | GTCTTTCGCGCAGCTCTGTGCGAGAGAAAGCCCATTTGTGCGGAAATTCAGGCTTTGCA | 3180 | |
| QY | 2041 | CCGGGTGTCTGCTGAGAGCGAAATGCCATTTGTTTGGGATGGGGAGCCCAACTG | 2100 | | Db | 3121 | GTCTTTCGCGCAGCTCTGTGCGAGAGAAAGSCCCCATTTGTGCGGAAATTCAGGCTTTGCA | 3180 | |
| Db | 2041 | CCGGGTGTCTGCTGAGAGCGAAATGCCATTTGTTTGGGATGGGGAGGCAACCACTG | 2100 | | QY | 3181 | GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGAGCCCC | 3240 | |
| QY | 2101 | CGAGACCCCGAGGCGCACATGCTTAGACCAAGTGTTCAGGCGACGGAACCTTCTCCCGGA | 2160 | | Db | 3181 | GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGAGCCCC | 3240 | |
| Db | 2101 | CGAGACCCCGAGGCGCACATGCTTAGACCAAGTGTTCAGGCGACGGAACCTTCTCCCGGA | 2160 | | QY | 3241 | TGGCTACAAATCTGCTCCTGAGGATCAGCCTCACCCACCCGACCATCCCTTCAACCTCAT | 3300 | |
| QY | 2161 | CACCGGCTTTGACGCTGTGACCCCAAGCTGGACTGGAACAGCTGTTTCTATCGAGATCTG | 2220 | | Db | 3241 | TGGCTACAAATCTGCTCCTGAGGATCAGCCTCACCCACCCGACCATCCCTTCAACCTCAT | 3300 | |
| Db | 2161 | CACCGGCTTTGACGCTGTGACCCCAAGCTGGACTGGAACAGCTGTTTCTATCGAGATCTG | 2220 | | QY | 3301 | GAAGTGTGACCTCATGCTAGCGGTGGAGGCGCCCTCTTTCAGGAAGTGGTTCTGCTGAGC | 3360 | |
| QY | 2221 | TGCTGCCGACTGTGGTGCCATGCGCTGTGAGGGGGACCTTCCGCTGCGAGATGG | 2280 | | Db | 3301 | GAAGTGTGACCTCATGCTAGCGGTGGAGGCGCCCTCTTTCAGGAAGTGGTTCTGCTGAGC | 3360 | |
| Db | 2221 | TGCTGCCGACTGTGGTGCCATGCGCTGTGAGGGGGACCTTCCGCTGCGAGATGG | 2280 | | QY | 3361 | CCGAGACCTGTCTATTTATTTTCATTTTGGGCAAGAAGACAGAGCTCTACAAACAGAGGTGT | 3420 | |
| QY | 2281 | CTGGATGGGGGAGCCTGCGACAGCGGGCTGCGACCCGCTGTGCGGAGCATGGGAC | 2340 | | Db | 3361 | CCGAGACCTGTCTATTTATTTTCATTTTGGGCAAGAAGACAGAGCTCTACAAACAGAGGTGT | 3420 | |
| Db | 2281 | CTGGATGGGGGAGCCTGCGACAGCGGGCTGCGACCCGCTGTGCGGAGCATGGGAC | 2340 | | QY | 3421 | TGGGCTTTCAGAGCCTTTGTTTCCGTTGGTTATGAATCTGCTCCCGCCAGATCTTAAT | 3480 | |
| QY | 2341 | CTGCGCGAGCGGCAAGTGCAGTGCAGCTCCTGGCTGGAATGGCGAAACACTGCACTCCG | 2400 | | Db | 3421 | TGGGCTTTCAGAGCCTTTGTTTCCGTTGGTTATGAATCTGCTCCCGCCAGATCTTAAT | 3480 | |
| Db | 2341 | CTGCGCGAGCGGCAAGTGCAGTGCAGCTCCTGGCTGGAATGGCGAAACACTGCACTCCG | 2400 | | QY | 3481 | CCTGTGGGAAAAAAGAACCAACAGTGTGAGGGCTATGAAATTCAGCGCTCCAAAGCTTGG | 3540 | |
| QY | 2401 | TCATATCTGATAGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGCGAG | 2460 | | Db | 3481 | CCTGTGGGAAAAAAGAACCAACAGTGTGAGGGCTATGAAATTCAGCGCTCCAAAGCTTGG | 3540 | |
| Db | 2401 | TCATATCTGATAGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGCGAG | 2460 | | QY | 3541 | AGGATGGAGCCTTAGACAAACATCATGCCCTCAAATTCAAAAGTGGTATCTCTGCACAAAGG | 3600 | |
| QY | 2461 | ATGTACCTTAGACCTGAATGGTTGGCACTGCGCTGCGAGCTGGGCTGGAGAGGAGCTGG | 2520 | | | | | | |

Db 3541 AGGATGGAGCCTAGACAAACATCATGCGCTCAACATTCAAAGTGGTATCTCTGCACAAAGG 3600
Qy 3601 GAAATGGGAGACCAAGTTTGTGCTCAGACGCTCCTCTCATTTGGGAGCATCATGGGCAA 3660
Db 3601 GAAATGGGAGAACCAAGTTTGTGCTCAGAGGCTCCTGTCTATGGGAGCATCATGGGCAA 3660
Qy 3661 TGGGCGCGGAGAACATCTCTGCGCCCGAGCTGCAACGGGCCCTTGCTGACGGCAACAAGCT 3720
Db 3661 TGGGCGCGGAGNAGCATCTCTGCGCCCGAGCTGCAACGGGCCCTTGCTGACGGCAACAAGCT 3720
Qy 3721 CCTGCGCCAGTGGCCCTCAACTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAA 3780
Db 3721 CCTGCGCCAGTGGCCCTCAACTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAA 3780
Qy 3781 CTACATTTAGNAGGATCTTCCCTCTCGGAATGCTACCAACATCTCTAGAGCTGAGGAATAA 3840
Db 3781 CTACATTTAGNAGGATCTTCCCTCTCGGAATGCTACCAACATCTCTAGAGCTGAGGAATAA 3840
Qy 3841 AGATTTTCAGACATAGTCAAGTCCAGCACACAAATACTACCTGGGCCACAGACCCCATGAG 3900
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Db 3901 TGGGCGCGCTTCTCTTTCTGACAGCAAAGCGCGGGTCTTTTAAATCAAGTCCACTGT 3960
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Db 4561 CCCCAAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTTGTTTTCTGGAGACGATGG 4620
Qy 4621 TTATGCCAAGGATGCAAAATTTAAATACCCCATCTTCTCTGGCTGTGTGCTGATGGGA 4680
Db 4621 TTATGCCAAGGATGCAAAATTTAAATACCCCATCTTCTCTGGCTGTGTGCTGATGGGA 4680

Qy 4681 GCTCTACGTGGCCGACCTTGGGAAACATCCGAATTCGGTTTATTCGGGAAGAACAGCCTTT 4740
Db 4681 GCTCTACGTGGCCGACCTTGGGAAACATCCGAATTCGGTTTATTCGGGAAGAACAGCCTTT 4740
Qy 4741 CCTCAACACCCAGAACATGTATGAGCTGTCTTCAACAAATGACCAAGAGCTCTATCTGTT 4800
Db 4741 CCTCAACACCCAGAACATGTATGAGCTGTCTTCAACAAATGACCAAGAGCTCTATCTGTT 4800
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Db 4801 TGATACACCGGCAAGCCTGTGTACACCCAAAGCCTGCCACAGGAGACTACCTGTACAA 4860
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Db 5461 CTTGGTGGAGTGGCGCCAGCGCAAAAGAGAGGTTCGGGGCCAGGTCACTGTCTTTGGCG 5520
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Db 5701 TGGGGGTTACATTTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCA 5760

| | | | | |
|----|------|--|------|--|
| Qy | 5761 | GGCGGCGCATCATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATCTT | 5820 | |
| Db | 5761 | GGCGGCGCATCATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATCTT | 5820 | |
| Qy | 5821 | AGAGAACTCCATGGTGTGCTATACACAGCCAGGAGCATATCTTTGAGTTGACAA | 5880 | |
| Db | 5821 | AGAGAACTCCATGGTGTGCTATACACAGCCAGGAGCATATCTTTGAGTTGACAA | 5880 | |
| Qy | 5881 | GAATGACCGGCTCTCTCTGTGAGATGCCAAGCTGCGCGGCGAGACATAGAGACAT | 5940 | |
| Db | 5881 | GAATGACCGGCTCTCTCTGTGAGATGCCAAGCTGCGCGGCGAGACATAGAGACAT | 5940 | |
| Qy | 5941 | CCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCGCTGAGGGCAATGCCTCAGTCAT | 6000 | |
| Db | 5941 | CCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCGCTGAGGGCAATGCCTCAGTCAT | 6000 | |
| Qy | 6001 | ACAGGACTTCACTGAGGATGGCAACCTCTCTTCAACCTTCTACCTGGGCACTGGCCGAG | 6060 | |
| Db | 6001 | ACAGGACTTCACTGAGGATGGCAACCTCTCTTCAACCTTCTACCTGGGCACTGGCCGAG | 6060 | |
| Qy | 6061 | GGTGATATCAAGTATGGCAACTGTCAAGCTGGCAGACGCTCTATGACACCACAA | 6120 | |
| Db | 6061 | GGTGATATCAAGTATGGCAACTGTCAAGCTGGCAGACGCTCTATGACACCACAA | 6120 | |
| Qy | 6121 | GGTCAGTTTCACTTACAGGACGGCAGGATGCTGAAGACCATCAACCTACAGAAATGA | 6180 | |
| Db | 6121 | GGTCAGTTTCACTTACAGGACGGCAGGATGCTGAAGACCATCAACCTACAGAAATGA | 6180 | |
| Qy | 6181 | GGGCTTCACTGCAACCTTCCGCTACCGTCAAGATTTGGGCCCCCTGATCAACGACAGATCTT | 6240 | |
| Db | 6181 | GGGCTTCACTGCAACCTTCCGCTACCGTCAAGATTTGGGCCCCCTGATCAACGACAGATCTT | 6240 | |
| Qy | 6241 | CCGCTTCACTGAGGAAGGCAATGCTCAAGCCCGCTTTTGACTACAACTATGACAAACGCTT | 6300 | |
| Db | 6241 | CCGCTTCACTGAGGAAGGCAATGCTCAAGCCCGCTTTTGACTACAACTATGACAAACGCTT | 6300 | |
| Qy | 6301 | CCGGTGACAGCATGAGGCTGTGATCAAGACGCCCATCTGCCATTTGATCTCTATCG | 6360 | |
| Db | 6301 | CCGGTGACAGCATGAGGCTGTGATCAAGACGCCCATCTGCCATTTGATCTCTATCG | 6360 | |
| Qy | 6361 | CTATGATGATGTGTGAGCAAGACAGAGCAGTTTGGGAAGTTTGGTGCTATTAATGA | 6420 | |
| Db | 6361 | CTATGATGATGTGTGAGCAAGACAGAGCAGTTTGGGAAGTTTGGTGCTATTAATGA | 6420 | |
| Qy | 6421 | CATTAAACAGATCATACACAGCTGTCTAGACCCACACCAAGCATTTTGATGATATGG | 6480 | |
| Db | 6421 | CATTAAACAGATCATACACAGCTGTCTAGACCCACACCAAGCATTTTGATGATATGG | 6480 | |
| Qy | 6481 | CAGGATGAAGAGTCAAGTATGATCTTCCGCTCGCTCATGTGATGACCGTCCA | 6540 | |
| Db | 6481 | CAGGATGAAGAGTCAAGTATGATCTTCCGCTCGCTCATGTGATGACCGTCCA | 6540 | |
| Qy | 6541 | GTATGATAACTGGGCGGAGTAGTGAAGAGGAGCTGAAGGTAGGACCTACGCGCAATAC | 6600 | |
| Db | 6541 | GTATGATAACTGGGCGGAGTAGTGAAGAGGAGCTGAAGGTAGGACCTACGCGCAATAC | 6600 | |
| Qy | 6601 | CACCTCGCTACTCTATGATGATGTGACGGCCAGCTGACAGACAGTCTCCATCAATGA | 6660 | |
| Db | 6601 | CACCTCGCTACTCTATGATGATGTGACGGCCAGCTGACAGACAGTCTCCATCAATGA | 6660 | |
| Qy | 6661 | CAAGCCACTCTGGGCGCTACAGCTAGACCTCAATGGGAACCTGACATTACTGAGCCCTGG | 6720 | |
| Db | 6661 | CAAGCCACTCTGGGCGCTACAGCTAGACCTCAATGGGAACCTGACATTACTGAGCCCTGG | 6720 | |
| Qy | 6721 | GAAAGTGCAGGGCTCACACCACTACGGTATGACATCCGCGACCGCATCACTCCGGCTGGG | 6780 | |
| Db | 6721 | GAAAGTGCAGGGCTCACACCACTACGGTATGACATCCGCGACCGCATCACTCCGGCTGGG | 6780 | |
| Qy | 6781 | TGACGTGCAATACAGATGGATGGATGGCTTCTGAGGCGAGCGGGCGGTGATATCTT | 6840 | |
| Db | 6781 | TGACGTGCAATACAGATGGATGGATGGCTTCTGAGGCGAGCGGGCGGTGATATCTT | 6840 | |
| Qy | 6841 | TGAGTACAACTCAGTGGCCTGCTCATCAAGGCCCTACACCGGCGTGGCAGCTGGAGTGT | 6900 | |

| | | | | |
|----|------|--|------|--|
| Db | 6841 | TGAGTACAACTCAGTGGCCTGCTCATCAAGGCTTCAACCGGCGTGGCAGCTGGAGTGT | 6900 | |
| Qy | 6901 | CAGGTACCGCTACGATGGCTGGGCGGCGGTCCAGCAAGAGCAGCCACAGCCACCA | 6960 | |
| Db | 6901 | CAGGTACCGCTACGATGGCTGGGCGGCGGTCCAGCAAGAGCAGCCACAGCCACCA | 6960 | |
| Qy | 6961 | CCTGCAAGTTCTTCTATGACAGACCTGACCAACCCACCAAGGTCAACCACTGTACAACCA | 7020 | |
| Db | 6961 | CCTGCAAGTTCTTCTATGACAGACCTGACCAACCCACCAAGGTCAACCACTGTACAACCA | 7020 | |
| Qy | 7021 | CTCAGGCTTGAGATCACTTCCCTCTACTACGATTTGCAAGGACACCTCTTTGGCATGGA | 7080 | |
| Db | 7021 | CTCAGGCTTGAGATCACTTCCCTCTACTACGATTTGCAAGGACACCTCTTTGGCATGGA | 7080 | |
| Qy | 7081 | GCTGACAGTGGTGTGATGATTTTACATAGCTTGTGCAACATCGGACCCCTCTTGTCTGT | 7140 | |
| Db | 7081 | GCTGACAGTGGTGTGATGATTTTACATAGCTTGTGCAACATCGGACCCCTCTTGTCTGT | 7140 | |
| Qy | 7141 | CTTTAGTGGAAAGGTTTGTATGATCAAGCAAAATCTGTACACAGCCTATGGGAGATCTA | 7200 | |
| Db | 7141 | CTTTAGTGGAAAGGTTTGTATGATCAAGCAAAATCTGTACACAGCCTATGGGAGATCTA | 7200 | |
| Qy | 7201 | CATGGATAACAAACCCCAACTTTTCCAGATCATATAGGCTACCATGGTGGCCTCTATGATCC | 7260 | |
| Db | 7201 | CATGGATAACAAACCCCAACTTTTCCAGATCATATAGGCTACCATGGTGGCCTCTATGATCC | 7260 | |
| Qy | 7261 | ACTCAACAGCTTGTCCACATGGCGCGGAGATTTATGATGCTGGCCCGGACGCTGGAC | 7320 | |
| Db | 7261 | ACTCAACAGCTTGTCCACATGGCGCGGAGATTTATGATGCTGGCCCGGACGCTGGAC | 7320 | |
| Qy | 7321 | TAGCCACAGACACGAGCTGTGGAAGACACCTTTAGTAGCAGCAAGCTCATGCTTTTAAATCT | 7380 | |
| Db | 7321 | TAGCCACAGACACGAGCTGTGGAAGACACCTTTAGTAGCAGCAAGCTCATGCTTTTAAATCT | 7380 | |
| Qy | 7381 | CTATATGTTTCAAAAAACAAACCCCATCAGCAATCTCCAGGACATCAAGTGTTCATGAC | 7440 | |
| Db | 7381 | CTATATGTTTCAAAAAACAAACCCCATCAGCAATCTCCAGGACATCAAGTGTTCATGAC | 7440 | |
| Qy | 7441 | AGATGTTTAAAGCTGGCTGCTCACTTTGATTTCCAGTACACCACTGATCCCTGGTTA | 7500 | |
| Db | 7441 | AGATGTTTAAAGCTGGCTGCTCACTTTGATTTCCAGTACACCACTGATCCCTGGTTA | 7500 | |
| Qy | 7501 | TCCCAACACAGACATGATGCCATGGAAACCTCTCTACAGCTCATCCACACACAGATGAA | 7560 | |
| Db | 7501 | TCCCAACACAGACATGATGCCATGGAAACCTCTCTACAGCTCATCCACACACAGATGAA | 7560 | |
| Qy | 7561 | AACGCGAGGTGGGACAAACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTACAGAAGCA | 7620 | |
| Db | 7561 | AACGCGAGGTGGGACAAACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTACAGAAGCA | 7620 | |
| Qy | 7621 | GCTCAAGGCTTTTGTCACTTTAGAAACCGTTTGACAGCTCTATGGCTCCCAATCACCAG | 7680 | |
| Db | 7621 | GCTCAAGGCTTTTGTCACTTTAGAAACCGTTTGACAGCTCTATGGCTCCCAATCACCAG | 7680 | |
| Qy | 7681 | CTGCCAGCGCTCCAAAGACCAAGAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG | 7740 | |
| Db | 7681 | CTGCCAGCGCTCCAAAGACCAAGAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG | 7740 | |
| Qy | 7741 | GGTCAAGTTTTCCTTGAAGGATGGCCGAGTGAACCAAGACATCATAGTGTGGCCAAATGA | 7800 | |
| Db | 7741 | GGTCAAGTTTTCCTTGAAGGATGGCCGAGTGAACCAAGACATCATAGTGTGGCCAAATGA | 7800 | |
| Qy | 7801 | GGATGGCGAAGGGTGTCTGCCATCTTTGAACCATATGACCACTA CTAAGAGAACCTTGACATT | 7860 | |
| Db | 7801 | GGATGGCGAAGGGTGTCTGCCATCTTTGAACCATATGACCACTA CTAAGAGAACCTTGACATT | 7860 | |
| Qy | 7861 | CACCATTTGATGGGTGATACCCATTTACTTTGTGAACACAGGACCTTTCAGAGGTGACCT | 7920 | |
| Db | 7861 | CACCATTTGATGGGTGATACCCATTTACTTTGTGAACACAGGACCTTTCAGAGGTGACCT | 7920 | |
| Qy | 7921 | GGCCATCTCTGGGCTCAGTGGGGGCGGCAACCTCGGAGAAATGGGGTCAACGTCACCTGT | 7980 | |

Db 7921 GGCCATCTCGGCTCAGTGGGGGGCGGAACCTCGAGAAATGGGTCAACGTCACCTGT 7980
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Qy 8041 GTACGGGCACTGCTTGAACACACGCTACGGGCAACGTTGGATGAGGAGAGGCACG 8100
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Qy 8101 GGTCTGAGCTGGCGCGGAGAGAGCGTGGCCCAAGCGTGGGCGCCCGCAGCAGCAGAG 8160
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Qy 8161 ACTCGGGAAGGGAGGAGGCTCGCGGCTTGACAGAGGGGGGAGAGAGCAGAGGTGCT 8220
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Qy 8221 GAGCACAGGGGGTGGCAAGCTACGACGGCTTTTTCGTGATCTCTGTCGAGCAGTACCC 8280
Db 8221 GAGCACAGGGGGTGGCAAGCTACGACGGCTTTTTCGTGATCTCTGTCGAGCAGTACCC 8280
Qy 8281 AGAAGCTGTCAGACAGCGCAACACATCCACTTCATGAGACAGAGCAGATGGGCGCGAG 8340
Db 8281 AGAAGCTGTCAGACAGCGCAACACATCCACTTCATGAGACAGAGCAGATGGGCGCGAG 8340
Qy 8341 GTGACAGAGAGGAC 8354
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RESULT 2

ID ADF74829
ID ADF74829 standard; cDNA; 8354 BP.

AC ADF74829;

DT 26-FEB-2004 (first entry)

DE Murine NOVX cDNA to treat human pathological conditions (SeqID 43).

KW gene; ss; mouse; murine; NOVX; metabolic disorder; diabetes; anorexia;
cancer; cardiovascular; infectious; neurodegenerative; immune;
haematopoietic disease; dyslipidaemia; anorectic; virucide; nontropic;
antiinflammatory; neuroprotective; antilipaemic; anabolic; cardiant;
neurogenesis; wound healing; angiogenesis; chromosome mapping;
tissue typing; preventive medicine; pharmacogenomic;
single nucleotide polymorphism; SNP.

OS Mus musculus.

| | |
|-----------|--|
| Key | Location/Qualifiers |
| variation | replace(536,a) |
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| | /tag= d |
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| | replace(4687,t) |
| | /tag= e |
| variation | /standard_name= "Single nucleotide polymorphism" |
| | replace(6909,c) |
| | /tag= f |
| variation | /standard_name= "Single nucleotide polymorphism" |

WO2003076578-A2.

XX

PD 18-SEP-2003.
XX 06-MAR-2003; 2003WO-US006794.
FF 06-MAR-2002; 2002US-0361974P.
XX 08-MAR-2002; 2002US-00093463.
PR 08-MAR-2002; 2002WO-US007288.
PR 15-MAR-2002; 2002US-0365034P.
PR 19-MAR-2002; 2002US-0365477P.
PR 20-MAR-2002; 2002US-0365884P.
PR 20-MAR-2002; 2002US-0365984P.
PR 20-MAR-2002; 2002US-0365985P.
PR 22-MAR-2002; 2002US-0366928P.
PR 12-APR-2002; 2002US-0372018P.
PR 12-APR-2002; 2002US-0372022P.
PR 23-APR-2002; 2002US-0374682P.
PR 12-JUN-2002; 2002US-0388096P.
PR 14-JUN-2002; 2002US-0389143P.
PR 26-JUN-2002; 2002US-0391779P.
PR 15-AUG-2002; 2002US-0403743P.
PR 13-SEP-2002; 2002US-0410755P.
PR 23-SEP-2002; 2002US-0412957P.
PR 22-OCT-2002; 2002US-0420382P.
PR 05-MAR-2003; 2003US-00420382.
XX (CURA-) CURAGEN CORP.

XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chaudhuri A;
PI Colman SD, Edinger SR, Ettenberg S, Gangolli EA, Gerlach VL;
PI Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malyanar UM;
PI Mezes PS, Miller CE, Millet I, Padigar M, Patturajan M, Peyman J;
PI Qian X, Rastelli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;
PI Sukumaran S, Vernet CM, Voas EZ, Zhong M;
XX WPI; 2003-697890/66.
DR P-PSDB; ADF74830.

XX New isolated NOVX polypeptides and polynucleotides, useful for
preventing, diagnosing or treating NOVX-associated disorders, e.g.
osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
asthma, or infections.

Claim 20; SEQ ID NO 43; 282pp; English.

XX This invention relates to a novel nucleic acid, and encoded polypeptides
thereof, which have properties related to the stimulation of biochemical
or physiological responses in a cell, tissue, organ or organism.
Specifically, it refers to the use of biologically active fragments for
diagnostic and prognostic assays and furthermore in the treatment of
diverse pathological conditions. The present invention describes novel
human and murine NOVX proteins, as well as methods to modulate their
expression using antisense oligos, ribozymes and peptide nucleic acids.
The polypeptides, nucleic acid molecules and antibodies are useful in the
manufacture of a medicament for treating metabolic disorders, diabetes,
anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune
and haematopoietic diseases as well as various dyslipidaemias.
Accordingly, these molecules have many activities including anorectic,
virucide, nontropic, antiinflammatory, neuroprotective, antilipaemic,
anabolic and cardiant. Furthermore, they are useful in screening assays
to identify small molecules that modulate or inhibit, for example,
neurogenesis, wound healing and angiogenesis. The nucleic acids are also
used as in chromosome mapping, tissue typing, preventive medicine and
pharmacogenomics. This polynucleotide is a murine NOVX cDNA of the
invention.

SQ Sequence 8354 BP; 1968 A; 2437 C; 2271 G; 1678 T; 0 U; 0 Other;

Query Match 100.0%; Score 8354; DB 10; Length 8354;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTTGTGGATGTGGAGGAGCGCGCGGAGGCCATGAGCGTGAAGAGAGGAAGCCTTAA 60
QY
61 CGCCTGCCTGACCCGCGCGCGAGCCGCGCTACACAGCTCGTCCGCGACAG 120
Db
61 CGCCTGCCTGACCCGCGCGCGAGCCGCGCTACACAGCTCGTCCGCGACAG 120
QY
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Db
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Db
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Db
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901 TGGAGGACCTCCCGCTCTTTCTGCACACATCACAGGGTACCCTAGACGTCCAGCAC 960
QY
961 AGTGTACTCTCTCCCGCCGACCCCTGCCCCGAGCACTTTCGCCCGCGCGCTTTTAA 1020
Db
961 AGTGTACTCTCTCCCGCCGACCCCTGCCCCGAGCACTTTCGCCCGCGCGCTTTTAA 1020
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QY
1201 TTGGCCTGTGGCCAAACCGAGCTCTCCTATATACCCCTCAGGGGGCACTGGCTTAGAGACCCC 1260
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1261 TCACAGGAAAGGCAAGGAACACACAGAGGAAGCCAGTAGTTTCTTTTCCAGAGACACAG 1320
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1321 TTTTCATAGATTTCTGGAGAAATTTGATGTGGAAAGGGAGCCTCCAGAAATTTCTCTCTGG 1380
Db
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1381 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTGTGTCATCTGAAATTTCAATGTTC 1440
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1381 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTGTGTCATCTGAAATTTCAATGTTC 1440
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1501 ACAGTTTGTACTTTGTGGAGCTCTGATGGCAGAGGCTCTTAAACCCAGAGGCGGGAG 1560
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1621 CTTTCATCCAGTATTTGGATTTCAGGATCTGGCACTTGGCTTTTAAATGACGGGAAGGA 1680
Db
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| | | | |
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| QY | 2221 | TGCTGCGCAGCTGTGTGGCCATGGCTGTGCTAGGGGGCACCTGCGCTCGGAGGATGG | 2280 |
| Db | 2221 | | 2280 |
| QY | 2281 | TGCTGCCACCTGTGTGTGCCATGGCGTGTGCTAGGGGGCACCTGCCCTCGGAGGATGG | 2340 |
| Db | 2281 | | 2340 |
| QY | 2341 | CTGATGAGGGGCGAGCTCGCGACCGAGCGGCGCTGCCACCCGCGCTGTGCGGAGCATGGGAC | 2400 |
| Db | 2341 | | 2400 |
| QY | 2401 | TCACCTATCTGGATAGGGTAGTTAAAGAGGGTTGCCCTGCGGTGTGCAATGCAACCGGCGAG | 2460 |
| Db | 2401 | | 2460 |
| QY | 2461 | ATGTACCTTAGACCTTGAATGGTTGGCACTGTGCGTCTGCCAGCTGGGCTGGAGAGGCTGG | 2520 |
| Db | 2461 | | 2520 |
| QY | 2521 | CTGTGACACTTCCATGGAGACTGCCCTGCGGTGACAGCAACATGATGGAGATGGCCT | 2580 |
| Db | 2521 | | 2580 |
| QY | 2581 | GGTGACTGCAATGGACCTGACTGCTGCTCCAGCCCTGTGCCATATCAACCCGCTGTG | 2640 |
| Db | 2581 | | 2640 |
| QY | 2641 | CTTGGCTCCCTTAAACCTCTGGACATCATCCAGGAGACACAGTCCCTGTGTCAACGCA | 2700 |
| Db | 2641 | | 2700 |
| QY | 2701 | GAACTACACTCTTATATGACCGCATCAAGTTCCTGTGGCGGAGGACAGGACGACAT | 2760 |
| Db | 2701 | | 2760 |
| QY | 2761 | AATCCCCGGGAGAACCCCTTTGATGGAGGGCATCTTGTGTATTCGTGGCCAAAGTGTAT | 2820 |
| Db | 2761 | | 2820 |
| QY | 2821 | GACATCAGATGGAAACCCCTCGTTGGTGTGAACATCAAGTTTGTCAATAACCCCTCTCTT | 2880 |
| Db | 2821 | | 2880 |
| QY | 2881 | TGGATATACAAATCAGCAGGCAAGATGGCAGCTTTGACTTGTGTGACAAATGGCGGATCTC | 2940 |
| Db | 2881 | | 2940 |
| QY | 2941 | CATCATCTCGCGTTTCGAGCGGGCACCTTTTCATCACAGGAGCACACCTGTGGCTGCC | 3000 |
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| QY | 3001 | ATGGGATCGCTTTTGTATGGAAACCAATCATATGACATGAGGAGAAATGAGATTCC | 3060 |
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| QY | 3121 | GTCTTTGGCGAGCTCTGTGACAGAAAGGGCCCAATTTGCGGGAATTCAGGCTTTGCA | 3180 |
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| QY | 3181 | GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGTGGCTACCTGAGCAGCGGACCC | 3240 |
| Db | 3181 | | 3240 |
| QY | 3241 | TGGCTACAAATCTGCTTGGATCAGCTTCAACCCAGCCATCCCTTCAACCTCAT | 3300 |
| Db | 3241 | | 3300 |
| QY | 3301 | GAAAGTGCACTCATGGTAGCGGTGGAGGGCGGCCTCTTTCAGGAAATGGTTCGCTGCAGC | 3360 |
| Db | 3301 | | 3360 |

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| Db | 3361 | GAAAGTGCACTCATGTAGCGTGGAGGGCGGCCTCTTCAGGAATGGTTCGCTGCAGC | 3420 |
| QY | 3361 | | 3420 |
| Db | 3361 | CCAGACCTGCTCTATTTATTTTGGGACAGACAGAGCTCTACAAACAGAAAGTGT | 3420 |
| QY | 3421 | | 3420 |
| Db | 3421 | TGGCTTTCAAGAACCTTTGTTCCGTTGGGTATGAATATGAATCTCTGCCAGATCTAAT | 3480 |
| QY | 3421 | | 3480 |
| Db | 3481 | CTGTGGGAAAAAAGAACCAACAGTCTGACAGGCTATGAAATTTGACGCGTCCAAGCTTGG | 3540 |
| QY | 3481 | | 3540 |
| Db | 3541 | AGGATGGAGCCTAGACAAACATCATGCCCTCAACATTTCAAAGTGGTATCTCTGCACAAAGG | 3600 |
| QY | 3541 | | 3600 |
| Db | 3601 | GAAATGGGGAGAACAGTTCCTGCTCAGACGCTCTCTGTCAATTTGGGAGCATCATGGGCAA | 3660 |
| QY | 3601 | | 3660 |
| Db | 3661 | TGGCGCGGAGAGCATCTCTGCCCGACGCTGCAACGGCTTGTGACGGCAACAAGCT | 3720 |
| QY | 3661 | | 3720 |
| Db | 3721 | CCTGGCCCCAGTGGCCTCACCTGTGGCTCTGACGGGAGCTCTATGTGGGTGATTTCAA | 3780 |
| QY | 3721 | | 3780 |
| Db | 3781 | CTACATTTAGAAAGGATCTTCCCTCTCGAAATGTCAACCAATCTCTAGAGCTGAGGAATAA | 3840 |
| QY | 3781 | | 3840 |
| Db | 3841 | AGATTTCAGACATAGTCACAGTCAGCACAAATACTACTCTGCGCCACAGACCCCATGAG | 3900 |
| QY | 3841 | | 3900 |
| Db | 3901 | TGGGGCGCTCTTCCCTTCTGACAGCAACAGCGCGGGTCTTTAAATCAAAGTCCACTGT | 3960 |
| QY | 3901 | | 3960 |
| Db | 3961 | GTTGGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTCGCGGGACAGGTGACCATGCT | 4020 |
| QY | 3961 | | 4020 |
| Db | 4021 | CCCCCTTTGATGACACTCGCTGCGGGGATGGTGGGAAAGCCACAGAGCCACACTCACCAA | 4080 |
| QY | 4021 | | 4080 |
| Db | 4081 | TCCCAGGGGTATTTACAGTGGACAAGTTTGGGCTCATCTACTTCGTGGATGGCAACATGAT | 4140 |
| QY | 4081 | | 4140 |
| Db | 4141 | TCCCAGGGGTATTTACAGTGGACAAGTTTGGGCTCATCTACTTCGTGGATGGCAACATGAT | 4200 |
| QY | 4141 | | 4200 |
| Db | 4201 | AGCCCGGCACTCAGCTGTGATTTCTGTCATGGATATTTCCAGGTGAGACTGGAGTGCC | 4260 |
| QY | 4201 | | 4260 |
| Db | 4261 | AGCCCGGCACTCAGCTGTGATTTCTGTCATGGATATTTCCAGGTGAGACTGGAGTGCC | 4320 |
| QY | 4261 | | 4320 |
| Db | 4321 | CCTGAAATCTCTGAAACCAACAGGTGCGCATTTGTGCGCGGGAGGCCATTCACATGCCA | 4380 |
| QY | 4321 | | 4380 |
| Db | 4381 | GTTCCCTGGGATTTGACCACTTCTGCTTAAGCAAGGTGGCCATCCACGCAACCTTGGAGTC | 4440 |
| QY | 4381 | | 4440 |

| | | | | | | | | | |
|---|---|------|---|------|---|---|------|--|------|
| D | b | 4381 | GGTCCCTGGCATTGACCACTTCCTGTAAGCAAGGTGGCCATCCACGCAACCCCTGGAGTC | 4440 | Q | y | 5521 | COGGCTGCGGGTGCAAAACCGAAATCTCCTATCTCTGGACTTTTGATCGGTAACACGCAC | 5580 |
| Q | y | 4441 | AGCCACCGCTTTGGCTGTTTACACAATGGGTCCTGTATATTGCTGAGACTCATGAGAA | 4500 | D | b | 5521 | COGGCTGCGGGTGCAAAACCGAAATCTCCTATCTCTGGACTTTTGATCGGTAACACGCAC | 5580 |
| D | b | 4441 | AGCCACCGCTTTGGCTGTTTACACAATGGGTCCTGTATATTGCTGAGACTCATGAGAA | 4500 | Q | y | 5581 | AGAGAAAGATCTATGATGACCAACCGCAAGTTCACCCCTTCGGATTCGTGTACGACCAAGGGGG | 5640 |
| Q | y | 4501 | AAAGATCAACCGCATCAGGAGGTCACCACTAGTGGAGAGATCTCACTCGTTCCTGGGC | 4560 | D | b | 5581 | AGAGAAAGATCTATGATGACCAACCGCAAGTTCACCCCTTCGGATTCGTGTACGACCAAGGGGG | 5640 |
| D | b | 4501 | AAAGATCAACCGCATCAGGAGGTCACCACTAGTGGAGAGATCTCACTCGTTCCTGGGC | 4560 | Q | y | 5641 | GGGGCCACGCTCTGTGTACCCAGCAGCAGGCTGAAATGTTGTCAAAGTGTACATCTCCCC | 5700 |
| Q | y | 4561 | CCCAGTGGCTGTGACTGTAAATATGATGCAACTGTGATGTTTCTCGAGACGATGG | 4620 | D | b | 5641 | GGGGCCACGCTCTGTGTACCCAGCAGCAGGCTGAAATGTTGTCAAAGTGTACATCTCCCC | 5700 |
| D | b | 4561 | CCCAGTGGCTGTGACTGTAAATATGATGCAACTGTGATGTTTCTCGAGACGATGG | 4620 | Q | y | 5701 | TGGGGGTTACATTTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCA | 5760 |
| Q | y | 4621 | TTATGCCAAGATGCAAGTAAATATGATGCAACTGTGATGTTTCTCGAGACGATGG | 4680 | D | b | 5701 | TGGGGGTTACATTTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCA | 5760 |
| D | b | 4621 | TTATGCCAAGATGCAAGTAAATATGATGCAACTGTGATGTTTCTCGAGACGATGG | 4680 | Q | y | 5761 | GGGGCCCGGATCACAATCCAGGATCTTCGTGATGGAAGACATGTAGAGCTTACATATCTT | 5820 |
| Q | y | 4681 | GCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACCAAGCCCTT | 4740 | D | b | 5761 | GGGGCCCGGATCACAATCCAGGATCTTCGTGATGGAAGACATGTAGAGCTTACATATCTT | 5820 |
| D | b | 4681 | GCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACCAAGCCCTT | 4740 | Q | y | 5821 | AGAGAAAGTCCATGGTGTCTACTACAGCCAGAGGCGAGTATCTTTTGAGTTCGACAA | 5880 |
| Q | y | 4741 | CCTCAACACCCAGAACATGATGATGATGCTGTCTTACCAATTTGACAGAGCTCTATCTGTT | 4800 | D | b | 5821 | AGAGAAAGTCCATGGTGTCTACTACAGCCAGAGGCGAGTATCTTTTGAGTTCGACAA | 5880 |
| D | b | 4741 | CCTCAACACCCAGAACATGATGATGATGCTGTCTTACCAATTTGACAGAGCTCTATCTGTT | 4800 | Q | y | 5881 | GAATGACCGCCTCTCTTCTGTGACGATGCCCACGTTGGCGCGCAGACATCTAGAGACCAT | 5940 |
| Q | y | 4801 | TGATACACCGGCAAGCCTGTACACCAAGCCTGCCACAGGAGCTACCTGTACAA | 4860 | D | b | 5881 | GAATGACCGCCTCTCTTCTGTGACGATGCCCACGTTGGCGCGCAGACATCTAGAGACCAT | 5940 |
| D | b | 4801 | TGATACACCGGCAAGCCTGTACACCAAGCCTGCCACAGGAGCTACCTGTACAA | 4860 | Q | y | 5941 | COGCTCAGTGGGCTACTACAGAAACATCTATACGCCCTGTAGGGGNAATGCCTCAGTCAT | 6000 |
| Q | y | 4861 | CTTCACCTACACTGGGCGCGGACATCACACTCATCACAGACAACAAATGGCAACATGGT | 4920 | D | b | 5941 | COGCTCAGTGGGCTACTACAGAAACATCTATACGCCCTGTAGGGGNAATGCCTCAGTCAT | 6000 |
| D | b | 4861 | CTTCACCTACACTGGGCGCGGACATCACACTCATCACAGACAACAAATGGCAACATGGT | 4920 | Q | y | 6001 | ACAGGACTTCACTGAGATGGGCACCTCTTACACCTTCTACCTCTGCGGCACCTGCGCCGAG | 6060 |
| Q | y | 4921 | AAATGTCGCGGAGACTCTACTGGGATGCCCCCTCTGCTGGTGGTCCAGATGGCCAGGT | 4980 | D | b | 6001 | ACAGGACTTCACTGAGATGGGCACCTCTTACACCTTCTACCTCTGCGGCACCTGCGCCGAG | 6060 |
| D | b | 4921 | AAATGTCGCGGAGACTCTACTGGGATGCCCCCTCTGCTGGTGGTCCAGATGGCCAGGT | 4980 | Q | y | 6061 | GGTGATATACAAATATGCGCAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACAA | 6120 |
| Q | y | 4981 | GTACTGGGTGACCATGGGCAACCAAGTGCATCAAGAGTGTGACCAACAGGACACGA | 5040 | D | b | 6061 | GGTGATATACAAATATGCGCAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACAA | 6120 |
| D | b | 4981 | GTACTGGGTGACCATGGGCAACCAAGTGCATCAAGAGTGTGACCAACAGGACACGA | 5040 | Q | y | 6121 | GGTCAGTTTCACTATGACGAGACGGCAGCATGTCTGAAAGACCATCAACCTACAGAAATGA | 6180 |
| Q | y | 5041 | GTTGGCCATGATGATACATACCATGCAATTCGGGCTTCTGGCAACCAAAAGCAATGAAAA | 5100 | D | b | 6121 | GGTCAGTTTCACTATGACGAGACGGCAGCATGTCTGAAAGACCATCAACCTACAGAAATGA | 6180 |
| D | b | 5041 | GTTGGCCATGATGATACATACCATGCAATTCGGGCTTCTGGCAACCAAAAGCAATGAAAA | 5100 | Q | y | 6181 | GGGCTTCACTGACCATCCGCTACCGTACAGATTTGGCCCTCTGATGACCGACAGATCTT | 6240 |
| Q | y | 5101 | CGGATGGACAAATTTTATGATGACGACAGCTTTGGCCGCTGACAAATGTGACCTTCCC | 5160 | D | b | 6181 | GGGCTTCACTGACCATCCGCTACCGTACAGATTTGGCCCTCTGATGACCGACAGATCTT | 6240 |
| D | b | 5101 | CGGATGGACAAATTTTATGATGACGACAGCTTTGGCCGCTGACAAATGTGACCTTCCC | 5160 | Q | y | 6241 | CCGCTTCACTGAGGAAGGATGGTCAACGCCCTTTTGACTACAACTATGACCAACAGCTT | 6300 |
| Q | y | 5161 | TACTGGCCAGGTGAGCAGTTTCCGAAGTATACAGACAGTTTCAGTGCATGTCCAGGTAGA | 5220 | D | b | 6241 | CCGCTTCACTGAGGAAGGATGGTCAACGCCCTTTTGACTACAACTATGACCAACAGCTT | 6300 |
| D | b | 5161 | TACTGGCCAGGTGAGCAGTTTCCGAAGTATACAGACAGTTTCAGTGCATGTCCAGGTAGA | 5220 | Q | y | 6301 | COGGGTGACCCAGCATCAGGCTGTGATCAACAGAGACCCCACTGCCCATTTGATCTTATCG | 6360 |
| Q | y | 5221 | GACCTCAGCAAGGATGATGTACCATACCAACCAACTGTCTGCCCTCAGCGCTTCTTA | 5280 | D | b | 6301 | COGGGTGACCCAGCATCAGGCTGTGATCAACAGAGACCCCACTGCCCATTTGATCTTATCG | 6360 |
| D | b | 5221 | GACCTCAGCAAGGATGATGTACCATACCAACCAACTGTCTGCCCTCAGCGCTTCTTA | 5280 | Q | y | 6361 | CTATGATGATGTCTCAGGCAAGACAGACGATTTGGGAAGTTTGGTGTCAATTACTATGA | 6420 |
| Q | y | 5281 | CACACTGCTGCAAGACCAAGTCCGGAAACAGCTACTACATCGGGCCGATGGCTCTTTGGG | 5340 | D | b | 6361 | CTATGATGATGTCTCAGGCAAGACAGACGATTTGGGAAGTTTGGTGTCAATTACTATGA | 6420 |
| D | b | 5281 | CACACTGCTGCAAGACCAAGTCCGGAAACAGCTACTACATCGGGCCGATGGCTCTTTGGG | 5340 | Q | y | 6421 | CATTAAACAGATCATCACACAGCTGTCTATGACCCACACCAAGCATTTTGTGATGATATGG | 6480 |
| Q | y | 5341 | GCTGCTGTGCGCAACCGCATGGAGGTGGCGCTGCAGACTGAGGCCCACTTGTGGCTGG | 5400 | D | b | 6421 | CATTAAACAGATCATCACACAGCTGTCTATGACCCACACCAAGCATTTTGTGATGATATGG | 6480 |
| D | b | 5341 | GCTGCTGTGCGCAACCGCATGGAGGTGGCGCTGCAGACTGAGGCCCACTTGTGGCTGG | 5400 | Q | y | 6481 | CAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGTGATGACCGTCCA | 6540 |
| Q | y | 5401 | CACCGTCAACCCACCGTGGCAAGAGGAATGTCAAGCTGCCCATCGACCAACGCGCTCAA | 5460 | D | b | 6481 | CAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGTGATGACCGTCCA | 6540 |
| D | b | 5401 | CACCGTCAACCCACCGTGGCAAGAGGAATGTCAAGCTGCCCATCGACCAACGCGCTCAA | 5460 | Q | y | 6541 | GTATGATTAACATGGGGGAGTGTGAAAGAGGAGCTGAAAGGTAGGACCTTACGCCAATAC | 6600 |
| Q | y | 5461 | CCTGGTGGAGTGGCGGACGCAAGAGAGGCTCGGGGCCAGGCTCACTGTCTTTTGGGCG | 5520 | D | b | 6541 | GTATGATTAACATGGGGGAGTGTGAAAGAGGAGCTGAAAGGTAGGACCTTACGCCAATAC | 6600 |
| D | b | 5461 | CCTGGTGGAGTGGCGGACGCAAGAGAGGCTCGGGGCCAGGCTCACTGTCTTTTGGGCG | 5520 | | | | | |

QY 6601 CACTCGCTACTCCTATGAGTATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA 6660
DB 6601 CACTCGCTACTCCTATGAGTATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA 6660
QY 6661 CAAGCCACTCTGGCGCTACAGCTACGACTCACTCAATGGGAACCTGCACTTACTTGAGCCCTGG 6720
DB 6661 CAAGCCACTCTGGCGCTACAGCTACGACTCACTCAATGGGAACCTGCACTTACTTGAGCCCTGG 6720
QY 6721 GAACAGTGCACGGCTCACACCACTACGATATGACATCCGCGACCGCATCACTCGGCTGGG 6780
DB 6721 GAACAGTGCACGGCTCACACCACTACGATATGACATCCGCGACCGCATCACTCGGCTGGG 6780
QY 6781 TGACGTGCAATACAGATGAGTATGAGTGGCTTCTGAGGAGCGGGCGGTGATATCTT 6840
DB 6781 TGACGTGCAATACAGATGAGTATGAGTGGCTTCTGAGGAGCGGGCGGTGATATCTT 6840
QY 6841 TGAGTACAACTCAGCTGGCTGCTCATCAAGGCTTACAACCGGGCTGGCAGCTGAGTGT 6900
DB 6841 TGAGTACAACTCAGCTGGCTGCTCATCAAGGCTTACAACCGGGCTGGCAGCTGAGTGT 6900
QY 6901 CAGGTACCGCTACGATGGCTGGGGCGGCGGTGTCAGAGAGAGACGCCACAGCCACCA 6960
DB 6901 CAGGTACCGCTACGATGGCTGGGGCGGCGGTGTCAGAGAGAGACGCCACAGCCACCA 6960
QY 6961 CCTGCAGTTCTTCTATGACAGCTGACCAACCCCAACCAAGTTCACCCACCTGTACAACCA 7020
DB 6961 CCTGCAGTTCTTCTATGACAGCTGACCAACCCCAACCAAGTTCACCCACCTGTACAACCA 7020
QY 7021 CTCCAGCTCTGAGATCACTCCCTCTACTACGACTTGAAGGACACCTCTTTGGCATGGA 7080
DB 7021 CTCCAGCTCTGAGATCACTCCCTCTACTACGACTTGAAGGACACCTCTTTGGCATGGA 7080
QY 7081 GCTGAGAGTGTGATGATGATTTTATAGCTTGTGACAACTATCGGAGATCTA 7140
DB 7081 GCTGAGAGTGTGATGATGATTTTATAGCTTGTGACAACTATCGGAGATCTA 7140
QY 7141 CTTTATGTGAAACAGTTTATGATATCAAGCAATCTGTACAGCTTATGGGAGATCTA 7200
DB 7141 CTTTATGTGAAACAGTTTATGATATCAAGCAATCTGTACAGCTTATGGGAGATCTA 7200
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DB 7201 CATGGATACCAACCCCAACTTTTTCAGATCATATAGGCTACCAATGGTGGCTCTATGATCC 7260
QY 7261 ACTCAGCAAGCTGTGTCATATGAGCGGGGAGATTTATGATGTGTCGGCGGAGCGTGGAC 7320
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DB 7321 TAGCCAGACACGAGCTGTGGAAGCACCCTTAGTAGCAGCAACGTCATGCGCTTTTAAATCT 7380
QY 7381 CTATATGTTTCAAAAAACAACCCCATCAGCAACTCCCAGGACATCAAGTGTCTTATGAC 7440
DB 7381 CTATATGTTTCAAAAAACAACCCCATCAGCAACTCCCAGGACATCAAGTGTCTTATGAC 7440
QY 7441 AGATGTTTAAACAGTGGCTGCTCACCTTTGGATTCCAGCTTACACAGCTGATCCCTGGTTA 7500
DB 7441 AGATGTTTAAACAGTGGCTGCTCACCTTTGGATTCCAGCTTACACAGCTGATCCCTGGTTA 7500
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DB 7501 TCCCAAAACAGACATGGATGTCATGGAACCTCTTACGAGCTTATCCACACACAGATGAA 7560
QY 7561 AACGCAAGGAGTGGGACAAACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTACAGAGCA 7620
DB 7561 AACGCAAGGAGTGGGACAAACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTACAGAGCA 7620
QY 7621 GCTCAAGGCTTTGTTCACCTTACAGGTTTACAGCAGCTTATGCTCCACCAATCACCAG 7680
DB 7621 GCTCAAGGCTTTGTTCACCTTACAGGTTTACAGCAGCTTATGCTCCACCAATCACCAG 7680
QY 7681 CTGCCAGAGGCTTCCAAAGACCAAGAAAGTTTGCATCCAGCGGCTCAGTCTTTTGGCAAGGG 7740

DB 7681 CTGCCAGAGGCTTCCAAAGACCAAGAAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG 7740
QY 7741 GGTCAAGTTTTCCTTTGAGAGTGGCCGAGTGACCAAGACATCATCAGTGTGGCCAAATGA 7800
DB 7741 GGTCAAGTTTTCCTTTGAGAGTGGCCGAGTGACCAAGACATCATCAGTGTGGCCAAATGA 7800
QY 7801 GGATGGSCGAAGGTTGCTGCCATCTTGAACCACTGACCCTTACCTAGAGAACCTGCACTT 7860
DB 7801 GGATGGSCGAAGGTTGCTGCCATCTTGAACCACTGACCCTTACCTAGAGAACCTGCACTT 7860
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DB 7861 CACCATTGATGGGTGGATACCCATTATTTTGTGAAACCAAGGACCTTTAGAGGTGACCT 7920
QY 7921 GGCCATCTCGGGCTCAGTGGGGGGGGCGAACCCTGGAGNATGGGGTCAACGTCACCTGT 7980
DB 7921 GGCCATCTCGGGCTCAGTGGGGGGGGCGAACCCTGGAGNATGGGGTCAACGTCACCTGT 7980
QY 7981 GTCCAGATCAACACAGTACTTAAATGGCAGGACTAGACGCTTACACAGACATCCAGTCCA 8040
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QY 8041 GTACGGGGCACTGTGCTTGAACACACGCTACGGGACAACTTTGGATGAGGAGAAAGGCACG 8100
DB 8041 GTACGGGGCACTGTGCTTGAACACACGCTACGGGACAACTTTGGATGAGGAGAAAGGCACG 8100
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QY 8161 ACTCGGGAAGGGAGGAAGGCTTGGCGGCTGTGACAGAGGGGGAAGCAGCAGGTGCT 8220
DB 8161 ACTCGGGAAGGGAGGAAGGCTTGGCGGCTGTGACAGAGGGGGAAGCAGCAGGTGCT 8220
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DB 8221 GAGCACAGGGCGGTGCAAGGCTTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCC 8280
QY 8281 AGAAGTCTGACAGAGCCCAACATCCATTCATGACAGAGCAGATGGGCCCGAG 8340
DB 8281 AGAAGTCTGACAGAGCCCAACATCCATTCATGACAGAGCAGATGGGCCCGAG 8340
QY 8341 GTGACAGAGAGGAC 8354
DB 8341 GTGACAGAGAGGAC 8354
RESULT 3
ABS78652
ID ABS78652 standard; cDNA; 8645 BP.
XX ABS78652;
AC ABS78652;
XX
DT 16-DEC-2002 (first entry)
XX
XX Human cDNA encoding CGDD10, INCYTE 7488573CB1.
DE
XX Human; ss; gene; cell growth; differentiation; death; CGDD; cancer;
KW cell proliferative disorder; arteriosclerosis; atherosclerosis;
KW cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis;
KW polycythaemia vera; primary thrombocytopaenia; developmental disorder;
KW renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS;
KW neurological disorder; Alzheimer disease; Parkinson's disease; asthma;
KW reproductive disorder; infertility; autoimmune disorder; gout; allergy;
KW inflammatory disorder; acquired immunodeficiency syndrome; uveitis;
KW autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection;
KW diabetes mellitus; glomerulonephritis; irritable bowel syndrome;
KW multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
rheumatoid arthritis.
XX Homo sapiens.
OS

1261 TGACAGGAAGCAAGGAACACACAGAGGAAGCCAGTAGTTCCTTTCCAGAGGACAG 1320
1331 TGACAGGAAGCAAGGAACACACAGAGGAAGCCAGTAGTTCCTTTCCAGAGGACAG 1390
1321 TTTTCATAGATTCCTGGAGAAATTTGATGTGGGAAGGGAGCCTCCACAGAAAGATTCCTCCTGG 1380
1391 TTTTCATAGATTCCTGGAGAAATTTGATGTGGGAAGGGAGCCTCCACAGAAAGATTCCTCCTGG 1450
1381 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTGTGCATCTGAAATTCAAATGTGTC 1440
1451 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTGTGCATCTGAAATTCAAATGTGTC 1510
1441 TCTGGGAAGGACGCCCTGTTGGCATTTATGSCAGAAAGGCCCTCCCTCTTACATAC 1500
1511 TCTGGGAAGGACGCCCTGTTGGCATTTATGSCAGAAAGGCCCTCCCTCTTACATAC 1570
1501 ACAGTTTGAATTTGTGGAGCTGCTGGATGGCAGAGGCTCTTAACCCAGAGGCGCGGAG 1560
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1621 CTTTCATCCAGTATTTGGATTACAGGAATCTGGCACTTGGCTTTTACAATGACGGAAGGA 1680
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1751 GTCAGAAAGTGTTCCTTTCTCACCACTGCCATGAGTCGGTGGATAACTGCCCCAGCAA 1810
1741 CTGCTATGGCAATGTGACTGCATCTCTGGGAACTGTGCCCTCCCTCGGTTCTCGGG 1800
1811 CTGCTATGGCAATGTGACTGCATCTCTGGGAACTGTGCCCTCCCTCGGTTCTCGGG 1870
1801 CCCCAGCTGTGGCAGAGCTCTGCCCGTGTCTGTAGCGGAATGCCAATACATGAA 1860
1871 CCCCAGCTGTGGCAGAGCTCTGCCCGTGTCTGTAGCGGAATGCCAATACATGAA 1930
1861 AGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGCGCTGAGTCGATGTGCCCAACCA 1920
1931 AGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGCGCTGAGTCGATGTGCCCAACCA 1990
1921 GTGTATCGATGTGGCTCGACCAACCATGGCACTGTGCATCAGGCACTGCATCTGCAA 1980
1991 GTGTATCGATGTGGCTCGACCAACCATGGCACTGTGCATCAGGCACTGCATCTGCAA 2050
1981 CCTGGCTACAGGGCGAGAGCTGTGAGGAAGTGGACTGCAATGGACCCCATGTTCAAG 2040
2051 CCTGGCTACAGGGCGAGAGCTGTGAGGAAGTGGACTGCAATGGACCCCATGTTCAAG 2110
2041 CCGGGGTGTCTCGTGAGAGGCGAAATGCCATTTGTTGTGGATGGGAGGACCAACTG 2100
2111 CCGGGGTGTCTCGTGAGAGGCGAAATGCCATTTGTTGTGGATGGGAGGACCAACTG 2170
2101 CGAGACCCCGAGGCCCATGCTTTAGACCAAGTGTTCAGGCCACGGAACCTTCTCCCGGA 2160
2171 CGAGACCCCGAGGCCCATGCTTTAGACCAAGTGTTCAGGCCACGGAACCTTCTCCCGGA 2230
2161 CACCGGGCTTTGACGCTGTGACCCCAAGCTGGACATGGACACGACTGTTCTATCGAGATCTG 2220
2231 CACCGGGCTTTGACGCTGTGACCCCAAGCTGGACATGGACACGACTGTTCTATCGAGATCTG 2290
2221 TGCTCCGACATGTGTGGCCATGCGGTGTGCGTAGGGGCACTGCGCGCTCGAGGATGG 2280
2291 TGCTCCGACATGTGTGGCCATGCGGTGTGCGTAGGGGCACTGCGCGCTCGAGGATGG 2350
2281 CTGGATGGGGCAGCTCGGACCAAGCGGCTGCCACCCGCGCTGTGCCGAGCATGGAC 2340
2351 CTGGATGGGGCAGCTCGGACCAAGCGGCTGCCACCCGCGCTGTGCCGAGCATGGAC 2410

2341 CTGCCGCGAGCGCAAGTGCAGTGCAGCCCTGGCTGGAATGGCGAAACACTGCACCATCGC 2400
2411 CTGCCGCGAGCGCAAGTGCAGTGCAGCCCTGGCTGGAATGGCGAAACACTGCACCATCGC 2470
2401 TCACATCTGGATAGGGTAGTTAAAGAGGGTTCGCCCTGGGTGTGCAATGGCAACGCGAG 2460
2471 TCACATCTGGATAGGGTAGTTAAAGAGGGTTCGCCCTGGGTGTGCAATGGCAACGCGAG 2530
2461 ATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCAGCTGGGCTGGAGAGAGCTGG 2520
2531 ATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCAGCTGGGCTGGAGAGAGCTGG 2590
2521 CTGTGACACTTCCATGAGAGACTGCTCGCGTGCAGCAAAAGACAATGATGAGAGATGSCCT 2580
2591 CTGTGACACTTCCATGAGAGACTGCTCGCGTGCAGCAAAAGACAATGATGAGAGATGSCCT 2650
2581 GGTGGACTGCATGGACCCCTGACTGCTGCTCCAGCCCCCTGTGCCATATCAACCCGCTGTG 2640
2651 GGTGGACTGCATGGACCCCTGACTGCTGCTCCAGCCCCCTGTGCCATATCAACCCGCTGTG 2710
2641 CTTGGCTCCCTTAAACCTCTTGACATCATCCAGGAGACACAGGTCCCTGTGTACAGCA 2700
2711 CTTGGCTCCCTTAAACCTCTTGACATCATCCAGGAGACACAGGTCCCTGTGTACAGCA 2770
2701 GAACCTACACTCCTTCTATGACCGCATCAAGTTCTCTGGGAGGAGACAGCAGCAGCAT 2760
2771 GAACCTACACTCCTTCTATGACCGCATCAAGTTCTCTGGGAGGAGACAGCAGCAGCAT 2830
2761 AATCCCCGGGAGAACCCCTTTGATGGAGGCAATGCTTGTGTTATTTCTGTGGCCAAAGTAT 2820
2831 AATCCCCGGGAGAACCCCTTTGATGGAGGCAATGCTTGTGTTATTTCTGTGCCAAAGTAT 2890
2821 GACATCAGATGGAAACCCCTCTGGTGTGAACATCAGTTTGTCAATAACCTCTCTTT 2880
2891 GACATCAGATGGAAACCCCTCTGGTGTGAACATCAGTTTGTCAATAACCTCTCTTT 2950
2881 TGATATATCAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC 2940
2951 TGATATATCAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC 3010
2941 CATCATCTCTCGGTTTCGAGCGGCACTTTTCATCACAAGGAGCACACCTGTGGCTGCC 3000
3011 CATCATCTCTCGGTTTCGAGCGGCACTTTTCATCACAAGGAGCACACCTGTGGCTGCC 3070
3001 ATGGGATCGCTTCTTGTGCATGGAACCAATCATCATGAGACATGAGGAGAAATGAGATTCC 3060
3071 ATGGGATCGCTTCTTGTGCATGGAACCAATCATCATGAGACATGAGGAGAAATGAGATTCC 3130
3061 CAGCTGTGACCTGAGCAATTTTCCCGCCCCCAACCCAGTCTCTCTCCATCCCCACTGAC 3120
3131 CAGCTGTGACCTGAGCAATTTTCCCGCCCCCAACCCAGTCTCTCTCCATCCCCACTGAC 3190
3121 GTCTTTGCCAGCTCTCTGTGCAGAGAAAGGCCCAATTTGTGCCCGGAAATTCAGGCTTTGCA 3180
3191 GTCTTTGCCAGCTCTCTGTGCAGAGAAAGGCCCAATTTGTGCCCGGAAATTCAGGCTTTGCA 3250
3181 GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACTGAGCAGCGGACCCC 3240
3251 GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACTGAGCAGCGGACCCC 3310
3241 TGGCTCAAAATCTGTCTGAGGATCAGCTTCAACCCAGCCACCCAGCCATCCCCCTCAACCTCAT 3300
3311 TGGCTCAAAATCTGTCTGAGGATCAGCTTCAACCCAGCCACCCAGCCATCCCCCTCAACCTCAT 3370
3301 GAAAGGTGCACCTCATGGTAGCGGTGAGGGCGCGCTCTTCAGGAAAGTGGTTCGCTGAGC 3360
3371 GAAAGGTGCACCTCATGGTAGCGGTGAGGGCGCGCTCTTCAGGAAAGTGGTTCGCTGAGC 3430
3361 CCAGAGCTGTCTCTATTTATTTATTTGGGACAGACAGCCTCTCAACCCAGAGGTGTT 3420
3431 CCAGAGCTGTCTCTATTTATTTATTTGGGACAGACAGCCTCTACACCAAGAGGTGTT 3490
3421 TGGGCTTTTCAGAAAGCCCTTTGTTTTCGTTGTTATGAAATGAAATCTCTGCCCCAGATCTAAT 3480

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| QY | 5641 | GGGGCCAGCCTCTGGTCAACCAGCAGCAGGCTGAATGSGTGTCAACGTGACATATCTCCCC | 5700 |
| DB | 5690 | GGGGCCAGCCTCTGGTCAACCAGCAGCAGGCTGAATGSGTGTCAACGTGACATATCTCCCC | 5749 |
| QY | 5701 | TGGGGGTTACATTGTCTGGGCATCCAGAGGGGCATCATGTCTGAAGAAATGGAATACGACCA | 5760 |
| DB | 5750 | TGGGGGTTACATTGTCTGGGCATCCAGAGGGGCATCATGTCTGAAGAAATGGAATACGACCA | 5809 |
| QY | 5761 | GGCGGGCCGCATCAATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATCTT | 5820 |
| DB | 5810 | GGCGGGCCGCATCAATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATCTT | 5869 |
| QY | 5821 | ACAGAAATGTCATGGTCTCTACTACAGCCAGAGGCGAGTATATCTTTGAGTTCGACAA | 5880 |
| DB | 5870 | AGAGAAATGTCATGGTCTCTACTACAGCCAGAGGCGAGTATATCTTTGAGTTCGACAA | 5929 |
| QY | 5881 | GAATGACCGCCTCTCTTCTGTGACGATGCCAACTGGCGGGCAGACACTAGAGACCAT | 5940 |
| DB | 5930 | GAATGACCGCCTCTCTTCTGTGACGATGCCAACTGGCGGGCAGACACTAGAGACCAT | 5989 |
| QY | 5941 | CGGCTCAGTGGGCTACTACAGAAAATCTATCAGCCCCCTGAGGGCAATGCGTCAGTCAAT | 6000 |
| DB | 5990 | CGGCTCAGTGGGCTACTACAGAAAATCTATCAGCCCCCTGAGGGCAATGCGTCAGTCAAT | 6049 |
| QY | 6001 | ACAGAGCTTCACTGAGGATGGGCACCTCTTACACACCTTCTACCTGGGCACCTGGCCGCGAG | 6060 |
| DB | 6050 | ACAGAGCTTCACTGAGGATGGGCACCTCTTACACACCTTCTACCTGGGCACCTGGCCGCGAG | 6109 |
| QY | 6061 | GGTGATATACAAGTATGGCAACTGTCAAAGCTGGCAGAGAGCGTCTATGACACACCACAA | 6120 |
| DB | 6110 | GGTGATATACAAGTATGGCAACTGTCAAAGCTGGCAGAGAGCGTCTATGACACACCACAA | 6169 |
| QY | 6121 | GGTCAAGTTTCACTATGACGAGACGGCAGGCGATGCTGAAGACCATCAACCTACAGAATGA | 6180 |
| DB | 6170 | GGTCAAGTTTCACTATGACGAGACGGCAGGCGATGCTGAAGACCATCAACCTACAGAATGA | 6229 |
| QY | 6181 | GGGCTTCACTTCACCTCCGCTACCGTACAGATGGGGCCCTGATGGCCGACGACAGATCTT | 6240 |
| DB | 6230 | GGGCTTCACTTCACCTCCGCTACCGTACAGATGGGGCCCTGATGGCCGACGACAGATCTT | 6289 |
| QY | 6241 | CGGCTTCACTGAGGAAGGCATGGTCAACGGCCGTTTTGACTACAACTATGACAAACAGCTT | 6300 |
| DB | 6290 | CGGCTTCACTGAGGAAGGCATGGTCAACGGCCGTTTTGACTACAACTATGACAAACAGCTT | 6349 |
| QY | 6301 | CGGGTGACACGATGCGAGGCTGTGATCAACGAGACCCCACTGGCCCATTTGATCTATCG | 6360 |
| DB | 6350 | CGGGTGACACGATGCGAGGCTGTGATCAACGAGACCCCACTGGCCCATTTGATCTATCG | 6409 |
| QY | 6361 | CTATGATGATGTGCAGGCAACAGACAGAGTTCGGGAAGTTTGGTGTCAATTTACTATGA | 6420 |
| DB | 6410 | CTATGATGATGTGTGAGGCAACAGACAGAGTTCGGGAAGTTTGGTGTCAATTTACTATGA | 6469 |
| QY | 6421 | CATTAAACAGATCATCACACAGCTGTCTATGACCCACACCAAGCATTTTGATGCAATATGG | 6480 |
| DB | 6470 | CATTAAACAGATCATCACACAGCTGTCTATGACCCACACCAAGCATTTTGATGCAATATGG | 6529 |
| QY | 6481 | CAGGATGAAGGAAGTGCAGTATGAGATCTTCGGCTCGCTCATGTACTGGATGACCGGTCCA | 6540 |
| DB | 6530 | CAGGATGAAGGAAGTGCAGTATGAGATCTTCGGCTCGCTCATGTACTGGATGACCGGTCCA | 6589 |
| QY | 6541 | GTATGATTAACATGGGGCGAGTGTCAAGAAAGAGCTGAAGGTAGGACCCCTACGCCAATAC | 6600 |
| DB | 6590 | GTATGATTAACATGGGGCGAGTGTCAAGAAAGAGCTGAAGGTAGGACCCCTACGCCAATAC | 6649 |
| QY | 6601 | CACCTCGCTACTCCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA | 6660 |
| DB | 6650 | CACCTCGCTACTCCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA | 6709 |
| QY | 6661 | CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACTTGCACTTACTGAGCCCTGG | 6720 |
| DB | 6710 | CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACTTGCACTTACTGAGCCCTGG | 6769 |

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| QY | 6721 | GAACAGTGCAGGCTCACACCACTACCGTATGATCATCCGGACCCGCATCACTCGGCTGGG | 6780 |
| DB | 6770 | GAACAGTGCAGGCTCACACCACTACCGTATGATCATCCGGACCCGCATCACTCGGCTGGG | 6829 |
| QY | 6781 | TGACGTGCAATACAAAGATGAGATGCGTTCCTGAGGACGCGGGCGGTGATATCTT | 6840 |
| DB | 6830 | TGACGTGCAATACAAAGATGAGATGCGTTCCTGAGGACGCGGGCGGTGATATCTT | 6889 |
| QY | 6841 | TGAGTACAACTCAGCTGGCCTGCTCATCAAGGCTCAACCGGGCTGGCAGCTGGAGTGT | 6900 |
| DB | 6890 | TGAGTACAACTCAGCTGGCCTGCTCATCAAGGCTCAACCGGGCTGGCAGCTGGAGTGT | 6949 |
| QY | 6901 | CAGGTACCGCTACGATGGCGCGCGCTGTCCAGAAAGAGCAGCAGCACCACCA | 6960 |
| DB | 6950 | CAGGTACCGCTACGATGGCGCGCGCTGTCCAGAAAGAGCAGCAGCACCACCA | 7009 |
| QY | 6961 | CTGSCAGTTCTTCTATGACAGACTTGACCAACCCCAACCAAGGTCAACCACTGTACAACCA | 7020 |
| DB | 7010 | CTGSCAGTTCTTCTATGACAGACTTGACCAACCCCAACCAAGGTCAACCACTGTACAACCA | 7069 |
| QY | 7021 | CTCCAGCTCTGAGATCACTCCCTCTACTAGACTTGCAGAGGACACCTCTTTGCCATGGA | 7080 |
| DB | 7070 | CTCCAGCTCTGAGATCACTCCCTCTACTAGACTTGCAGAGGACACCTCTTTGCCATGGA | 7129 |
| QY | 7081 | GCTGAGCAGTGGTGTGATGAGTTTTACATAGCTTTGTGACAAACATCGGGACCCCTCTTGCTGT | 7140 |
| DB | 7130 | GCTGAGCAGTGGTGTGATGAGTTTTACATAGCTTTGTGACAAACATCGGGACCCCTCTTGCTGT | 7189 |
| QY | 7141 | CTTTAGTGGAAACAGGTTTGATGATCAAGCAAAATCTCTGTACACAGCCTATGSGGAGATCTA | 7200 |
| DB | 7190 | CTTTAGTGGAAACAGGTTTGATGATCAAGCAAAATCTCTGTACACAGCCTATGSGGAGATCTA | 7249 |
| QY | 7201 | CATGATATACCAACCCCAACTTTCAGATCATATAGGCTCATCTGCTCGCTCTATGATCC | 7260 |
| DB | 7250 | CATGATATACCAACCCCAACTTTCAGATCATATAGGCTCATCTGCTCGCTCTATGATCC | 7309 |
| QY | 7261 | ACTCACAAGCTTGTCCACATGGCGCGGAGATTAATGATGTGTGCGCGGACGCTGGAC | 7320 |
| DB | 7310 | ACTCACAAGCTTGTCCACATGGCGCGGAGATTAATGATGTGTGCGCGGACGCTGGAC | 7369 |
| QY | 7321 | TAGCCACAGACGAGCTGTGGAAAGCACTTTAGTAGCAGCAACGTCATGCTCTTTTAATCT | 7380 |
| DB | 7370 | TAGCCACAGACGAGCTGTGGAAAGCACTTTAGTAGCAGCAACGTCATGCTCTTTTAATCT | 7429 |
| QY | 7381 | CTATATGTTCAAAACCAACCCCACTCCAGAGCATCAAGTGTCTCATGAC | 7440 |
| DB | 7430 | CTATATGTTCAAAACCAACCCCACTCCAGAGCATCAAGTGTCTCATGAC | 7489 |
| QY | 7441 | AGATGTTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAAACGTCCTGGTTA | 7500 |
| DB | 7490 | AGATGTTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAAACGTCCTGGTTA | 7549 |
| QY | 7501 | TCCCAAAACAGACATGATGCCATGGAAACCTCTCTACGAGTCTATCCACACAGATGAA | 7560 |
| DB | 7550 | TCCCAAAACAGACATGATGCCATGGAAACCTCTCTACGAGTCTATCCACACAGATGAA | 7609 |
| QY | 7561 | AACGACAGGTTGGGACAAACAGCAAGTCTATCTCGGGGTACAGTGTCAAGTACAGAGCA | 7620 |
| DB | 7610 | AACGACAGGTTGGGACAAACAGCAAGTCTATCTCGGGGTACAGTGTCAAGTACAGAGCA | 7669 |
| QY | 7621 | GCTCAAGGCTTTTGTCACTTTAGAACGGTTTGGACAGCTCTATGGCTCCCAATCACCCAG | 7680 |
| DB | 7670 | GCTCAAGGCTTTTGTCACTTTAGAACGGTTTGGACAGCTCTATGGCTCCCAATCACCCAG | 7729 |
| QY | 7681 | CTGCCACAGGCTCCAAAGACCCCAAGAAATTTGCATCCAGCGGCTCAGTCTTTTGGCAAGGG | 7740 |
| DB | 7730 | CTGCCACAGGCTCCAAAGACCCCAAGAAATTTGCATCCAGCGGCTCAGTCTTTTGGCAAGGG | 7789 |
| QY | 7741 | GGTCAAGTTTGGCTTGAAGGATGGCCGAGTGACCACAGACATCATCATGTGGGCAATGA | 7800 |
| DB | 7790 | GGTCAAGTTTGGCTTGAAGGATGGCCGAGTGACCACAGACATCATCATGTGGGCAATGA | 7849 |
| QY | 7801 | GGATGGGCGAAGGTTTGTCTCCATCTTTGAACCACTTACCTAGAGAACCTTGCATCTT | 7860 |

Db 181 AAGACATTGTGCGCAGGAGCGGAGGAATTTCTGCGCACAGGTGCCAACTTCACCCCTG 240
Qy 275 CGGGAGCTGGGGCTGGAAGAATAAGCCCCCTCAGGGGACCTGTATCGGGACAGACATTT 334
Db 241 CGGGAGCTGGGGCTGGAAGAATAAGCCCCCTCAGGGGACCTGTATCGGGACAGACATTT 300
Qy 335 GGCCTGCCCAATGGGCTACTCCATGGGGGTGGCTCTGTATGCCAGACATGGAGGCTGAC 394
Db 301 GGCCTCCCCACTGGGGTACTTCCATGGGGGTGGCTCTGTATGCCAGACATGGAGGCTGAC 360
Qy 395 ACGTGCTGTCCCTTGAGCACCCCGTGGGTCTGTGGGGCGGAGACACGGTCAAGGGCGC 454
Db 361 ACGGTGCTGTCCCTTGAGCACCCCGTGGGTCTGTGGGGCGGAGACACGGTCAAGGGCGC 420
Qy 455 AGCTCTGCTGTCCAGCGGGGCCAATTCCAATCTCACACTCACCGACACCGAGGATGAA 514
Db 421 AGCTCTGCTGTCCAGCGGGGCCAATTCCAATCTCACACTCACCGACACCGAGGATGAA 480
Qy 515 AACACTGAGACTGATCATCCGGGGCGCTTGAGAACACACGGCGGCTCCGAGCGCGCG 574
Db 481 AACACTGAGACTGATCATCCGGGGCGCTTGAGAACACACGGCGGCTCCGAGCGCGCG 540
Qy 575 CCGCGCTCTCGACGCCACACCCCCAAACAGCACACCGGGCTTCCATTAATCCCTG 634
Db 541 CCGCGCTCTCGACGCCACACCCCCAAACAGCACACCGGGCTTCCATTAATCCCTG 600
Qy 635 AACCGGGCACTTCAGCGGAGGAGCAACCCAGCGCGGCGGCGGCGGCGGCGGCTC 694
Db 601 AACCGGGCACTTCAGCGGAGGAGCAACCCAGCGCGGCGGCGGCGGCGGCGGCTC 660
Qy 695 TCCGAGAGCCCCCTGCGGGCGGCGCCAGAGAGCTGCGCACCGCCAGGAACTGGGCTG 754
Db 661 TCCGAGAGCCCCCTGCGGGCGGCGCCAGAGAGCTGCGCACCGCCAGGAACTGGGCTG 720
Qy 755 CTCAAACAGCAACATCCCCCTGGAGACACAGGAACTTAGGCAAGCAACCTTCTAGGGACA 814
Db 721 CTCAAACAGCAACATCCCCCTGGAGACACAGAACTTAGGCAAGCAACCTTCTAGGGACA 780
Qy 815 TTGAGGAGACACTATTGAGATGACATTTCTGGGGCTCCCGGCTATGATGGGGCTTAC 874
Db 781 TTGAGGAGACACTATTGAGATGACATTTCTGGGGCTCCCGGCTATGATGGGGCTTAC 840
Qy 875 AGTGACGGGCACTTCTCTTCAAGGCTGGAGGACCTCCCGCTCTTCTGCACACACATCA 934
Db 841 AGTGACGGGCACTTCTCTTCAAGGCTGGAGGACCTCCCGCTCTTCTGCACACATCA 900
Qy 935 CCAGGGTACCCACTGAGCTCAGACACAGTGTACTCTCTCGCGCCGACCCCTGCGCGCG 994
Db 901 CCAGGGTACCCACTGAGCTCAGACACAGTGTACTCTCTCGCGCCGACCCCTGCGCGCG 960
Qy 995 AGCACCTTCGCGCGCGGCGCTTTAACTCAAGAGCCCTCCAAGTACTGTAACTGGGAG 1054
Db 961 AGCACCTTCGCGCGCGGCGCTTTAACTCAAGAGCCCTCCAAGTACTGTAACTGGGAG 1020
Qy 1055 TGCAGGCGCTGAGCGCCATCGTCACTCAGCACCTTGGTCACTCTCTGGCATACTTT 1114
Db 1021 TGCAGGCGCTGAGCGCCATCGTCACTCAGCACCTTGGTCACTCTCTGGCATACTTT 1080
Qy 1115 GTGGCCATGCACCTGTTGGCTTAACTTGGCACTTGACGCCGATGGAGGGGACAGTGTAT 1174
Db 1081 GTGGCCATGCACCTGTTGGCTTAACTTGGCACTTGACGCCGATGGAGGGGACAGTGTAT 1140
Qy 1175 GAGATCACGGAGGACACAGCAGGATTTGGGCTTGCCACCGAGCTCCCTCATACCC 1234
Db 1141 GAGATCACGGAGGACACAGCAGGATTTGGGCTTGCCACCGAGCTCCCTCATACCC 1200
Qy 1235 TCAGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAGGAAACACAGAAAGGAAAG 1294
Db 1201 TCAGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAGGAAACACAGAAAGGAAAG 1260
Qy 1295 CCAGTAGTCTTTCAGAGGACAGTCTTCAAGATTTCTAGATTTCTGAGAAATTTGATGTGGGAGG 1354
Db 1261 CCAGTAGTCTTTCAGAGGACAGTCTTCAAGATTTCTAGATTTCTGAGAAATTTGATGTGGGAGG 1320

Qy 1355 CGAGCCTCCAGAGATTTCTCTCGGCACATTTCTGGAGATCTCAAGTGTTCATAGACAT 1414
Db 1321 CGAGCTTCCAGAGATTTCTCTCGGCACATTTCTGGAGATCTCAAGTGTTCATAGACAT 1380
Qy 1415 CTTGTGATCTGAAATTAATTTCTCTGGAAAGGACGCCCTGGTGTGGCATTTATGGC 1474
Db 1381 CTTGTGATCTGAAATTAATTTCTCTGGAAAGGACGCCCTGGTGTGGCATTTATGGC 1440
Qy 1475 AGAAAGGCTCCCTCTTACATACACAGTTTGAATTTGTGGAGCTGTGGATGGGAGG 1534
Db 1441 AGAAAGGCTCCCTCTTACATACACAGTTTGAATTTGTGGAGCTGTGGATGGGAGG 1500
Qy 1535 AGGCTCTTAACCCAGAGGCGCGAGCTTAGAGGGACCCCGCGCCAGTCTCGGGGAAT 1594
Db 1501 AGGCTCTTAACCCAGAGGCGCGAGCTTAGAGGGACCCCGCGCCAGTCTCGGGGAAT 1560
Qy 1595 GTGCCCCCTCCAGCCATGAGACAGGCTTCACTCAGTATTTGGATTCAGGAATCTGGCAC 1654
Db 1561 GTGCCCCCTCCAGCCATGAGACAGGCTTCACTCAGTATTTGGATTCAGGAATCTGGCAC 1620
Qy 1655 TTGGCTTTTACAATGACGAAAGGAGTCAAGATGGTTCCTTTCTCACACATGCCAT 1714
Db 1621 TTGGCTTTTACAATGACGAAAGGAGTCAAGATGGTTCCTTTCTCTCCCC-----A 1674
Qy 1715 GAGTCGGTGTAACTGCCCCAGCACTGCTATGGCAATGGTGAATCTGACATCTTGGGACC 1774
Db 1675 GAGTCGGTGTAACTGCCCCAGCACTGCTATGGCAATGGTGAATCTGACATCTTGGGACC 1734
Qy 1775 TGCCACTGCTTCTCTGGGTTTCTTGGGCCCCGACTGTGGCAGAGCCTCCTGCCCGTCTC 1834
Db 1735 TGCCACTGCTTCTCTGGGTTTCTTGGGCCCCGACTGTGGCAGAGCCTCCTGCCCGTCTC 1794
Qy 1835 TGTAGCGGAAATGGCCAAATACATGAAGGACAGATGCTTGTGCCACAGTGGCTGGAAGGC 1894
Db 1795 TGTAGCGGAAATGGCCAAATACATGAAGGACAGATGCTTGTGCCACAGTGGCTGGAAGGC 1854
Qy 1895 GCTGAGTGCCATGTGCCCAACCACTGATCGATGTGGCTGCGCTGACAGCAACCATGGCACC 1954
Db 1855 GCTGAGTGCCATGTGCCCAACCACTGATCGATGTGGCTGCGCTGACAGCAACCATGGCACC 1914
Qy 1955 TGCACTACCGGCACTGCACTCTGCAACCTTGGCTACAAAGGCGGAGAGCTGTGAGGAAGTG 2014
Db 1915 TGCACTACCGGCACTGCACTCTGCAACCTTGGCTACAAAGGCGGAGAGCTGTGAGGAAGTG 1971
Qy 2015 GACTGATGAGACCCCACTGTTTCAAGCGGGGTGTCTGCGTGAAGCGGAGATGGCATTCG 2074
Db 1972 GACTGATGAGACCCCACTGTTTCAAGCGGGGTGTCTGCGTGAAGCGGAGATGGCATTCG 2031
Qy 2075 TTTGTGGGATGGGAGGACCAACTGCGAGACCCCGAGGCCACATGCTTTAGACCAGTGT 2134
Db 2032 TCTGTGGGATGGGAGGACCAACTGCGAGACCCCGAGGCCACATGCTTTAGACCAGTGT 2091
Qy 2135 TCAGGCGACGGAACCTTCTTCCCGGACACCGGGCTTTTGCAGCTGTGACCCAAAGCTGACT 2194
Db 2092 TCAGGCGACGGAACCTTCTTCCCGGACACCGGGCTTTTGCAGCTGTGACCCAAAGCTGACT 2151
Qy 2195 GGAACAGACTGTTTATCGAGATCTGTGCTGCCAGTGTGGTGGCCATGGCGGTGCGTA 2254
Db 2152 GGAACAGACTGTTTATCGAGATCTGTGCTGCCAGTGTGGTGGCCATGGCGGTGCGTA 2211
Qy 2255 GGGGGCACTGCGCTGCGAGGATGCTGGATGGGGGACGCTTGCAGACCGCGGCTGC 2314
Db 2212 GGGGGCACTGCGCTGCGAGGATGCTGGATGGGGGACGCTTGCAGACCGCGGCTGC 2271
Qy 2315 CACCCGCGCTGTCCGAGCATGGGACCTGCGCGACGGCAAGTGCAGTGCAGCCCTGGC 2374
Db 2272 CACCCGCGCTGTCCGAGCATGGGACCTGCGCGACGGCAAGTGCAGTGCAGCCCTGGC 2331
Qy 2375 TGGAAATGGCGAACACTGACCATC-----GCTCACTATCTGATAGGGTAGTTAA----- 2424
Db 2332 TGGAAATGGCGAACACTGACCATCCTCCCTAGCTCACTATCTGATAGGGTAGTTAACTT 2391

Db 4552 GGGCCCCCAGTGGCTGTGACTGTAATAAAATGATGCCAACTGTGATGTTTTCCTGGAGAC 4611
Qy 4616 GATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCTTGGCTGTGTGCTGTAT 4675
Db 4612 GATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCTTGGCTGTGTGCTGTAT 4671
Qy 4676 GGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTATCCGGAAGAACAAAG 4735
Db 4672 GGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTATCCGGAAGAACAAAG 4731
Qy 4736 CTTTTCCTCAACACCAGAACATGATGAGCTGTCTTCAACAAATTGACAGGAGCTCTAT 4795
Db 4732 CTTTTCCTCAACACCAGAACATGATGAGCTGTCTTCAACAAATTGACAGGAGCTCTAT 4791
Qy 4796 CTGTTTGATACACCGGCAAGCACTGTGTAACCCAAAGCCTGCCACAGGAGACTACCTG 4855
Db 4792 CTGTTTGATACACCGGCAAGCACTGTGTAACCCAAAGCCTGCCACAGGAGACTACCTG 4851
Qy 4856 TACAACCTTCACTACACTGGGAGCGGCACATCACTCATCACAGACAAACAATGGCAAC 4915
Db 4852 TACAACCTTCACTACACTGGGAGCGGCACATCACTCATCACAGACAAACAATGGCAAC 4911
Qy 4916 ATGTTAAATGTCCGCCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCCAAGTGGC 4975
Db 4912 ATGTTAAATGTCCGCCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCCAAGTGGC 4971
Qy 4976 CAGTGTACTGGGTGACCATGGGCACCAAGTGCACCTCAAGAGTGTGACACACAAGGA 5035
Db 4972 CAGTGTACTGGGTGACCATGGGCACCAAGTGCACCTCAAGAGTGTGACACACAAGGA 5031
Qy 5036 CACGAGTTGGCCATGATGACATACCATGGCAATTCGGGCCCTTTCGGCAACCAAAAGCAAT 5095
Db 5032 CACGAGTTGGCCATGATGACATACCATGGCAATTCGGGCCCTTTCGGCAACCAAAAGCAAT 5091
Qy 5096 GAAAAACGATGGACAACTTTTATCAGTACGACAGCTTTTGGCCGCTTGACAAATGTGACC 5155
Db 5092 GAAAAACGATGGACAACTTTTATCAGTACGACAGCTTTTGGCCGCTTGACAAATGTGACC 5151
Qy 5156 TTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAAGTGCATGTCCAG 5215
Db 5152 TTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAAGTGCATGTCCAG 5211
Qy 5216 GTAGAGACCTCCAGCAAGGATGTGTACCACTAACCCAACTGTCTGCTCAGGCGCC 5275
Db 5212 GTAGAGACCTCCAGCAAGGATGTGTACCACTAACCCAACTGTCTGCTCAGGCGCC 5271
Qy 5276 TTCTACACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTCC 5335
Db 5272 TTCTAC-----GACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTCC 5319
Qy 5336 TTGGCGCTGTGCTGGCCAAACGGCATGAGGTGGCGCTGCAAGCTGAGCCCACTTGGCTG 5395
Db 5320 TTGGCGCTGTGCTGGCCAAACGGCATGAGGTGGCGCTGCAAGCTGAGCCCACTTGGCTG 5379
Qy 5396 GCTGSCACCGTCAACCCACCGTGGGCAAGAGGAATGTCAGCTGCCCATCGACAAACGGC 5455
Db 5380 GCTGSCACCGTCAACCCACCGTGGGCAAGAGGAATGTCAGCTGCCCATCGACAAACGGC 5439
Qy 5456 CTCAACTGTGGTGGTGGCGGCGAGGCAAGAGAGGCTCGGGGCCAGGTCACTGTCTTT 5515
Db 5440 CTCAACTGTGGTGGTGGCGGCGAGGCAAGAGAGGCTCGGGGCCAGGTCACTGTCTTT 5499
Qy 5516 GGGCGCCGGCTGGGGTG-----CACAAACCGAAATCTCTATCTCTGGACTTTGAT 5566
Db 5500 GGGCGCCGGCTGGGGTGCTCCAGGTTTCACAAACCGAAATCTCTATCTCTGGACTTTGAT 5559
Qy 5567 GCGGTAAACGACACAGAGAAGATCTATGATGACACCGCAAGTTTCAACCTTCGGATTCTG 5626
Db 5560 GCGGTAAACGACACAGAGAAGATCTATGATGACACCGCAAGTTTCAACCTTCGGATTCTG 5619
Qy 5627 TACGACAGGGGGCGGCCAGCCTCTGGTCACCCAGCAGCGCTGAATGGTGTCAAC 5686
Db 5620 TACGACAGGGGGCGGCCAGCCTCTGGTCACCCAGCAGCGCTGAATGGTGTCAAC 5679

Qy 5687 GTGACATACCTCCCTGGGGTTACATTTCTGGCATCCAGAGGGGCATCATGTCTGAAGA 5746
Db 5680 GTGACATACCTCCCTGGGGTTACATTTCTGGCATCCAGAGGGGCATCATGTCTGAAGA 5739
Qy 5747 ATGGAATACGACAGGCGGGCCGCATCACATCCAGGATCTTCGTGTATGGGAACACATGG 5806
Db 5740 ATGGAATACGACAGGCGGGCCGCATCACATCCAGGATCTTCGTGTATGGGAACACATGG 5799
Qy 5807 AGCTACACATCTTAGAGAAAGTCCATGGTGTCTACTACACAGCCAGAGCATATATC 5866
Db 5800 AGCTACACATCTTAGAGAAAGGAGTG----- 5827
Qy 5867 TTTGAGTTCCACAGAAATGACCGCTCTCTTCTGTGACGATGCCAACTGGCGCGGCAG 5926
Db 5828 -TCGAGTTCCACAGAAATGACCGCTCTCTTCTGTGACGATGCCAACTGGCGCGGCAG 5886
Qy 5927 ACCTAGAGACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCTTGAGGGC 5986
Db 5887 ACCTAGAGACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCTTGAGGGC 5946
Qy 5987 AATGCCCTCAGTACATACAGGACTTCACTGAGGATGGGCACCTCTTCAACCTTTTACCTG 6046
Db 5947 AATGCCCTCAGTACATACAGGACTTCACTGAGGATGGGCACCTCTTCAACCTTTTACCTG 6006
Qy 6047 GGCACCTGGCCGCGAGGTGATACAAAGTATGGCAAACTGTCAAAGCTGGCAGACCGCTC 6106
Db 6007 GGCACCTGGCCGCGAGGTGATACAAAGTATGGCAAACTGTCAAAGCTGGCAGACCGCTC 6066
Qy 6107 TATGACACCAACCAAGGTCACTTTTACCTATGACAGACGGCAGCATGTCTGACACCATC 6166
Db 6067 TATGACACCAACCAAGGTCACTTTTACCTATGACAGACGGCAGCATGTCTGACACCATC 6126
Qy 6167 AACCTACAGAATGAGGGCTTCACTGCAACCATCCGCTACCGTACAGTTGGGCCCTGATT 6226
Db 6127 AACCTACAGAATGAGGGCTTCACTGCAACCATCCGCTACCGTACAGTTGGGCCCTGATT 6186
Qy 6227 GACCGACAGATCTTCGCTTCACTGAGGAAGGATGTCAACGCCCGTTTTTGACTACAAC 6286
Db 6187 GACCGACAGATCTTCGCTTCACTGAGGAAGGATGTCAACGCCCGTTTTTGACTACAAC 6246
Qy 6287 TATGACAAACAGCTTCCGGGTGACCGAGCATCAGGCTGTGATCAACGAGACCCCACTGCC 6346
Db 6247 TATGACAAACAGCTTCCGGGTGACCGAGCATCAGGCTGTGATCAACGAGACCCCACTGCC 6306
Qy 6347 ATTGATCTCTATCGCTATGATGTGTCAAGGCAAGACAGAGCATTTTGGGAAGTTTGGT 6406
Db 6307 ATTGATCTCTATCGCTATGATGTGTCAAGGCAAGACAGAGCATTTTGGGAAGTTTGGT 6366
Qy 6407 GTCAATTTTACTATGACATTAACCAAGATCATCAACAGCTGTCTATGACCCCAACCAAGCAT 6466
Db 6367 GTCAATTTTACTATGACATTAACCAAGATCATCAACAGCTGTCTATGACCCCAACCAAGCAT 6426
Qy 6467 TTTGATGCATATGGCAGGATGAAGAAAGTGCAGTATCAGATCTTCCGCTCGCTCATGTAC 6526
Db 6427 TTTGATGCATATGGCAGGATGAAGAAAGTGCAGTATCAGATCTTCCGCTCGCTCATGTAC 6486
Qy 6527 TGGATGACCGTCCAGTATGATAACATGGGGGAGTAGTGAAGAAAGGAGCTGAAGGTAGGA 6586
Db 6487 TGGATGACCGTCCAGTATGATAACATGGGGGAGTAGTGAAGAAAGGAGCTGAAGGTAGGA 6546
Qy 6587 CCCTTACGCCAATACCACTCGCTACTCTATGATGTATGCTGACGGCAGCTGCAGACA 6646
Db 6547 CCCTTACGCCAATACCACTCGCTACTCTCTATGATGTATGCTGACGGCAGCTGCAGACA 6606
Qy 6647 GTCTCCAATGAAGCCCACTTGGCGCTTACAGCTACGACCTCAATGGGAACTTGAC 6706
Db 6607 GTCTCCAATGAAGCCCACTTGGCGCTTACAGCTACGACCTCAATGGGAACTTGAC 6666
Qy 6707 TTACTGAGCCCTGGGAAACAGTGCACGGCTCACACCATACGGTATGACATCCGCGACCGC 6766
Db 6667 TTACTGAGCCCTGGGAAACAGTGCACGGCTCACACCATACGGTATGACATCCGCGACCGC 6726

| | | | |
|----|------|---|------|
| Qy | 6767 | ATCACTCGGCTGGGTGACGTGGCAATACAAGATGATGAGGATGGCTTCTGTGAGGCGACGCG | 6822 |
| Db | 6727 | ATCACTCGGCTGGGTGACGTGGCAATACAAGATGATGAGGATGGCTTCTGTGAGGCGACGCG | 6786 |
| Qy | 6827 | GGCGGTGATATCTTTGAGTACAACCTCAGCTGGCTGCTCATCAAGGCGCTACAACCGGGCT | 6886 |
| Db | 6787 | GGCGGTGATATCTTTGAGTACAACCTCAGCTGGCTGCTCATCAAGGCGCTACAACCGGGCT | 6846 |
| Qy | 6887 | GGCAGCTGGAGTGTCAAGTACCGCTACGATGGCTGGGGCGGGCGGTGTCCAGCAAGAGC | 6946 |
| Db | 6847 | GGCAGCTGGAGTGTCAAGTACCGCTACGATGGCTGGGGCGGGCGGTGTCCAGCAAGAGC | 6906 |
| Qy | 6947 | AGCCACAGCCACCACTGCAAGTTCTTCTATGCGAGACTGACACCAACCCCAAGAGTCAAC | 7006 |
| Db | 6907 | AGCCACAGCCACCACTGCAAGTTCTTCTATGCGAGACTGACACCAACCCCAAGAGTCAAC | 6966 |
| Qy | 7007 | CACCTGTACAACCACTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAGAGACAC | 7066 |
| Db | 6967 | CACCTGTACAACCACTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAGAGACAC | 7026 |
| Qy | 7067 | CTCTTTGCCATGGAGCTGAGCAGTGTGATGAGTTTATACATAGCTTGTGACAACATCGGG | 7126 |
| Db | 7027 | CTCTTTGCCATGGAGCTGAGCAGTGTGATGAGTTTATACATAGCTTGTGACAACATCGGG | 7086 |
| Qy | 7127 | ACCCCTCTTGCTCTTTAGTGGAAACAGGTTTGATGATCAAGCAAAATCTGTATACAGCC | 7186 |
| Db | 7087 | ACCCCTCTTGCTCTTTAGTGGAAACAGGTTTGATGATCAAGCAAAATCTGTATACAGCC | 7146 |
| Qy | 7187 | TATGGGAGATCTACATGATACCAACCCCAACTTTTCAGATCATATAGGCTACCATGGT | 7246 |
| Db | 7147 | TATGGGAGATCTACATGATGATACCAACCCCAACTTTTCAGATCATATAGGCTACCATGGT | 7206 |
| Qy | 7247 | GGCCTCTATGATCCACTCACCAGCTTGTCCACATGGCGCGGAGATTATGATGTGCTG | 7306 |
| Db | 7207 | GGCCTCTATGATCCACTCACCAGCTTGTCCACATGGCGCGGAGATTATGATGTGCTG | 7266 |
| Qy | 7307 | GCCGGACGCTGACATAGCCCCAGACCAACGAGCTGTGGAAAGCACTTGTAGCAGCAACGTC | 7366 |
| Db | 7267 | GCCGGACGCTGACATAGCCCCAGACCAACGAGCTGTGGAAAGCACTTGTAGCAGCAACGTC | 7326 |
| Qy | 7367 | ATGCTCTTTAATCTCTATATGTTTCAAAAACCAACCCCATCAGCAACTCCAGGACATC | 7426 |
| Db | 7327 | ATGCTCTTTAATCTCTATATGTTTCAAAAACCAACCCCATCAGCAACTCCAGGACATC | 7386 |
| Qy | 7427 | AAGTGCTTCATGACAGATGTTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAAC | 7486 |
| Db | 7387 | AAGTGCTTCATGACAGATGTTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAAC | 7446 |
| Qy | 7487 | GTGATCCCTGGTTATCCCAAACACAGACATGATGCCATGGAAACCCCTCTACAGAGCTCATC | 7546 |
| Db | 7447 | GTGATCCCTGGTTATCCCAAACACAGACATGATGCCATGGAAACCCCTCTACAGAGCTCATC | 7506 |
| Qy | 7547 | CACACACAGATGA AAAACGAGGAGTGGGACAAACGCA----- | 7593 |
| Db | 7507 | CACACACAGATGA AAAACGAGGAGTGGGACAAACGCAAGGTAAATTCCTGCACAAGGCTGC | 7566 |
| Qy | 7584 | -AGTCTATCTCCGCGGTACAGTGTGAAGTACAGAAAGCAGCTCAAGGCTTTGTCAACCTTA | 7642 |
| Db | 7567 | CAGTCTATCTCCGCGGTACAGTGTGAAGTACAGAAAGCAGCTCAAGGCTTTGTCAACCTTA | 7626 |
| Qy | 7643 | GAACGGTTTGACCAAGCTCTATGGCTTCCACAATCAACAGCTGCCAGCAGGCTCCAAAGCC | 7702 |
| Db | 7627 | GAACGGTTTGACCAAGCTCTATGGCTTCCACAATCAACAGCTGCCAGCAGGCTCCAAAGCC | 7686 |
| Qy | 7703 | AAGAAAGTTTGATCCAGCGGCTCAGTCTTTGGCAAGGGGTCAAGTTTGCTTTGAAAGAT | 7762 |
| Db | 7687 | AAGAAAGTTTGATCCAGCGGCTCAGTCTTTGGCAAGGGGTCAAGTTTGCTTTGAAAGAT | 7746 |
| Qy | 7763 | GGCCGAGTGACACACAGACATCATCAGTGTGGCCAAATGAGGATGGCGAAGGGTTGCTGCC | 7822 |
| Db | 7747 | GGCCGAGTGACACACAGACATCATCAGTGTGGCCAAATGAGGATGGCGAAGGGTTGCTGCC | 7806 |
| Qy | 7823 | ATCTTTGAACCAATGCCCACTACTAGAGAAACCTGCACCTTCACCAATGATGGGGTGGATACC | 7882 |

| | | | |
|----------|--|---|------|
| Db | 7807 | ATCTTGAACCATGCCACCTACCTAGAGAACCTTGCACTTTACCAATTGATGGGTGGATACC | 7886 |
| Qy | 7883 | CATTACTTTTGTGAACCCAGGACCTTCAGAAAGGTGACCTCGGCCATCTCTGGGCCCTCAGTGGG | 7942 |
| Db | 7867 | CATTACTTTTGTGAACCCAGGACCTTCAGAAAGGTGACCTCGGCCATCTCTGGGCCCTCAGTGGG | 7926 |
| Qy | 7943 | GGCGCGCGAACCCCTGAGAAATGGGGTCAACGTCACCTGTGTCTCCAGATCAACACAGTACTT | 8002 |
| Db | 7927 | GGCGCGCGAACCCCTGAGAAATGGGGTCAACGTCACCTGTGTCTCCAGATCAACACAGTACTT | 7986 |
| Qy | 8003 | AATGGCAGGACTAGACGCTACACAGACATCCAGCTCCAGTACGCGGGCACCTGTGCTTGAAC | 8062 |
| Db | 7987 | AATGGCAGGACTAGACGCTACACAGACATCCAGCTCCAGTACGCGGGCACCTGTGCTTGAAC | 8046 |
| Qy | 8063 | ACACGCTACGGGCAACCTTTGGATGAGGAGAAAGGCACCGGTCTCTGGAGCTTGCCCCGCGCAG | 8122 |
| Db | 8047 | ACACGCTACGGGCAACCTTTGGATGAGGAGAAAGGCACCGGTCTCTGGAGCTTGCCCCGCGCAG | 8106 |
| Qy | 8123 | AGACCGTGGCCCAAGCTGGGCCCCGGAGCAGACAGACTGCGGGAGGGGAGGAGAGGC | 8182 |
| Db | 8107 | AGACCGTGGCCCAAGCTGGGCCCCGGAGCAGACAGACTGCGGGAGGGGAGGAGAGGC | 8166 |
| Qy | 8183 | CTCGGGCCCTGGACAGAGGGGGAGAGCAGCAGGTGCTGAGCACAGGGCGGCTGCAAGGC | 8242 |
| Db | 8167 | CTCGGGCCCTGGACAGAGGGGGAGAGCAGCAGGTGCTGAGCACAGGGCGGCTGCAAGGC | 8226 |
| Qy | 8243 | TACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAACTGTTCAGACAGCGCCCAAC | 8302 |
| Db | 8227 | TACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAACTGTTCAGACAGCGCCCAAC | 8286 |
| Qy | 8303 | AACATCCACTTCATGACAGAGCGAGATGGCGGGAGGTGACAGAGGAC | 8354 |
| Db | 8287 | AACATCCACTTCATGACAGAGCGAGATGGCGGGAGGTGACAGAGGAC | 8338 |
| RESULT 5 | | | |
| ABN85378 | | | |
| ID | ABN85378 standard; DNA; 8438 BP. | | |
| XX | AC | | |
| AC | ABN85378; | | |
| XX | AC | | |
| XX | 21-OCT-2002 (first entry) | | |
| DT | Human NOV1, TEN-M4 like protein, coding sequence. | | |
| XX | Human NOV1, TEN-M4 like protein, coding sequence. | | |
| XX | Human; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive; | | |
| KW | Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic; | | |
| KW | Antiaesthetic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic; | | |
| KW | Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant; | | |
| KW | Gene Therapy; NOV; cancer; heart disease; Inflammation; | | |
| KW | autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; | | |
| KW | asthma; IgA nephropathy; cirrhosis; arthritis; Alzheimer's disease; | | |
| KW | infection; stroke; muscular dystrophy; epilepsy; wasting disorder; | | |
| XX | TEN-M4 like protein; chromosome 11; Gene; ds. | | |
| XX | Homo sapiens. | | |
| OS | Homo sapiens. | | |
| XX | FH | | |
| XX | Key | | |
| FT | CDS | | |
| FT | 4..8395 | | |
| FT | /*tag= a | | |
| FT | /trans_except= (pos: 1138..1147,aa:Met) | | |
| FT | /product= "NOV1 protein" | | |
| XX | XX | | |
| XX | W0200255704-A2. | | |
| PN | XX | | |
| XX | XX | | |
| FD | 18-JUL-2002. | | |
| XX | XX | | |
| PF | 09-JAN-2002; 2002WO-US000554. | | |
| XX | XX | | |
| PR | 09-JAN-2001; 2001US-0260417P. | | |
| PR | 10-JAN-2001; 2001US-0260831P. | | |
| PR | 28-FEB-2001; 2001US-0272338P. | | |

1645 AATCTGGCACTTGGCTTTTACAAATGACGGAAAGGAGTCAGAAAGTGGTTTCTCTTCTCAC 1704
1621 AATCTGGCACTTGGCTTTTACAAATGACGGAAAGGAGTCAGAAAGTGGTTTCTCTCTCAC 1680
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1765 CTCTGGGACCTGCGCACTGCTTCTCGGTTTCTGGGGCCCGGCTGCGGAGAGCCCTCCCTG 1824
1732 TTCTGGAACCTGGCAATGTTTTCAGGAATTCCTGGGTCCGGATGTTTCAAGAGCCGCCCTG 1791
1825 CCCCGTGTCTGTAGCGGAAATGCCCCAATACATCAAAAGGCAGATGCTGTGCGCACAGTGG 1884
1792 TCCAGTGTATGATGGCAACGGGCACTACTCCAGGGCCGCTGCTGTGTTTACGCGG 1851
1885 CTGGAAGGCGCTGAGTGGCATGTGCCCAACCAACAGTGTATCGATGTGGCCCTGCGACGAA 1944
1852 CTGGAAGGCGCACCGAGTGTATGTGCCCACTACCCAGTGTATTTGACCCACAGTGTGGGG 1911
1945 CCATGGCACTGATCAGGGGCACTGCACTCTGCAACCTCGCTACAAAGGCGGAGAGCTG 2004
1912 TCGTGGGATTTGATCATGGGCTCTGTGTCTTGAACCTCAGGATACAAAGGAGAAAGTTG 1971
2005 TGAGGAAGTGGCACTGCAATGACCCACATGTTGAGGCGGGGTGTCTGCGTGAGAGCGGA 2064
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2932 GTTCGAGCGGGCACCTTTTCATCACAGGAGCACACCTGTGTGCTGCCATGGGATCGCTT 2991
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Db 5932 GATGCCCAACGTGGCGGCGAGACACTAGAGACCATCCGCTCAGTGGGCTACTACAGAA 5991

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|----|------|--|------|--|------|--|------|
| QY | 5965 | CATCTATACGCCCCCTGAGGCAATGCCTCAGTCATACAGGACTTCACTGAGGATGGCA | 6024 | | 7072 | CTATACGACTTGAAGGACACCTCTTTGCCATGAGCTGAGCATGGTGGATGATTTTA | 7131 |
| Db | 5992 | CATCTATACGCCCCCTGAGGCAATGCCTCAGTCATACAGGACTTCACTGAGGATGGCA | 6051 | | 7105 | CATAGCTTGTGACAAATCGGACCCCTCTTCTGCTCTTTAGTGAAACAGAGTTTGATGAT | 7164 |
| QY | 6025 | CTTCTTTCAACACTTCTTCTTCTGAGGCACTGGCCGCGAGGGTGATATACAAGTATGGCAACT | 6084 | | 7132 | CATAGCTTGTGACAAATCGGACCCCTCTTCTGCTCTTTAGTGAAACAGAGTTTGATGAT | 7191 |
| Db | 6052 | CTTCTTTCAACACTTCTTCTTCTTCTGAGGCACTGGCCGCGAGGGTGATATACAAGTATGGCAACT | 6111 | | 7165 | CAAGCAAAATCTGTGTACACAGCCTATGGGGAGATCTATACATGATACCAACCCCACTTTCA | 7224 |
| QY | 6085 | GTCAAAAGCTGGCAGAGAGCGCTCTATGACACCAACCAAGGTCAAGTTTCACTATGACGAGAC | 6144 | | 7192 | CAAGCAAAATCTGTGTACACAGCCTATGGGGAGATCTATACATGATACCAACCCCACTTTCA | 7251 |
| Db | 6112 | GTCAAAAGCTGGCAGAGAGCGCTCTATGACACCAACCAAGGTCAAGTTTCACTATGACGAGAC | 6171 | | 7225 | GATCATCATAGGCTACCATGGTGGCTCTATGATCCATCACCACAGCTTGTCCACATGGG | 7284 |
| QY | 6145 | GGCAGGCACTGCTGAAGACCACTCAACCTACAGATGAGGGCTTCACTGACCACTCCGCTA | 6204 | | 7252 | GATCATCATAGGCTACCATGGTGGCTCTATGATCCATCACCACAGCTTGTCCACATGGG | 7311 |
| Db | 6172 | GGCAGGCACTGCTGAAGACCACTCAACCTACAGATGAGGGCTTCACTGACCACTCCGCTA | 6231 | | 7285 | CGCGGAGATTAATGATGTGCTGGCCGAGCGCTGGACTAGCCAGACCCAGAGCTGTGGAA | 7344 |
| QY | 6205 | CGGTCAAGTTGGGCCCTGATTTGACCGCAGATCTTCCGTTTCACTGAGGAAGCATGCT | 6264 | | 7312 | CGCGGAGATTAATGATGTGCTGGCCGAGCGCTGGACTAGCCAGACAGCTGTGGAA | 7371 |
| Db | 6232 | CGGTCAAGTTGGGCCCTGATTTGACCGCAGATCTTCCGTTTCACTGAGGAAGCATGCT | 6291 | | 7345 | GCACCTTAGTAGCAGCAACGTCATGCTTTTAAATCTCTATATGTTCAAAAAACAACCC | 7404 |
| QY | 6265 | CAACGCCGTTTGACTACAACTATGACCAAGCTTCCGCGTGACAGATGCGAGCTGT | 6324 | | 7372 | GCACCTTAGTAGCAGCAACGTCATGCTTTTAAATCTCTATATGTTCAAAAAACAACCC | 7431 |
| Db | 6292 | CAACGCCGTTTGACTACAACTATGACCAAGCTTCCGCGTGACAGATGCGAGCTGT | 6351 | | 7405 | CATCAGCAACTCCAGGACATCAAGTGCTTTCATGACAGATGTTAACAGCTGGCTGCTAC | 7464 |
| QY | 6325 | GATCAAGGAGACCCCACTGCCATTTGATCTCTATCGCTATGATGATGTCTCAGGCAAGAC | 6384 | | 7432 | CATCAGCAACTCCAGGACATCAAGTGCTTTCATGACAGATGTTAACAGCTGGCTGCTAC | 7491 |
| Db | 6352 | GATCAAGGAGACCCCACTGCCATTTGATCTCTATCGCTATGATGATGTCTCAGGCAAGAC | 6411 | | 7465 | CTTTGGATTCAGCTACCAACGTCATCCCTGCTTATCCAAACCCAGACATGATGCCAT | 7524 |
| QY | 6385 | AGAGCAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATTAACAGATCATCACACAGC | 6444 | | 7492 | CTTTGGATTCAGCTACCAACGTCATCCCTGCTTATCCAAACCCAGACATGATGCCAT | 7551 |
| Db | 6412 | AGAGCAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATTAACAGATCATCACACAGC | 6471 | | 7525 | GGAAACCTCTCAGAGCTCATCCACACACAGATGAAACCGCAGGAGTGGGACAAACAGCA | 7583 |
| QY | 6445 | TGTCATGACCCACACCAAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT | 6504 | | 7552 | GGAAACCTCTCAGAGCTCATCCACACACAGATGAAACCGCAGGAGTGGGACAAACAGCA | 7611 |
| Db | 6472 | TGTCATGACCCACACCAAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT | 6531 | | 7584 | -----AGTCTATCTCGGGGTACAGTGTGAAGTACAGAGCA | 7620 |
| QY | 6505 | GATCTTCCGCTCGCTCATGTAAGTGGATGACCGTCCAGTATGATAAATGAGGGGAGTAGT | 6564 | | 7612 | GGTAAATCTCGCAAGGCTGCCAGTCTATCTCGGGGTACAGTGTGAAGTACAGAGCA | 7671 |
| Db | 6532 | GATCTTCCGCTCGCTCATGTAAGTGGATGACCGTCCAGTATGATAAATGAGGGGAGTAGT | 6591 | | 7621 | GCTCAAGGCTTTGTACCTTAGACCTTACAGCTTATGAGCTTATGCTTCCACATCACCAG | 7680 |
| QY | 6565 | GAAAGAGGAGCTGAAGGTAGGACCCCTAGCCCAATACCACTCGTACTCTCTATGATGATGA | 6624 | | 7672 | GCTCAAGGCTTTGTACCTTAGACCTTACAGCTTATGAGCTTATGCTTCCACATCACCAG | 7731 |
| Db | 6592 | GAAGAGGAGCTGAAGGTAGGACCCCTAGCCCAATACCACTCGTACTCTCTATGATGATGA | 6651 | | 7681 | CTGCCAGAGGCTTCAAAGACCAAGAAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG | 7740 |
| QY | 6625 | TGTCAGGCGCAGCTGACAGACAGTCTCCATCAATGACAGCCACTCTGGGGCTACAGCTA | 6684 | | 7732 | CTGCCAGAGGCTTCAAAGACCAAGAAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG | 7791 |
| Db | 6652 | TGTCAGGCGCAGCTGACAGACAGTCTCCATCAATGACAGCCACTCTGGGGCTACAGCTA | 6711 | | 7741 | GGTCAAGTTTGTGTAAGGATGGCGAGTGACCAACAGACATCATCAGTGTGGCCCAATGA | 7800 |
| QY | 6685 | CGACCTCAATGGGAACTGCACTTACTGAGCCCTGGGAAACAGTGACGGCTCACACCACT | 6744 | | 7792 | GGTCAAGTTTGTGTAAGGATGGCGAGTGACCAACAGACATCATCAGTGTGGCCCAATGA | 7851 |
| Db | 6712 | CGACCTCAATGGGAACTGCACTTACTGAGCCCTGGGAAACAGTGACGGCTCACACCACT | 6771 | | 7801 | GGATGGGCGAAGGGTTGCTGCCATCTTGAAACCAATGCCACTACCTAGAGAACCTGCACCT | 7860 |
| QY | 6745 | ACGGTATGACATCCGGACCGCATCACTCGGCTGGGTGACGTGCAATACAAAGATGGATGA | 6804 | | 7852 | GGATGGGCGAAGGGTTGCTGCCATCTTGAAACCAATGCCACTACCTAGAGAACCTGCACCT | 7911 |
| Db | 6772 | ACGGTATGACATCCGGACCGCATCACTCGGCTGGGTGACGTGCAATACAAAGATGGATGA | 6831 | | 7861 | CACCATTTGATGGGTGGATACCATTTACTTTGTGAAACCAAGACCTTACAGAGGTGACCT | 7920 |
| QY | 6805 | GGATGGCTTCTGAGGAGCGGGCGGTGATATCTTTGATGATCAAACTCAGCTGGCTGCT | 6864 | | 7912 | CACCATTTGATGGGTGGATACCATTTACTTTGTGAAACCAAGACCTTACAGAGGTGACCT | 7971 |
| Db | 6832 | GGATGGCTTCTGAGGAGCGGGCGGTGATATCTTTGATGATCAAACTCAGCTGGCTGCT | 6891 | | 7921 | GGCCATCTCGGGCTCAGTGGGGGCGGCAACCTTGGAGAAATGGGGTCAACGTCATGCT | 7980 |
| QY | 6865 | CATCAAGGCTTCAACCGGCTGGCAGCTGAGTGTGAGTACCGCTACCATGGCTGGG | 6924 | | 7972 | GGCCATCTCGGGCTCAGTGGGGGCGGCAACCTTGGAGAAATGGGGTCAACGTCATGCT | 8031 |
| Db | 6892 | CATCAAGGCTTCAACCGGCTGGCAGCTGAGTGTGAGTACCGCTACCATGGCTGGG | 6951 | | 7981 | GTCCAGATCAACACAGTACTTAAATGGCAGGACTAGACGCTACACAGATCCAGGTCCA | 8040 |
| QY | 6925 | CGCGGGGTGTCCAGCAAGAGAGCCACAGCCACCACTCGAGTTCTTCTATGACAGCT | 6984 | | 8032 | GTCCAGATCAACACAGTACTTAAATGGCAGGACTAGACGCTACACAGATCCAGGTCCA | 8091 |
| Db | 6952 | CGCGGGGTGTCCAGCAAGAGAGCCACAGCCACCACTCGAGTTCTTCTATGACAGCT | 7011 | | 8041 | GTACGGGGCAGCTGTGCTTGAACACACGCTACGGGCAACCTTGGATGAGGAGAGGCAGC | 8100 |
| QY | 6985 | GACCAACCCCAAGGTCAACCACTGTATCAACCACTCCAGCTCTGAGATACCTCCCT | 7044 | | 8092 | GTACGGGGCAGCTGTGCTTGAACACACGCTACGGGCAACCTTGGATGAGGAGAGGCAGC | 8151 |
| Db | 7012 | GACCAACCCCAAGGTCAACCACTGTATCAACCACTCCAGCTCTGAGATACCTCCCT | 7071 | | 8101 | GGTCTTGGAGCTGGCCCGGCGAGAGCCGTGGCCCAAGCGTGGGGCCCGGCGAGCAGAG | 8160 |
| QY | 7045 | CTACTACGACTTGCAGGACACCTCTTTGGCATGGAGCTGAGCAGTGGTATGAGTTTAA | 7104 | | | | |

| | | | | | | | |
|----|------|--|------|----|------|---|------|
| QY | 5575 | ACGCACAGAGAGATCTATGATGACCAACCGCAAGTTTCAACCTTCGGATTCTGTACGACCA | 5634 | QY | 6655 | CAATGACAAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCATCTACTGAG | 6714 |
| DB | 1081 | ACGCACAGAGAGATCTATGATGACCAACCGCAAGTTTCAACCTTCGGATTCTGTACGACCA | 1140 | DB | 2161 | CAATGACAAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCATCTACTGAG | 2220 |
| QY | 5635 | GGCGGGCGGCGCCAGCCTCTGGTCAACCCAGCAGCGCTGAATGGTGAACGTGACATA | 5694 | QY | 6715 | CCCTGGGAACAGTGCACGGCTCACACCTACGGTATGACATCCGGACCGCATCACTCG | 6774 |
| DB | 1141 | GGCGGGCGGCGCCAGCCTCTGGTCAACCCAGCAGCGCTGAATGGTGAACGTGACATA | 1200 | DB | 2221 | CCCTGGGAACAGTGCACGGCTCACACCTACGGTATGACATCCGGACCGCATCACTCG | 2280 |
| QY | 5695 | CTCCCTGGGGTTACATTTGCTGGCATCCAGAGGGGCATCATGCTCTGAAAGAAATGAATA | 5754 | QY | 6775 | GCTGGTGAAGTGCATAAAGATGGATGGATGGCTTTCTTGAGGACAGCGGGCGGTGA | 6834 |
| DB | 1201 | CTCCCTGGGGTTACATTTGCTGGCATCCAGAGGGGCATCATGCTCTGAAAGAAATGAATA | 1260 | DB | 2281 | GCTGGTGAAGTGCATAAAGATGGATGGATGGCTTTCTTGAGGACAGCGGGCGGTGA | 2340 |
| QY | 5755 | CGACACGGCGGCGGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGAGAGCTACAC | 5814 | QY | 6835 | TATCTTTGAGTAAACACTAGCTGGCTGTCTATCAAGGGCTTAAACCGGGCTGGCAGCTG | 6894 |
| DB | 1261 | CGACACGGCGGCGGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGAGAGCTACAC | 1320 | DB | 2341 | TATCTTTGAGTAAACACTAGCTGGCTGTCTATCAAGGGCTTAAACCGGGCTGGCAGCTG | 2400 |
| QY | 5815 | ATATTTAGAGAACTCCATGGTGTCTTACTATACAGCCAGAGGACGATATCTTTGAGTT | 5874 | QY | 6895 | GAGTGTACAGTACCGCTACGATGGCTGGGGCGGCGGTGTCAGCAAGAGACGACACAG | 6954 |
| DB | 1321 | ATATTTAGAGAACTCCATGGTGTCTTACTATACAGCCAGAGGACGATATCTTTGAGTT | 1380 | DB | 2401 | GAGTGTACAGTACCGCTACGATGGCTGGGGCGGCGGTGTCAGCAAGAGACGACACAG | 2460 |
| QY | 5875 | CGACAAGATGACCGCTCTCTTCTGTGACGATGCCAAGCTGGCGGGCGAGACACTAGA | 5934 | QY | 6955 | CCACCACTGTCAGTTCTTCTATGTCAGACCTGACCAACCCCAAGGTCAACCACCTGTA | 7014 |
| DB | 1381 | CGACAAGATGACCGCTCTCTTCTGTGACGATGCCAAGCTGGCGGGCGAGACACTAGA | 1440 | DB | 2461 | CCACCACTGTCAGTTCTTCTATGTCAGACCTGACCAACCCCAAGGTCAACCACCTGTA | 2520 |
| QY | 5935 | GACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCTTGAGGGCAATGCCTC | 5994 | QY | 7015 | CAACCACTCCAGCTCTGAGATCACCTCTCTACTACGACTTGCAGAGACACCTCTTTGC | 7074 |
| DB | 1441 | GACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCTTGAGGGCAATGCCTC | 1500 | DB | 2521 | CAACCACTCCAGCTCTGAGATCACCTCTCTACTACGACTTGCAGAGACACCTCTTTGC | 2580 |
| QY | 5995 | AGTCATACAGGACTTCACTGAGGATGGGCACTCTTTCACACCTTCTACCTGGGCACTGG | 6054 | QY | 7075 | CATGGAGCTGAGCAGTGGTGTGATGATCAAGCAAAATCCTGTACACAGCTTATGGGGA | 7134 |
| DB | 1501 | AGTCATACAGGACTTCACTGAGGATGGGCACTCTTTCACACCTTCTACCTGGGCACTGG | 1560 | DB | 2581 | CATGGAGCTGAGCAGTGGTGTGATGATCAAGCAAAATCCTGTACACAGCTTATGGGGA | 2640 |
| QY | 6055 | CCGAGGGTGATATACAAAGTATGGCAAACTGTCAAAGCTGGCAGAGCGCTCTATGACAC | 6114 | QY | 7135 | TGCTGTCTTTAGTGGAAACAGGTTTGTATGATCAAGCAAAATCCTGTACACAGCTTATGGGGA | 7194 |
| DB | 1561 | CCGAGGGTGATATACAAAGTATGGCAAACTGTCAAAGCTGGCAGAGCGCTCTATGACAC | 1620 | DB | 2641 | TGCTGTCTTTAGTGGAAACAGGTTTGTATGATCAAGCAAAATCCTGTACACAGCTTATGGGGA | 2700 |
| QY | 6115 | CACCAAGTTCAGTTTCACTATGACGAGCGGAGGATGCTGAAGACCATCAACCTTACA | 6174 | QY | 7195 | GATCTACATGGATAPACAAACCCCAACTTTTTCAGATCATATAGGCTACCATGGTGGCTCTA | 7254 |
| DB | 1621 | CACCAAGTTCAGTTTCACTATGACGAGCGGAGGATGCTGAAGACCATCAACCTTACA | 1680 | DB | 2701 | GATCTACATGGATAPACAAACCCCAACTTTTTCAGATCATATAGGCTACCATGGTGGCTCTA | 2760 |
| QY | 6175 | GAATGAGGGCTTCACTGACACCATCCGCTACCGTCAAGATTGGGCCCCCTGATTGACCGACA | 6234 | QY | 7255 | TGATTCACCTACCAAGCTTGTCCACATGGCGCGGAGATTATGATGCTGCGCCGAGCG | 7314 |
| DB | 1681 | GAATGAGGGCTTCACTGACACCATCCGCTACCGTCAAGATTGGGCCCCCTGATTGACCGACA | 1740 | DB | 2761 | TGATTCACCTACCAAGCTTGTCCACATGGCGCGGAGATTATGATGCTGCGCCGAGCG | 2820 |
| QY | 6235 | GATCTTCCGCTTCACTGAGGAAGGATGGTCAACGCCGCTTTTGAATAAATATGACAA | 6294 | QY | 7315 | CTGAGCTAGCCACAGACACAGAGCTGTGGAAAGCACTTATAGTAGCAGCAACCTCATGCTTT | 7374 |
| DB | 1741 | GATCTTCCGCTTCACTGAGGAAGGATGGTCAACGCCGCTTTTGAATAAATATGACAA | 1800 | DB | 2821 | CTGAGCTAGCCACAGACACAGAGCTGTGGAAAGCACTTATAGTAGCAGCAACCTCATGCTTT | 2880 |
| QY | 6295 | CAGCTTCCGGGTGACAGCATGAGGCTGTGATCAACGAGACCCCACTGCCATTTGATCT | 6354 | QY | 7375 | TATCTCTATATGTTCAAAAAACAAACCCCATCAGCAACTCCAGAGCATCAAGTGCTT | 7434 |
| DB | 1801 | CAGCTTCCGGGTGACAGCATGAGGCTGTGATCAACGAGACCCCACTGCCATTTGATCT | 1860 | DB | 2881 | TATCTCTATATGTTCAAAAAACAAACCCCATCAGCAACTCCAGAGCATCAAGTGCTT | 2940 |
| QY | 6355 | CTATCGCTATGATGATGTGTGAGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAITTA | 6414 | QY | 7435 | CATGACAGATGTTAAACAGCTGGCTGTCACTTTGGATTCCAGCTACACAACCTGATCCC | 7494 |
| DB | 1861 | CTATCGCTATGATGATGTGTGAGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAITTA | 1920 | DB | 2941 | CATGACAGATGTTAAACAGCTGGCTGTCACTTTGGATTCCAGCTACACAACCTGATCCC | 3000 |
| QY | 6415 | CTATGACATTAACAGATATATACCAACAGTGTATGACCCACCAAGCAITTTTGTATGC | 6474 | QY | 7495 | TGGTTATCCCAACACAGACATGATGATCCATGGAAACCTCTCTACAGCTCATCCACACACA | 7554 |
| DB | 1921 | CTATGACATTAACAGATATATACCAACAGTGTATGACCCACCAAGCAITTTTGTATGC | 1980 | DB | 3001 | TGGTTATCCCAACACAGACATGATGATCCATGGAAACCTCTCTACAGCTCATCCACACACA | 3060 |
| QY | 6475 | ATATGGCAGATGAGGAAGTGCAGATGATGATCTCCGCTCGCTCATGTACTGGATGAC | 6534 | QY | 7555 | GATGAAAAACGAGAGTGGGACAAACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTACA | 7614 |
| DB | 1981 | ATATGGCAGATGAGGAAGTGCAGATGATGATCTCCGCTCGCTCATGTACTGGATGAC | 2040 | DB | 3061 | GATGAAAAACGAGAGTGGGACAAACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTACA | 3120 |
| QY | 6535 | CGTCCAGTATGATAACATGGGGCGAGTAGTGAGAGAGGAGCTGAGGTAGGACCTTACGC | 6594 | QY | 7615 | GAAGAGCTCAAGGCTTTGTGACCTTTAGAACCGTTTGACAGCTCTATGGCTCCACAAT | 7674 |
| DB | 2041 | CGTCCAGTATGATAACATGGGGCGAGTAGTGAGAGAGGAGCTGAGGTAGGACCTTACGC | 2100 | DB | 3121 | GAAGAGCTCAAGGCTTTGTGACCTTTAGAACCGTTTGACAGCTCTATGGCTCCACAAT | 3180 |
| QY | 6595 | CAATACCACTCGCTACTCTCTATGATGATGATGCTGAGCGGCGAGCTGCAGACAGTCTCCAT | 6654 | QY | 7675 | CACCACTCCAGCAGGCTCCAAAGACCAAGAGTTTGTATCCAGGGCTCAGTCTTTGG | 7734 |
| DB | 2101 | CAATACCACTCGCTACTCTCTATGATGATGATGCTGAGCGGCGAGCTGCAGACAGTCTCCAT | 2160 | DB | 3181 | CACCACTCCAGCAGGCTCCAAAGACCAAGAGTTTGTATCCAGGGCTCAGTCTTTGG | 3240 |
| | | | | QY | 7735 | CAAGGGGCTCAAGTTTTCCTTGAAGGATGGCGGAGTGCACACAGACATCATAGTGTGGC | 7794 |

Db 3241 CAAGGGGCTCAAGTTTGCTTTGAAGATGGCCGAGTGACACAGACATCATCAGTGTGGC 3300
Qy 7795 CAATGAGATGGCGCAAGGGTTGCTGCCATCTTGAACCATGCCACTACCTAGAGAACCT 7854
Db 3301 CAATGAGATGGCGCAAGGGTTGCTGCCATCTTGAACCATGCCACTACCTAGAGAACCT 3360
Qy 7855 GCACCTTACCATGTATGGGTGGATACCATCTTGTGTAACCCAGGACCTTCAGAGG 7914
Db 3361 GCACCTTACCATGTATGGGTGGATACCATCTTGTGTAACCCAGGACCTTCAGAGG 3420
Qy 7915 TGACCTGGCCATCTCGGCGCTCAGTGGGGGGCGGCAACCCCTGGAGAAATGGGTCACGT 7974
Db 3421 TGACCTGGCCATCTCGGCGCTCAGTGGGGGGCGGCAACCCCTGGAGAAATGGGTCACGT 3480
Qy 7975 CACTGTGTCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGATCCA 8034
Db 3481 CACTGTGTCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGATCCA 3540
Qy 8035 GCTCCAGTACGGGGCACTGTGCTTGAACACACAGCTACGGGACAACTTTGGATGAGGAA 8094
Db 3541 GCTCCAGTACGGGGCACTGTGCTTGAACACACAGCTACGGGACAACTTTGGATGAGGAA 3600
Qy 8095 GGCACGGGTCTGGAGCTGGCCCGCAGAGAGCCGTGCGCCCAAGCGTGGGCCCCGCGAGCA 8154
Db 3601 GGCACGGGTCTGGAGCTGGCCCGCAGAGAGCCGTGCGCCCAAGCGTGGGCCCCGCGAGCA 3660
Qy 8155 GCAGAGACTGGCGAAGGGGAGGAGCGCTGGGGCCCTGGACAGAGGGGGAGAGCAGCA 8214
Db 3661 GCAGAGACTGGCGAAGGGGAGGAGCGCTGGGGCCCTGGACAGAGGGGGAGAGCAGCA 3720
Qy 8215 GGTGCTGAGCACAGGGCGGGTGCAAGGCTACGAGCGCTTTTTCGTGATCTCTGTGAGCA 8274
Db 3721 GGTGCTGAGCACAGGGCGGGTGCAAGGCTACGAGCGCTTTTTCGTGATCTCTGTGAGCA 3780
Qy 8275 GTACCCAGAACTGTGACAGAGCGGCCCAACACATCCACTTCATGACAGAGCGAGATGGG 8334
Db 3781 GTACCCAGAACTGTGACAGAGCGGCCCAACACATCCACTTCATGACAGAGCGAGATGGG 3840
Qy 8335 CCGGAGGTGACAGAGAGGAC 8354
Db 3841 CCGGAGGTGACAGAGAGGAC 3860

RESULT 7
ADQ24356
ID ADQ24356 standard; DNA; 8774 BP.

AC ADQ24356;

DT 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 7176.

DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW ds.

XX Homo sapiens.

OS WO2004048938-A2.

XX 10-JUN-2004.

PF 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/41.

XX

PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.

PS Example 2; SEQ ID NO 7176; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytosatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 8774 BP; 2210 A; 2279 C; 2190 G; 2060 T; 0 U; 35 Other;

Query Match 43.4%; Score 3621.6; DB 12; Length 8774;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 3758; Conservative 0; Mismatches 14; Indels 88; Gaps 4;

Qy 4578 GTAAAAATGATGCCCACTGTGATTTCTTGAGACGATGGTTATGCCAAGATGCAA 4637

Db 1 GTAAAAATGATGCCCACTGTGATTTCTTGAGACGATGGTTATGCCAAGATGCAA 60

Qy 4638 AGTTAAATACCCATCTTCTTGGCTGTGTGCTGATGGGAGCTCTACGTGCGCCGACC 4697

Db 61 AGTTAAATACCCATCTTCTTGGCTGTGTGCTGATGGGAGCTCTACGTGCGCCGACC 120

Qy 4698 TTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAGCCTTTCCTCAACACCCAGAAC 4757

Db 121 TTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAGCCTTTCCTCAACACCCAGAAC 180

Qy 4758 TGTATGAGCTGTCTTACCAATTTGACCCAGGAGCTCTATCTGTTTGATACCCAGCGCAGC 4817

Db 181 TGTATGAGCTGTCTTACCAATTTGACCCAGGAGCTCTATCTGTTTGATACCCAGCGCAGC 240

Qy 4818 ACCTGTACACCCAAAGCTGCCACAGGAGACTACCTGTACAACTTCACCTACACTGCGG 4877

Db 241 ACCTGTACACCCAAAGCTGCCACAGGAGACTACCTGTACAACTTCACCTACACTGCGG 300

Qy 4878 ACGCGACATCACACTCATCACAGAACAAATGGCAACATGGTAAATGTCGCGCGAGACT 4937

Db 301 ACGCGACATCACACTCATCACAGAACAAATGGCAACATGGTAAATGTCGCGCGAGACT 360

Qy 4938 CTACTGGGATGCCCTCTGGCTGGTCCAGATGGCCAGGTGCTACTGGGTGACCATGG 4997

Db 361 CTACTGGGATGCCCTCTGGCTGGTCCAGATGGCCAGGTGCTACTGGGTGACCATGG 420

Qy 4998 GCACCAACAGTGCCTCAAGAGTGTGACCAACAGGACACGAGTGGCCATGATGACAT 5057

Db 421 GCACCAACAGTGCCTCAAGAGTGTGACCAACAGGACACGAGTGGCCATGATGACAT 480

Qy 5058 ACCATGGCAATTCGGGCTCTTGTGCAACCAAAAGCAATGAAAACGGATGGCAACATTTT 5117

Db 481 ACCATGGCAATTCGGGCTCTTGTGCAACCAAAAGCAATGAAAACGGATGGCAACATTTT 540

Qy 5118 ATGA----- 5121

Db 541 ATGCAACCTCAGATGGCAGGAATTATCATCCATTTTTTACATATGAAAGTACAGAGAG 600

Qy 5122 -----GTACGACAGCTTTGGCCGCTTGACAAATGTGAC 5154

Db 601 ATTAGATAACAGCCTGAAACACACCGTACGACAGCTTTGGCCGCTTGACAAATGTGAC 660

Qy 5155 CTTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTCAAGTGCATGTCCA 5214

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| | | | |
|----|------|--|------|
| Db | 661 | CTTCCCTACTGCGCAGGTGAGCAGTTTCCGAAAGTGATACAGACAGTTTCAGTGCATGTCCA | 720 |
| Qy | 5215 | GGTAGAGACCTCAGCAAGATGATGTACCAATTAACCAACCAACCTGTCTGCCTCAGGCGC | 5274 |
| Db | 721 | GGTAGAGACCTCAGCAAGATGATGTACCAATTAACCAACCAACCTGTCTGCCTCAGGCGC | 780 |
| Qy | 5275 | CTTCTACACACTGCTCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCGATGGCTC | 5334 |
| Db | 781 | CTTCTACACACTGCTCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCGATGGCTC | 840 |
| Qy | 5335 | CTTGGGCTGCTGCTGGCCAAACGGCATGAGGTGGCGCTGCGAGACTGAGCCCCACCTGTCT | 5394 |
| Db | 841 | CTTGGGCTGCTGCTGGCCAAACGGCATGAGGTGGCGCTGCGAGACTGAGCCCCACCTGTCT | 900 |
| Qy | 5395 | GGCTGGCAACCTCAACCCACCGTGGGCAAGAGGATGTCAACGCTGCCCATCGACAACGG | 5454 |
| Db | 901 | GGCTGGCAACCTCAACCCACCGTGGGCAAGAGGATGTCAACGCTGCCCATCGACAACGG | 960 |
| Qy | 5455 | CCTCAACCTGGTGGAGTGGCGCCAGCGCAAGAGCAGGCTCGGGGCGCAGGTCACTGTCTT | 5514 |
| Db | 961 | CCTCAACCTGGTGGAGTGGCGCCAGCGCAAGAGCAGGCTCGGGGCGCAGGTCACTGTCTT | 1020 |
| Qy | 5515 | TGGGCGCGGCTGCGGGTGCACAACCGAAATCTCTATCTCTGGACTTTGATCGCGTAAC | 5574 |
| Db | 1021 | TGGGCGCGGCTGCGGGTGCACAACCGAAATCTCTATCTCTGGACTTTGATCGCGTAAC | 1080 |
| Qy | 5575 | AGCAACAGAGATCTATGATGACCAACCGAAAGTTCAACCTTCGGATTTCTGTACACCA | 5634 |
| Db | 1081 | AGCAACAGAGATCTATGATGACCAACCGAAAGTTCAACCTTCGGATTTCTGTACACCA | 1140 |
| Qy | 5635 | GGCGGGCGCGCAGGCTCTGTGTCACCCAGCAGCGCTGAATGTCAACGTGACATA | 5694 |
| Db | 1141 | GGCGGGCGCGCAGGCTCTGTGTCACCCAGCAGCGCTGAATGTCAACCGACATA | 1200 |
| Qy | 5695 | CTCCCTGGGGTTACATTTGCTGGCATCCAGAGGGCATCATCTCTGAAAGAAATGGAATA | 5754 |
| Db | 1201 | CTCCCTGGGGTTACATTTGCTGGCATCCAGAGGGCATCATCTCTGAAAGAAATGGAATA | 1260 |
| Qy | 5755 | CGACAGGGGGCGCATCAATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACAC | 5814 |
| Db | 1261 | CGACAGGGGGCGCATCAATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACAC | 1320 |
| Qy | 5815 | ATACTTAGAAGTCCATGGTGTCTACTACACGCGCAGGACGATATCTTTGAGTT | 5874 |
| Db | 1321 | ATACTTAGAAGTCCATGGTGTCTACTACACGCGCAGGACGATATCTTTGAGTT | 1380 |
| Qy | 5875 | CGACAAGATGACCGCTCTCTTCTGTGACGATGCCAACAGTGGCGCGGACACACTAGA | 5934 |
| Db | 1381 | CGACAAGATGACCGCTCTCTTCTGTGACGATGCCAACAGTGGCGCGGACACACTAGA | 1440 |
| Qy | 5935 | GACCATCCGCTCAGTGGGCTACTACAGAAACATCTATACGCCCTTGAGGGCAATGCCTC | 5994 |
| Db | 1441 | GACCATCCGCTCAGTGGGCTACTACAGAAACATCTATACGCCCTTGAGGGCAATGCCTC | 1500 |
| Qy | 5995 | AGTCATACAGGACTTCACTGAGATGGGCACTCTCTTACACCTTCTACTCGGGCACTGG | 6054 |
| Db | 1501 | AGTCATACAGGACTTCACTGAGATGGGCACTCTCTTACACCTTCTACTCGGGCACTGG | 1560 |
| Qy | 6055 | CCGAGGGTGATATACAAGTATGGCAACTGTCAAGCTGGCAGAGACGCTCTATGACAC | 6114 |
| Db | 1561 | CCGAGGGTGATATACAAGTATGGCAACTGTCAAGCTGGCAGAGACGCTCTATGACAC | 1620 |
| Qy | 6115 | CACCAAGGTGAGTTTCACTTATGACGAGCGGAGGATGCTGAAGACCAATCAACCTTACA | 6174 |
| Db | 1621 | CACCAAGGTGAGTTTCACTTATGACGAGCGGAGGATGCTGAAGACCAATCAACCTTACA | 1680 |
| Qy | 6175 | GAATGAGGGCTTCACTGACACCATCCGCTACCGTCAGATTGGGCGGCTGATTCACCGACA | 6234 |
| Db | 1681 | GAATGAGGGCTTCACTGACACCATCCGCTACCGTCAGATTGGGCGGCTGATTCACCGACA | 1739 |
| Qy | 6235 | GATCTTCGCTTCACTGAGGAGGATGTCACGCGCGGTTTGGACTTACAACTATGACAA | 6294 |
| Db | 1740 | GATCTTCGCTTCACTGAGGAGGATGTCACGCGCGGTTTGGACTTACAACTATGACAA | 1795 |
| Qy | 6295 | CAGCTTCCGGGTGACAGCATGCGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCT | 6354 |
| Db | 1796 | CCAGCTCCGGGTGACAGCATGCGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCT | 1855 |
| Qy | 6355 | CTATCGCTATGATGATGTGTAGGCAAGACAGAGCAGTTTGGAGAGTTTGGTGTCAATTA | 6414 |
| Db | 1856 | CTATCGCTATGATGATGTGTAGGCAAGACAGAGCAGTTTGGAGAGTTTGGTGTCAATTA | 1915 |
| Qy | 6415 | CTATGACATTAACACAGATCATCACACAGCTGTGATGACCCACACCAACCAATTTTGATGC | 6474 |
| Db | 1916 | CTATGACATTAACACAGATCATCACACAGCTGTGATGACCCACACCAACCAATTTTGATGC | 1975 |
| Qy | 6475 | ATATGGCAGGATGAAGAGAGTGCAGTATGAGATCTTTCGCTCGCTCATGTACTCTGGATGAC | 6534 |
| Db | 1976 | ATATGGCAGGATGAAGAGAGTGCAGTATGAGATCTTTCGCTCGCTCATGTACTCTGGATGAC | 2035 |
| Qy | 6535 | CGTCAGATGATATAACATGGGGCGAGTGTGAAGAAGAGCTGAAGGTAGGACCCCTACGC | 6594 |
| Db | 2036 | CGTCAGATGATATAACATGGGGCGAGTGTGAAGAAGAGCTGAAGGTAGGACCCCTACGC | 2095 |
| Qy | 6595 | CAATACCACTCGCTACTCTCTATGAGTATGATCTGACGGCCAGCTGCAGACAGTCTCCAT | 6654 |
| Db | 2096 | CAATACCACTCGCTACTCTCTATGAGTATGATCTGACGGCCAGCTGCAGACAGTCTCCAT | 2155 |
| Qy | 6655 | CAATGACAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACTCTGCACCTTACTGAG | 6714 |
| Db | 2156 | CAATGACAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACTCTGCACCTTACTGAG | 2215 |
| Qy | 6715 | CCCTGGGAAACAGTGCACGGCTCACACCTACGGTATGATATCCGGGACCGCATCTCTCG | 6774 |
| Db | 2216 | CCCTGGGAAACAGTGCACGGCTCACACCTACGGTATGATATCCGGGACCGCATCTCTCG | 2275 |
| Qy | 6775 | GCTGGTGAAGTGAATACAAAGATGAGATGGCTTCTTCTGAGCAGCGGGCGGTGA | 6834 |
| Db | 2276 | GCTGGTGAAGTGAATACAAAGATGAGATGGCTTCTTCTGAGCAGCGGGCGGTGA | 2335 |
| Qy | 6835 | TATCTTTGAGTACAACCTCAGCTGGCTGTCTCATCAAGGCTTACAAACGGGCTGGCAGCTG | 6894 |
| Db | 2336 | TATCTTTGAGTACAACCTCAGCTGGCTGTCTCATCAAGGCTTACAAACGGGCTGGCAGCTG | 2395 |
| Qy | 6895 | GAGTGTGAGTACCGCTACGATGGCTGGGGCGGCGGTGTCCAGCAAGACAGCAGCAG | 6954 |
| Db | 2396 | GAGTGTGAGTACCGCTACGATGGCTGGGGCGGCGGTGTCCAGCAAGACAGCAGCAG | 2455 |
| Qy | 6955 | CCACCACTTGCAGTTCTTCTATGACAGCTGACCAACCCCAACCAAGGTCAACCACTGTA | 7014 |
| Db | 2456 | CCACCACTTGCAGTTCTTCTATGACAGCTGACCAACCCCAACCAAGGTCAACCACTGTA | 2515 |
| Qy | 7015 | CAACCACTCCAGCTCGAGATCAACCTTCTTACTAGACTTTCGAAGGACACCTCTTTGTC | 7074 |
| Db | 2516 | CAACCACTCCAGCTCGAGATCAACCTTCTTACTAGACTTTCGAAGGACACCTCTTTGTC | 2575 |
| Qy | 7075 | CATGAGCTGAGCAGTGGTGTGATGATTTTATACATGCTTTGTGACCAACATCGGACCCCTCT | 7134 |
| Db | 2576 | CATGAGCTGAGCAGTGGTGTGATGATTTTATACATGCTTTGTGACCAACATCGGACCCCTCT | 2635 |
| Qy | 7135 | TGCTGTCTTTAGTGGAAACAGTTTGTATGATCAAGCAAAATCTCTGTACACAGCTTATGGGA | 7194 |
| Db | 2636 | TGCTGTCTTTAGTGGAAACAGTTTGTATGATCAAGCAAAATCTCTGTACACAGCTTATGGGA | 2695 |
| Qy | 7195 | GATCTACATGGATACCAACCCCAACCTTTCAGATCATCATAGGCTTACCATGGTGGCTCTTA | 7254 |
| Db | 2696 | GATCTACATGGATACCAACCCCAACCTTTCAGATCATCATAGGCTTACCATGGTGGCTCTTA | 2755 |
| Qy | 7255 | TGATCCACTCACCAAGCTTGTCCACATGGGCGGCGAGATTTATGATGTGTGCGCGGACG | 7314 |
| Db | 2756 | TGATCCACTCACCAAGCTTGTCCACATGGGCGGCGAGATTTATGATGTGTGCGCGGACG | 2815 |
| Qy | 7315 | CTGAGCTAGCCACAGACCGAGCTGTGGAAAGCACTTATGATGAGCAACGTCATGCGCTTT | 7374 |
| Db | 2816 | CTGAGCTAGCCACAGACCGAGCTGTGGAAAGCACTTATGATGAGCAACGTCATGCGCTTT | 2875 |

| | | | |
|----|-----|--|--|
| XX | SQ | Sequence | 8964 BP; 2391 A; 2261 C; 2321 G; 1991 T; 0 U; 0 Other; |
| | | Query Match | 42.4%; Score 3544.6; DB 12; Length 8964; |
| | | Beet Local Similarity | 65.6%; Pred. No. 0; |
| | | Matches 5458; Conservative | 0; Mismatches 2679; Indels 186; Gaps 12; |
| Qy | 35 | ATGACCTGAAGGAGAGAAAGCCTTACCGCTCGCTGACCCGGCGC---- | CGCGACCGCGAG 91 |
| Db | 50 | ATGGATGTGAAGAAACGCGAGCCTTACTGCTCTTGACCAAGAGCAGACGGGAAAGGAA | 109 |
| Qy | 92 | CGCGCTACACCACTGTCGCGGACAGCGAGGAGGCAAGGCC---- | CGCAGAAATCG 148 |
| Db | 110 | AGGCGCTATACAAATTCGTGCGCGGACAAATGAGAGGTGAGGGTCCCGCACGAGAATGCC | 169 |
| Qy | 149 | TACAGCTCCACGCGAGACCTCAAGCGCTTACGACACAGG---- | ACGCCCGCTAGCCTATGGC 205 |
| Db | 170 | TATAGTTCAGTGAAACCTTGAAAGCTTTCGATCATGATATTTACCGGCTGTTTATGGA | 229 |
| Qy | 206 | AGCGCGTCAAGGACATTTGTGCCGAGAGGCGAGGAATTTCTGCCGCACAGGTGCCAAC | 265 |
| Db | 230 | AACAGAGTAAAGGATTTGGTCCACAGAGAAACCGACGAGTATCTAGACAAAGGACAGAT | 289 |
| Qy | 266 | TTCAACCTGCGGGAGCTGGGCTGGAAGAATAACGCCCCCTCACGGGACCTGTACGGG | 325 |
| Db | 290 | TTTACCCTTAAGCGAGTTAGGAGTGTGGAATCCGCAACTCTCGAAGAGGAGTGGCAATCTGT | 349 |
| Qy | 326 | ACAGACATTTGGCTGCCCAATGCGGTACTCTCCATGGGGCTGGCTCTGATCGCGACATG | 385 |
| Db | 350 | CGGAAATTTGGGCTCCCTTCACAGAGGTTACTTCCATCATGTGAGGGGTGATGTGCGGATCG | 409 |
| Qy | 386 | GAGGCTGACACGGTGCTGCCCTGAGCACCCCGCTGCGTCTGTGGGGCGGAGCACACGG | 445 |
| Db | 410 | GAAACGAAGCAGTGATGTCCCTGAGCATGCCATGAGACTTTTGGGCGAGGGGGTCAAA | 469 |
| Qy | 446 | TCAGGCGCAGCTCTGCTGCTCOAGCCGGGCGCAATTTCCAATCTCACTCACCGACACC | 505 |
| Db | 470 | TCGGCGCGCAGTTCTGCTGCTCAAGCGCGTCCAACCTCCGCCCTCACCCCTGACAGACG | 529 |
| Qy | 506 | GAGCATGAACACCTGAGACTGATCATCCGGCGCGCTGCAGAACCCACCGCGGCTCCGG | 565 |
| Db | 530 | GAGCACGAGAACAGGTGCGGACAGTGGAGCGAGCAACCTTCAAAACAACCCAGGGCAACCC | 589 |
| Qy | 566 | ACGCGCGCGCGCGCTCTCGCAGCGCCACACCCGCCAACACGACACCGCGGCTCCCAT | 625 |
| Db | 590 | ACCTGCGAGCTTTGGCGGCATCCACAAGCAGCACCGCGCGAGCATCACCCGCTCCATC | 649 |
| Qy | 626 | AATCCCTGAAACCGGGGCAATTCAACGCCGAGGAGCAACCCAGCCCGGCCCCCACGGAC | 685 |
| Db | 650 | ACTTCCCTCAATAGAAACTCCCTGACCAATAGAAGGAACACAGAGTCCGGCCCCCGCGCT | 709 |
| Qy | 686 | CACCTGCTCTCGGAGAGCCCTTCGCGCGCGCCGAGGAGCTTGCCACGCCCGCAGGAG | 745 |
| Db | 710 | GCTTTGCCCGCGAGCTGCAAAAC-----CACACCCGAGTCCGTCCAGCTCGGAGC | 760 |
| Qy | 746 | AATGGGCTGCTCAACAGCAACAATCCCTCGAGACCAAGGAACCTTAGGCAAGCAGCATTC | 805 |
| Db | 761 | AGCTGGGTCTTTGGCAGTAAATGTACCACTGGAAGAGGCGATTT----- | 804 |
| Qy | 806 | CTAGGGAATTGACGACAACCTCATTTGAGATGGACATTTCTCGCGCCTCCCGCCATGAT | 865 |
| Db | 805 | ----- | 804 |
| Qy | 866 | GGGGCTTACAGTGACGGGCACTTCTCTTTAAGCCTTGAGGACCTTCCCGGCTCTTTCGC | 925 |
| Db | 805 | -----CCTATTCAAAACAGGGACAGGGACGACGCCACTGTGTTTCACT | 844 |
| Qy | 926 | ACCACATCACAGGGTACCCTAGCTGACGTCAGCAGTACTCTCTCCGCCCGCACCC | 985 |
| Db | 845 | ACGGCAACCCCGGGATACAAATGGCATCTGGCTCTGTTTATTTCTCCGCTTACCGGGCA | 904 |
| Qy | 986 | CTGCCCGCGACACCTTCTCGCCGGCGCGCTTTAACTCTCAAGAAAGCCCTCCAAGTACTGT | 1045 |

QY 2126 GACAGTGTTCAGGCGACGGAACTTCTCCGGACACCGGCTTTGAGCTGTGACCCA 2185
DB 1997 GACCAAGTGTACGGCGACGGGACTTACCTTCAAGAAAGCGGTCTCGCACTTGGACCCA 2056
QY 2186 AGCTGGACTGGACAGCACTGTTCTATCAGATCTGTCTGCGGACTGTGGTGGCCATGGC 2245
DB 2057 AATTGGACTGGCCCCGACGTCTCAATGAATATATTTTCAGTGGACTCGGGCTCACACGGC 2116
QY 2246 GTGTGCGTAGGGGACCTTGCCTGCGAGATGGCTGGATGGGGGCGACCTTGGACCCAG 2305
DB 2117 GTCTCATGGGGGCTCTGTCTGCTGTGAAGAGCTGGAACGGCCCGCGTGTAAATCAG 2176
QY 2306 CGGGCTGCGACCCCGCTGTGCCAGCATGGGACCTGCCGGACGGCAAGTGTGGAGTGC 2365
DB 2177 AGAGCTTGCCACCTTCGTCTGTCTGAGCACGGGACGTGCAAGGACGGCAAGTGTGGAGTGC 2236
QY 2366 AGCCCTGGCTGGAATGGCGAACTGCACCTACCTCGCTCACTATCTGGATAGGTTAGTAAA 2425
DB 2237 AGCCAAGGATGGACGGAGAGCACTGCAAAATTTGCTCACTATTTGGATGAATAGTTAAA 2296
QY 2426 GAGGGTTCCTCGGTTGTGCAATGGCAACCGCAGATGTACTTTAGACCTGAATGGTTGG 2485
DB 2297 GAGGGTTCCTCGGCTTGTGCAACAGCAATGGAGATGCACACTGGACCAAAACGGCTGG 2356
QY 2486 CACTGCGTTCGCCAGCTGGCTGGAGAGAGTGGCTGTGACATTCATCGAGACTGCC 2545
DB 2357 CACTGCGTTTGCACGCCAGGGTGGAGAGGAGCGCTGTGACGTAGCCATGGAGACCTC 2416
QY 2546 TSCGTTGACAGCAAGACAAATGATGGAGATGGCTGTGGACTGCATGGACCTTGACTGC 2605
DB 2417 TGTACAGACAGCAAGACAAACGAGAGAGACGCACTCATTTGATCGATGATGATTCGATTGC 2476
QY 2606 TGCTTCCAGCCCCGTGCGCATATCAACCCGCTGTGCTTGGCTCCCTTAAACCTCTTGGAC 2665
DB 2477 TGCTTCCAGAGCTCTCTGCCAAACACAGCCCTACTGTCTGTGGCTTGCTGTGCTCCTCAGGAT 2536
QY 2666 ATCATCCAGGAGACAGAGTCCCTGTGTGACAGCAAGACCTTACACTCTTCTATGACCGC 2725
DB 2537 ATCATTTAGCCAAAGCTTTCAGACACCATCTCAGCAAGCTGCAAGTCTCTTATGACCGA 2596
QY 2726 ATCAAGTTCTCTGTGGGAGGACAGACGACATAATCCCGGGGAGAACCCCTTTGAT 2785
DB 2597 ATCAGTTTCTCGATTGGATCGGATAGCACCCAGCTGCTCCCTGGAGAAAGTCCGTTCAAT 2656
QY 2786 GGAGGGCATGTGTGTATTGTGTGGCCAAAGTGTATGACATCAGATGGAAACCCCTTGTT 2845
DB 2657 AAGAGTCTTGTGTCGTCATCAGAGGCCAAGTACTAACAGCTGATGGAAACCCACTTATT 2716
QY 2846 GGTGTGAACATCAGTTTGTCAATAACCTCTCTTTGGATATACATCAGCAGGCAAGAT 2905
DB 2717 GCGCTCAACGTTGCTGTTTTACACTCTCGGAATATGGATATACATTTACCGCGCAGGAT 2776
QY 2906 GGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCTCGCGTTCGAGCGGCA 2965
DB 2777 GGAATGTTTGACTTGGTGGCAAAATGGTGGCGCTTCTGTGACTTGGTATTGAGGGTTCC 2836
QY 2966 CTTTTCATCACAGGAGCACACCTGTGGTGGCCATGGATCGCTCTTTGTGATGGAA 3025
DB 2837 CCATTTCTCACTCAGTACACACTGTGTGGATTCCCTCGGAATGTCTTTATGTGTATGGAT 2896
QY 3026 ACCATCATCAGACATGAGGAGATGAGATTCACAGCTGCCAGCTGTGACCAATTTTGGC 3085
DB 2897 ACCCTTGTCTGAAGAAAGAGGAGAACGACATTTCCAGCTGTGACCTCAGTGGCTTTGTG 2956
QY 3086 CGCCCAACCAAGTGGTCTCTCCATCCCACTGACGTCTTCCAGCTCTTCCAGCTCTGTGACAG 3145
DB 2957 AGGCCAAGTCCCATCAATTGTGTCTTCACCGTTATCCACTTCTTCAGGCTCTTCCCTGAG 3016
QY 3146 AAAGCCCCCATTTGTCGGGAATTCAGGCTTTGACAGGAGGAAATCTCTATCTCTGGCTGC 3205
DB 3017 GACAGCCCCATCATCCCGGAGACAGGTCTCGATGAAAGAAACCACAATTTCCAGGAACA 3076

QY 3206 AAGATGAGGCTGAGCTACCTGAGCAGCGGACCCCTCGCTACAAATCTGTCTCTGAGGATC 3265
DB 3077 GATTGAAACTTTTCTTACCTGAGTTCCAGAGCGGCAGGGTACAAGTCAGTTCAGTTTAAAGATT 3136
QY 3266 AGCTCTACCCACCCGACATCCCTTCAAGCTCATGAAGGTGCACTCATCTGATAGCGGTG 3325
DB 3137 ACCATGACCCAGGCGGTATACCGTTTAACTCATGAAGGTCCATCTGATGTTGCCGTG 3196
QY 3326 GAGGCGCGCTCTTTCAGAAAGTGGTTCGCTGAGAGCCCGCAGACCTGTCTTATTTCAATT 3385
DB 3197 GTTGGGAGACTCTTCCAGAAAGTGGTTTCTCGCTCGCAAACTTTGGCTACACGTTTCATC 3256
QY 3386 TGGGACAGACAGACGCTTACAACCAAGSTGTTTGGGCTTTTCAGAGCCCTTTGTTTCC 3445
DB 3257 TGGGATGAAGACGGACGATATATACTAGAAAGTCTACGGCTTGTTCAGAGGCAAGTTGTGTCC 3316
QY 3446 GTGGGTTATGAATATGATCTCTGCCAGATCTTATCTCTGGGAAAGAAACCAACAGTG 3505
DB 3317 GTCGATACGAGTACGAGTCTGTCTTGGACCTGACTCTCTGGGAAAGAGGACTGCCGTT 3376
QY 3506 CTGACGGGCTATGAATTTGACGGCTCCAAGTTGGAGGATGGAGCCTTAGACAAACATCAT 3565
DB 3377 TTGCAAGGCTATGAGTTGGATGCTTTCGAACATGGGCGGCTGGACGTTTGGCAAGACCAT 3436
QY 3566 GCCCTCAACATTCAAAGTGGTATCTCTGCACAAAGGGAATGGGAGAACCAAGTTTGTGTCT 3625
DB 3437 GTACTGACGTTTCAGAACGGTATATATACAAGGAAATGGAGAAATTCAGTTTCATCTCT 3496
QY 3626 CAGCAGCCTCTCTGTTCATTGGGAGCATATGGGCAATGGGCGCCGGAGAGCATCTCTGC 3685
DB 3497 CAGCAGCCTCGGTGGTCAGCAGCATCATGGTAAATGCTCGGAGCGTAGCATCTCATGC 3556
QY 3686 CCAGCTGCAACCGGCTTGTGACGGCAACAGCTCTCGGCCCGCAGTGGCCCTCACCTGT 3745
DB 3557 CCAAGTTTGCATGGTCAAGCTGACGGGAAACAACTCTCGGCACCCGCTTGGCCTGT 3616
QY 3746 GGCTCTCAGCGGAGCCTTATGTGGGTGATTTCAACTACATTAAGAAGCATCTTCCCTCT 3805
DB 3617 GGGATCAGCGGAGTCTATACGTAGGGGATTTCAATTACGTCCGGCGGATATTCCTGCT 3676
QY 3806 GGAATGTCAACCACTCTTAGAGCTGAGGAATAAAGATTTTCAGACATAGTTCACAGTCCA 3865
DB 3677 GGGATGTGACAGAGTGTTTTAGAACAATAAGAAATAAAGATTTTAGACATAGTAGCAACCCA 3736
QY 3866 GCACAAATATCTACCTGGCCACAGACCCCATGAGTGGGGCGCTCTTCTTCTTGACAGC 3925
DB 3737 GCTCACAGATACTACTGGCTACGGACCCAGTCAACCGAGATTTGTACGCTCTCTGATACT 3796
QY 3926 AACAGCCGCGGGTCTTTAAATCAAGTCCACTGTGTGTGAGGAGCTTTGTCAAGAAC 3985
DB 3797 AACACCCGCAATCTATTCGGCCGAATCACTACGGGAGCCAAAGACCTGACTTAANAAC 3856
QY 3986 TCTGAGTGTGTGGGGGACAGGTGACAGTGCCTCCCTTTTGTATGACACTTCGCTGCGGG 4045
DB 3857 GCTGAAGTGTGGCAGGACCGGGGAACAGTGCCTTCCCTTTTGACGAGCGCAGGTGGG 3916
QY 4046 GATGTTGGGAAGGCCACAGAAAGCCACATCAACCATCCAGGGGTATTACAGTGGACAG 4105
DB 3917 GATGGAGGCAAGGTGTGGAAAGCAACGCTCATGAGTCCCAAGGAATGGCAATCGATAAG 3976
QY 4106 TTTGGGCTGATCTACTTCGTGGATGGCACCATGATCAGACGCTCATGATCAGATGGGATC 4165
DB 3977 AACGGACTGATCTACTTTGTTGATGGAAACCATGATCAGAAAGGTTGATCAAAATGGAAATC 4036
QY 4166 ATCTTCAACCTGTCTCGCTCTTAATGATCTCACATCAGCCCGGCCACTCAGCTGTGATTCT 4225
DB 4037 ATATCAACTCTCTGTGGCTCCACGACCTCAGCTCAGCTCGACCTTTAACTGTGATACT 4096
QY 4226 GTCATGATATTTTCCAGGTAAGACTGGAGTGGCCCAACAGACTTAGGCATCAACCCCAATG 4285
DB 4097 AGCATGATATCAGCCAGGTGCGTCTGGAATGGCCCACTGACCTCGCGGATCAACCCCATG 4156
QY 4286 GACAACTCACTTTTATGCTCGACAAACAAATGTGTGCTCTGCAAAATCTCTGAAAMACCAACAG 4345

| | | | | | | | | |
|----|------|-------|--|------|----|------|---|------|
| Db | 4157 | GATAA | CTCCATCTAGGTCCTGGATAATAACGTAAGTTTACAGATCACTGAAACCCGTCAG | 4216 | Db | 5234 | GACTCTCACTACACAGACAGAGCCCCACCGTTCTGGCTGGCACGCGCAATCCACAGTAGCC | 5293 |
| Qy | 4346 | GTGGG | CAATGTGCGGGAGGCCAATGCACTGCCAGGTCCCTGGCAATGACCACTTCCTG | 4405 | Qy | 5423 | AAAGGAATGTCAAGCTGCCCATCGAACACGGCTCAACTGGTGGAGTGGCGCCAGCGC | 5482 |
| Db | 4217 | GTCCG | ATCGTCTCCGGGCGGCCCATGCACTGTCAAGTCCCTGGAGTGG---AATACCCG | 4273 | Db | 5294 | AAAAGAAACATGACTCTTCCCGTGAGAAAGGCGCAGAAATCTGGTGGAGTGGAGATTC | 5353 |
| Qy | 4406 | CTAAG | CAAGGTGCCATCCACGCAACCCCTGGAGTCAAGCCAGCCGCTTTGGCTGTTTACAC | 4465 | Qy | 5483 | AAAGAGCAGGCTCGGGGCGCAGGTCACTGTCTTTGGCGCGGCTGCGGGTGCACAA | 5542 |
| Db | 4274 | GTGGG | GAAGCACGCGGTTTACACACCTTGAGTTCAGCCACGCGCATGCTGTGTCTTAC | 4333 | Db | 5354 | AAAGAACAGCCACAGGCAAGTCAACGTAATTCGCGCGGAAGCTCAGGGTCAATGG | 5413 |
| Qy | 4466 | AATGG | GTCTCTATATTTGCTGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAAGTC | 4525 | Qy | 5543 | AATCTCTATCTCTGACATTTGATCGCGTAAACAGCACAGAGAGATCTATGATGACC | 5602 |
| Db | 4334 | AGCGG | GTCTTTACATCACGGAACCTGATGAGAGAAGATCAACCGAATAAGCGCAGGTC | 4393 | Db | 5414 | AACTACTCTCTAGTGGACTTTGATCGGACCAACCAAGACGGAAGAAATCTATGAT | 5473 |
| Qy | 4526 | ACCA | TAGTGGAGATCTCACTCGTGTGCTGGGGCCCCAGTGGCTGTGACTGTAAAT | 4585 | Qy | 5603 | CGCAAGTTCACCTTCGGATTTCTGTACGACACAGCGGGGCGGCCAGCTCTCTGT | 5662 |
| Db | 4394 | ACGAC | AGACGGGAGATCTCCTTAGTGGCTGGGATACCTTCGGAATGTGACTGCAAGAC | 4453 | Db | 5474 | CGGAATTTCTCTGAGGATCGTTACGACACGTGCGGGGACCCGACTCTCTGGCTG | 5533 |
| Qy | 4586 | GATGC | CAACTGTGATTTTCTGGAGACGATGGTTTATGCCAAGGATGCAAAAGTTAAAT | 4645 | Qy | 5663 | AGCAGCAGGCTGAATGGTGTCAACGTGACATCTCCCTGGGGGTTTACATTTGTG | 5722 |
| Db | 4454 | GAGCC | AACTGTGACTGTCTACCAAGCGGAGACGGTACGCCAAAGATGCCAACTCAAT | 4513 | Db | 5534 | AGTAGCAAGCTAATGGCAGTGAACGTCACTACTCATCCCGTCAAAATGGCAGCAT | 5593 |
| Qy | 4646 | ACCC | CACTTTCTTGGTGTGTGCTGTGATGGGAGCTCTACGTGGCGCACCTTGGGAAC | 4705 | Qy | 5723 | CAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCGCGGGCCGCATCATCC | 5782 |
| Db | 4514 | GGCG | CTCTCCCTGGCGGCTCCAGATGGCACCTCTGTACATTCAGATCTGGGAAT | 4573 | Db | 5594 | CAGAGGGGACCAACGAGCGAAAGGTGGACTATGACAGCCAGGGGAGGATCGTAT | 5653 |
| Qy | 4706 | ATCCG | AAATTCGGTTTATCCGGAAGAAACAAGCCTTTCTCAACCCAGAAACATGTATGAG | 4765 | Qy | 5783 | ATCTTCGCTGATGGGAAGACATGGAGCTACACATCTTACAGAGTCCATGGTGT | 5842 |
| Db | 4574 | ATCAG | ATCCGGCGGCTTTCGAAGAAATAAACCTTTACTGAACTCAATGMACTTTACGA | 4633 | Db | 5654 | GTCTTTGCCGATGGGAAACATGAGGTACACGTACTTGGAAAGTCCATGGTTC | 5713 |
| Qy | 4766 | CTGCT | TTCAACATGACAGGAGCTTATCTGTTTGTATACACCGGACGACCTGTAC | 4825 | Qy | 5843 | CTACACGCGCAGAGGAGATATATCTTTGAGTTTCGACAAAGAAATGACCGCTCT | 5902 |
| Db | 4634 | GTTC | CTCTTCAACTGATCAAGAGCTCTCATCTTTGACATCAACGGTACTCACAGTAC | 4693 | Db | 5714 | CTCCATAGCCAGCGGAGTACATCTTCGAATACGACATGTGGACCGCTGTCCG | 5773 |
| Qy | 4826 | ACCAA | AGCTGCCACAGGAGACTACCTGTACAACTTCACTACACCTGCGGGACGGCAC | 4885 | Qy | 5903 | ACGATCCCAACGTGCGCGGCHAGACACTAGACACCATCGCTCAGTGGGCTACTA | 5962 |
| Db | 4694 | ACCG | TGAGCTGGTACAGGCTGACTACTATATAATTTAGTTACAGCAATGACAATGAC | 4753 | Db | 5774 | ACCATCCGAGTGTGCTCGCCACACCATGCGACCATCCGGTCCATTTGCTACTA | 5833 |
| Qy | 4886 | ATC | ACTCATACAGACAAACAATGGCAACATGGTAAATGTCGCGCAGACTCTACTGGG | 4945 | Qy | 5963 | ACATCTATCAGCCCTCGAGGCAATGCTCAGTCAATACAGGACTTCACTGAGGAT | 6022 |
| Db | 4754 | GTCA | CGCTGTAACTGACAGCAATGGCAACACCCCTCCGAATCCGAAGGGATCCGAAT | 4813 | Db | 5834 | ACATCTCAATCCCCCAGAAAGCAATGCTCTATCATCACCGACTCAACGAGGA | 5893 |
| Qy | 4946 | ATGCC | CTCTGGCTGGTCCAGATGGCCAGGTGACTGGGTGACCATGGGCACCAAC | 5005 | Qy | 6023 | CACCTCTTCAACCTTCTACCTGGGCACCTGGCGCGCAGGGTGTATATCAAGTAT | 6082 |
| Db | 4814 | ATGCG | GTGGGTGTCTCCTGTAAACAGGTGATGGTTGACCATAGGACCAAC | 4873 | Db | 5894 | CTGCTCTCGAAACACGCTTTCCTGGGAAACGAGTCGGAGGGTCTTATTCAGT | 5953 |
| Qy | 5006 | AGTG | CACTCAAGAGTGTGACCAACAAAGGACACGAGTTGGCCATGATGACATACCAT | 5065 | Qy | 6083 | CTGTCAAAGCTGCGCAGAGACGCTCTATGACACCAACCAAGGTGATTTTACCT | 6142 |
| Db | 4874 | GGTGT | CTGAAAGCATGACCGCTCAGGGCTTGGACTGGTTTGTATTACTTACCATGGC | 4933 | Db | 5954 | CAGACCAGGCTATCAGAAATTTTATACGACAGCACAAAGAGTCAAGTTTAC | 6013 |
| Qy | 5066 | AATTC | CGGCTTCTGGCAACAAAGCAATGAAACCGGATGGACAAATTTTATGAGTAC | 5125 | Qy | 6143 | ACGGCAGGCATGCTGAAGACCATCAACCTACAGAAATGAGGGCTTCACTGCA | 6202 |
| Db | 4934 | AACAG | TGGGCTTTTAGCCACAAAGGTGACGAACTGGATGGACAAATTTTGTGACTAT | 4993 | Db | 6014 | ACAGCGGAGTCTGTGAAACAGTAAACCTTCAGAGTGTGTTTATTTTGCA | 6073 |
| Qy | 5126 | GACAG | TTTTGGCGCTGACAAATGTGACCTTCCCTACTGCGCCAGGTGAGCAGTTTCCGA | 5185 | Qy | 6203 | TACCGTCAAGTTGGGCGGCTGATTGACCGACAGATCTTCCGCTTTCAC | 6262 |
| Db | 4994 | GACAG | TGAAGGTGCGCTGACGAATGTATCTTCCCACTGGGTGGTTTCAAACTCGCAC | 5053 | Db | 6074 | TACAGGCAATTTGGTCCCTGATTGACACAGATTTTCCGCTTCAGCGAGGATG | 6133 |
| Qy | 5186 | AGTG | ATACAGACAGTTCAGTGCATGTCCAGGTAGAGACCTCCAGCA---AGGATGAT | 5242 | Qy | 6263 | GTCAACCGCGCTTTTGACTACAACTATGACAAACAGCTTCCGGGTGACGAC | 6322 |
| Db | 5054 | GGGGA | CATGACAAAGGTATACCGGTGGACATCGAGTCACTCCAGCAGAGAGGAGATGTC | 5113 | Db | 6134 | GTAAATGCGAGATTTGACTATAGCTACGACAAACAGCTTTTCAGTGCACG | 6193 |
| Qy | 5243 | ACC | ATACCAACCAACCTGTCTGCTCAGGCGCTTCTTACACACTGTGTGCAAGACCA | 5302 | Qy | 6323 | GTGATCAACGAGACCCCACTGCCCATTTGATCTATCGCTATGATGATGTCAG | 6382 |
| Db | 5114 | AGCAT | CACTTTCGAACCTTGTCTCCATCGATTCCTTCTTACACCATGGTCCCAAGAC | 5173 | Db | 6194 | GTCAATCAATGAAACACCACTGCCCATTTGATCTATACAGTTTATGACATCT | 6253 |
| Qy | 5303 | CGNA | CAGCTTACTACATCGGGCGGATGGCTCTTGGCGCTGTGCTGGGCCAACGCGCAT | 5362 | Qy | 6383 | ACAGACAGTTCGGGAAGTTTGGTGTCAATTTACTATGACATTAACAGATCAT | 6442 |
| Db | 5174 | AGAA | ACAGTTTACCAAGATTTGGGTATGATGGCTCCCTTAGAATCTTCTATGCCAG | 5233 | Db | 6254 | GTGACAGGTTTGGAAAAATTCGGAGTGTATACTACGACATCAACCAATCAT | 6313 |
| Qy | 5363 | GAGT | GCGCTGCAGACTGAGGCCCACTTGTGCTGGCGCACCGTCAACCCCAACCGTGG | 5422 | Qy | 6443 | GCTGTATGACCCACCAACGACATTTTGTATGTCATATGGCAGGATGAAGGAT | 6502 |
| Db | | | | | Db | 6314 | GCGTGTGATGACTTATACAAAGCACTTTTGTGCTCATGGGCGCATCAAGGAGAT | 6373 |

QY 6503 GAGATCTTCCGCTCGCTCATGTACTGTGATGACCGTCCAGTATGATAACATGGGCGAGTA 6562
DB 6374 GAGATATTTAGGTCACTCATGTACTGTGATTAACAATTTCAATATGATAATATGGGCGGGTA 6433
QY 6563 GTGAAGAGGAGCTGAAGGTAGGACCTTACGCCAATACCACTCGCTACTCTATGAGTAT 6622
DB 6434 ACCAAGAGAGAGATTAAATTTGGGCTTTTGGCAACACTACCAATACCGGTACGAGTAC 6493
QY 6623 GATGCTGACGGCAGCTCGACAGCATCTCCATCAATGAACAAGCCACTCTGGCGGTACAGC 6682
DB 6494 GACGTCGATGACAGCTCCAAACAGTTTACCTTAACGAAAGATCATGTGGCGGTACAAAC 6553
QY 6683 TAGACCTCAATGGGAACCTGCATTACTAGAGCCCTGGGAACAGTGCAGCGCTCACACCA 6742
DB 6554 TACGACCTAAATGGAAACCTCCACTTGTCTCAACCCAGCAGCGCCGCTGACCCCT 6613
QY 6743 CTACGGTATGATCCGCGACCGCATCACTCGGCTGGGTGACGTGCAATACAAGATGGAT 6802
DB 6614 CTGCGCTATGACCTCGCGGACAGAAATCAACCGCTTGGCGGATGTTTCACTACGGCTGGAT 6673
QY 6803 GAGGATGGCTTCTGAGGACGCGGCGGTGATATCTTTGAGTACAACTCAGCTGGCCCTG 6862
DB 6674 GAAGATGGTTCTCGCTCAGAGGGGCACTGAAATTTTGAATACAGCTCCAAAGGGCTT 6733
QY 6863 CTCATCAAGGCTTACAAACGGGCTGGCAGCTGGAGTGTGAGTACCGCTACGATGGCCCTG 6922
DB 6734 CTGACTCAGTCTACAGTAAAGGCAAGTGGCTGGACAGTGATCTATCGGTACGACGGCCCTG 6793
QY 6923 GGGCGGCGGTGTCAGCAAGAGCAGCCACAGCCACCACTGCACTTCTTATGACAGC 6982
DB 6794 GGAAGACGTGTTCTAGCAAAACAGCTGGGACAGACCTTCAGTTTCTACGCCGAC 6853
QY 6983 CTGACCAACCCCAACAGGTACCCACTGTGTACAAACCACTCAGCTCTGAGATCACTCC 7042
DB 6854 CTGACATACCCCAAGAAATTACTCACGTCTACAAACCAATTCAGTTTCAGAAATCACTCC 6913
QY 7043 CTCTACTAGACTTCAAGGACACCTTTTGCATGGAGCTGAGCAGTGGTGTAGTGGTTT 7102
DB 6914 CTGTACTATGACTTCAAGGACATCTCTTCGCGCATGGAGATCAGCAGTGGGATGAGTTC 6973
QY 7103 TACATAGCTTGTGACAAATCGGACCCCTCTTGTGCTCTTTAGTGGAAACAGTGTGATG 7162
DB 6974 TACATCGCTCGGACAAACAGGGGACACGCTGGCTGTGTTTTCAGCAGCAACGGGCTCATG 7033
QY 7163 ATCAAGCAAAATCCTGTACACAGCTATGGGGAGATCTACATGGATACCAACCCCACTTT 7222
DB 7034 CTGAACACAGACCCAGTACACTGCCTATGGTGAGATCTACTTTGACTCCAAACGTCGACTTT 7093
QY 7223 CAGATCATCATAGGCTACCATGCTGGCCCTCTATGATCCACTCACCAAGCTTGTCCACATG 7282
DB 7094 CAGCTGGTAAATTGGATTCACCGGGGCTTGTATGATCCCGCTCACCAACTAATCCACTTT 7153
QY 7283 GGCCGCGAGATTTATGATGTGTCGGCGGACGCTGAGCTAGCCACAGACCAAGCTGTGG 7342
DB 7154 GGAGAAAGAGATTATGACATTTTGGGGGAAGATGGACCAACCGGACATTTGAATCTGG 7213
QY 7343 AAGCACTTTAGTAGCAGCAACGTCATGCGCTTTTAAATCTCTATATGTTTCAAAAACAAAC 7402
DB 7214 A---AAAGGATCGGAAGACCCCTGCTCCTTTTAACTCTGTATATGTTTTCGGAATAACAAAC 7270
QY 7403 CCCATCAGCACTCCAGGACATCAAGTCTTTCATGACAGATGTTAAACAGCTGGCTGCTC 7462
DB 7271 CCCGGAGCAAAATCCATGATGTGAAGATTACATACCGATGTTAAACAGCTGGCTGGTG 7330
QY 7463 ACCTTTGGATTCAGCTACACAACTGATCCCTGGTTATCCCAACCCAGACATGGATGCC 7522
DB 7331 ACGTTTGGCTTCCATCTGACAAATGCTATTCTCTGGATTCCCTGTTTCCCAAAATTGATTTA 7390
QY 7523 ATGGAAACCTCTCTACAGCTCATCCACACAGATGAACCCAGGATGGGACACAGC 7582
DB 7391 ACTGAGCCTTCTCTATGAGCT-----TGTGAAGAGTCAACAGTGGGGAAGATGG 7438

QY 7583 AAGTCTATCTCGGGGTACAGTGTGAAGTACAGAGCAGCTCAAGGCTTTTGTACCTTA 7642
DB 7439 CCGCCCATCTTTGGAGTTTACAGCAGCAAGTGGCAAGGCAAGCGCTTCTTGTCCCTG 7498
QY 7643 GAACGGTTTACAGCTCTATGGCTCCCAATACAGCTGCCAGCAGGCTCCAAAGACC 7702
DB 7499 GGGAAAGATGGCCGAGGTGAGTGCAGCGAAGCTGGCGCCGAG---CAGTCGTGG 7555
QY 7703 AAGNAAGTTTTCATCCAGCGGCTCAGTCTTTTGGCAAGGGGTCAAGTTTTCCTTCAAGGAT 7762
DB 7556 CTGTGGTTTCGCCACGGTCAAGTCTCATCGCAGAGGGCGTCTGCTGGCGTGAAGCAA 7615
QY 7763 GGGCGAGTGAACCAAGACATCATCAGTGTGGCCCAATCAGAGTGGCGAAGGGTTGTGACC 7822
DB 7616 GGGCGGCTGCAGACCAACGCTCAACATCGCCAAACGAGGACTGCATCAAGGTGGCGGCG 7675
QY 7823 ATCTTGAACCATGCCCCACTTACCTAGAGAACTGTGCACTTACCATTGATGGGGTGGATACC 7882
DB 7676 GTGCTCAACAACGCTTTTACTTGGAGAACCTGCACCTTCAACCATCGAGGGGCAAGGACACA 7735
QY 7883 CATTTACTTTGTGAACACGAGGACCTTTCAGAAAGTGCACCTGGGCATCTCTGGGCTCAGTGGG 7942
DB 7736 CACTACTTTCATCAAGACCAACACCCGAGAGCACTTGGGCACACTTGGGCTGACGAGC 7795
QY 7943 GGGCGGCAACCCCTGGAGAAATGGGGTCAACGTCACTGTGTCCCAGATCAACACAGTACTT 8002
DB 7796 GGTGCAAGGCCCTGGAGAACGGGATCAACGTGACCGTGTCTCAGTCCACACCGTGGTG 7855
QY 8003 AATGGCAGGACTAGACGCTACACAGATCCAGCTCCAGTACGGGGCACTGTGCTTGAAC 8062
DB 7856 AACGGCAGGACTCGCAGGTTTCCGCGACGTGGAGATGCAGTTTCGGTGGCTTGGCTGCTG 7915
QY 8063 ACAGCTACGGGCAACCGTTGGATGAGAGAAAGCAACGGGTCTCTGGAGCTGGCCCGGCGAG 8122
DB 7916 GTGCGCTATGTCATGACGCTGGACAGAGAAAGGGCGCATCTTGGAGCAGCGCGCCAG 7975
QY 8123 AGAGCCGTGGCCCAAGCTGGGCCCGCAGCAGCAGAGACTGCGGGAAGGGAGGAAGGC 8182
DB 7976 CGCGGCTCGCCCGGGCTGGGCACGGGACGAGCAGCGCGTGGCGACGGGAGAGGGT 8035
QY 8183 CTGGCGGCTGGACAGAGGGGAGAAAGCAGAGCTGTGAGCAGCAGGCGGGTGCAGGC 8242
DB 8036 CGCGGCTCTGGACGGAGGGTGAGAAACGGCAGCTGTGAGCGCTTGGCAAGGTGCAGGC 8095
QY 8243 TACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCAGAACTGTACAGACAGCGCCAAAC 8302
DB 8096 TACGATGGTACTAGTACTCTGCTGGAGCAGTACCCCGAGCTGGCTGACAGTGCCTAAC 8155
QY 8303 AACATCCACTTTCATGACAGAGGAGATGGGCGGAGGTGAC 8345
DB 8156 AACATCCAGTTCTTTCGCAACAAAGTGAGATCGCAAGAGGTAAAC 8198

RESULT 9
ABQ82344

ID ABQ82344 standard; cDNA; 8645 BP.

AC ABQ82344;

XX 17-DEC-2002 (first entry)

XX Human NOV15b encoding cDNA SEQ ID NO:37.

Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide; antianemic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy; Pick's disease; vesicular transport disease; cystic fibrosis; goitre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; Gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia;

| | | |
|----|---|--|
| KW | rheumatoid arthritis; gene; chromosome 4; ss. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PH | Location/Qualifiers | |
| FT | 151..8316 | |
| FT | /tag= a | |
| FT | /product= "NOV15b" | |
| XX | | |
| XX | WO200262999-A2. | |
| PN | | |
| XX | | |
| PD | 15-AUG-2002. | |
| XX | | |
| PF | 31-DEC-2001; 2001WO-US049976. | |
| XX | | |
| PR | 29-DEC-2000; 2000US-0258928P. | |
| PR | 02-JAN-2001; 2001US-0259415P. | |
| PR | 04-JAN-2001; 2001US-0259785P. | |
| PR | 20-FEB-2001; 2001US-0269614P. | |
| PR | 09-MAR-2001; 2001US-0279863P. | |
| PR | 29-MAR-2001; 2001US-0279832P. | |
| PR | 29-MAR-2001; 2001US-0279833P. | |
| PR | 13-APR-2001; 2001US-0283889P. | |
| PR | 18-APR-2001; 2001US-0284447P. | |
| PR | 25-APR-2001; 2001US-0286683P. | |
| PR | 29-MAY-2001; 2001US-0294080P. | |
| PR | 16-AUG-2001; 2001US-0312915P. | |
| PR | 17-AUG-2001; 2001US-0313325P. | |
| PR | 17-SEP-2001; 2001US-0322699P. | |
| PR | 26-NOV-2001; 2001US-0333350P. | |
| XX | | |
| PA | (CURA-) CURAGEN CORP. | |
| XX | | |
| PI | Spytek KA, Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X; | |
| PI | Malyankar U, Shinkets RA, Tchernev VT, Spaderna SK, Gorman L; | |
| PI | Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S; | |
| PI | Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K; | |
| PI | Gunther E, Smithson G, Millet I, Macdougall JR; | |
| XX | | |
| DR | WPI: 2002-732706/79. | |
| DR | P-PSDB; ABP53587. | |
| XX | | |
| PT | New NOVX polypeptides and polynucleotides useful for treating NOVX- | |
| PT | associated disorders, such as cancers, neurological disorders, disorders | |
| PT | of vesicular transport, gastrointestinal disorders, and autoimmune | |
| PT | diseases. | |
| XX | | |
| PS | Claim 8; Page 114-117; 444pp; English. | |
| XX | | |
| CC | The present invention describes novel human proteins designated NOVX, | |
| CC | where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, | |
| CC | cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, | |
| CC | antidiabetic, antiinflammatory, antirheumatic, antiarthritic, virucide, | |
| CC | immunosuppressive, antiallergic, antianemic, antibacterial, fungicide, | |
| CC | protozoicide and antihelminthic activities, and can be used in gene | |
| CC | therapy. The NOVX proteins, nucleotides or antibodies can be used in the | |
| CC | manufacture of a medicament for treating a syndrome associated with a | |
| CC | human disease selected from NOVX-associated disorder, such as cancers | |
| CC | (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, | |
| CC | ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, | |
| CC | ischemic cerebrovascular disease, Alzheimer's disease or Pick's | |
| CC | disease), disorders of vesicular transport (e.g. cystic fibrosis, | |
| CC | diabetes mellitus, Grave's disease, or goitre), gastrointestinal | |
| CC | disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), | |
| CC | autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic | |
| CC | anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic | |
| CC | and protozoal infections. The NOVX proteins can be used as immunogens to | |
| CC | produce antibodies and as vaccines. The NOVX nucleotide sequences may be | |
| CC | used in chromosome mapping, identifying individuals from minute | |
| CC | biological samples (tissue typing), and in forensic identification of a | |
| CC | biological sample. The present sequence encodes human NOV15b, which is | |
| CC | located on chromosome 4 | |
| XX | | |

| | | |
|----|---|-------------------------|
| SQ | Sequence 8645 BP; 2343 A; 2060 C; 2200 G; 2038 T; 0 U; 4 Other; | |
| | | |
| | Query Match 42.0%; Score 3504.6; DB 6; Length 8645; | |
| | Best Local Similarity 65.3%; Pred. No. 0; | |
| | Matches 5449; Conservative 1; Mismatches 2687; Indels 204; Gaps 13; | |
| | | |
| QY | 35 ATGACGTGAAGGAGAGAGACCTTACGGCTCGCTGACCCCGGCGC---- | CCGAGCGCGAG 91 |
| | | |
| DB | 151 ATGGATGTGAAGAAGACGAGGCGCTTACTGCTCCCTGACCAAGAGCAGACGAGAGAGGAA | 210 |
| | | |
| QY | 92 CGCGCTACACAGCTGCTCGCGGACAGCGAGGAGGGCAAG-- | CCCCGCGAGAATCG 148 |
| | | |
| DB | 211 CGCGCTACACAAATTTCTCCGAGACAAATGAGAGTGCCGGGTACCCACACAGAGATCC | 270 |
| | | |
| QY | 149 TACAGCTCCAGCGAGACCTTGAAGGCTTACGACACGAG-- | CGCCCGCCTTAGCTATGGC 205 |
| | | |
| DB | 271 TACAGTCCAGGAGACATTTGAAGCTTTTGTATCATGATTTCTCTCGGGCTGCTTTACGGC | 330 |
| | | |
| QY | 206 AGCGCGTCAAGGACATTTGTCCCGCAGGAGCGCGAGGAATTTCTGCCGACAGGTGCCAAC | 285 |
| | | |
| DB | 331 AACAGAGTGAAGGATTTTGGTTTCACAGAGAAGCAGACGAGTTTCACTAGACAAGACAGAAT | 330 |
| | | |
| QY | 266 TTCACCTCTCGGGAGCTGGGCTCGAAGAACTAAGCGCCCTCACGSGGACCTGTACCGG | 325 |
| | | |
| DB | 391 TTTACCTTAAGCGAGTTAGGAGTTTGTGAACACAGCAACTCGAAGAGACTTGGCATTTTGT | 450 |
| | | |
| QY | 326 ACAGACATTTGGCTGCCCAATGGGCTACTTCATATGGGGCTGGCTCTGATCGCGACATG | 385 |
| | | |
| DB | 451 GCGGAATGGGCTCCCTCACAGAGGTTACTTATCATGTGAGGGTTCAGATGCTGATACT | 510 |
| | | |
| QY | 386 GAGGCTGACACGGTGTCTCCCTTGAGACCCCGTGGCTCTGTGGGGCCCGAGACACACGG | 445 |
| | | |
| DB | 511 GAAATGAAGCAGTGATGTCGCCAGAGCATGCCATGAGACTTTTGGGCGCAGGGGGGTCAAA | 570 |
| | | |
| QY | 446 TCAGGGCGCAGCTCTGCTGCTCCAGCGCGGGCCCAATTTCCAATCTCACTACCGACACC | 505 |
| | | |
| DB | 571 TCAGGCGCGAGCTCTGCTGCTCAAGTCGGTTCAACTCAGCCCTCNCNCTGACAGATACG | 630 |
| | | |
| QY | 506 GAGCATGAAAAACACTGAGACTGATCATCCGGCGGCGCTGCGAAGAACACGCGCGCTCCGG | 565 |
| | | |
| DB | 631 GAGCAGGAAAACAGTCCGACAGTGAAGAYAGCAACTCTGCAGCAATCAAGGCCAGTCT | 690 |
| | | |
| QY | 566 AGCGCGCGCGCG | |

[illegible]

| | | | |
|----|------|---|------|
| QY | 5405 | GTCAACCCACCGTGGCAAGAGAAATGTCACGCTGCCATCGAACACGGCCTCAACCTTG | 5464 |
| Db | 5395 | GCTNAATCCGACGGTTGCCAAAGAAACATGACTTTGCTGCGGAGAACGGTCAAAACTTG | 5454 |
| QY | 5465 | GTGGAGTGGCCGCAAGCCAAAGAGCAGGCTCGGGGCCAGGTCTACTGCTTTTGGGCGCGG | 5524 |
| Db | 5455 | GTGGAAATGGAGATTCGGAAGAGCAAGCCAAAGGGAAATCAATGTCTTTGGCCGCAAG | 5514 |
| QY | 5525 | CTGGGGGTGCACAACCCAAATCTCTATCTCTGGACTTTGATCGCGTAACACGCACAGAG | 5584 |
| Db | 5515 | CTCAGGGTTAATGGCAGAAAACTCTTCAATTTGACTTTGATCGAAACAACAAAGACAGAA | 5574 |
| QY | 5585 | AAGATCTATGATGACACCGCAAGTTCACCCCTTCGGATTCGTACGACAGCGGGGCGG | 5644 |
| Db | 5575 | AAGATCTATGACGACCAACCGTAATTTCTACTGAGGATCGCCTACGACAGCTCTGGGCAC | 5634 |
| QY | 5645 | CCGAGCCTCTGGTCAACCCAGCAGCGCTGAATGGTGTCAACGTGACATACTCCCCGGG | 5704 |
| Db | 5635 | CCGACTCTCTGGCTGCCAACGACGACGATGATGGCCGTCAATGTCACTATTATCCACA | 5694 |
| QY | 5705 | GTTTACATTTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGATGGAATAGACACGAGCG | 5764 |
| Db | 5695 | GGTCAAAATTTGCCAGCATCCAGCAGGACCACTAGCGAGAAAGTAGATTATGACGGACAG | 5754 |
| QY | 5765 | GGCCGCATCACATCAGAGATCTTCGCTGATGGGAAGACATGGAGCTACACATCTTAGAG | 5824 |
| Db | 5755 | GGGAGGATCGTGTCTCGGGTCTTTGCTGATGTGTAACATAGGATTAACATATTTAGAA | 5814 |
| QY | 5825 | AAGTCCATGTGTCTACTACACAGCCAGAGGAGTATATCTTTGAGTTTCGAAGAAT | 5884 |
| Db | 5815 | AAGTCCATGGTTCTTCTGCTTATAGCCAGCGGAGTACATCTTCGAATACGATATGTGG | 5874 |
| QY | 5885 | GACCGCTCTCTTCTGTGAAGATGCCCAAAGTGGCGGCGGACACACTAGAGACCATCCG | 5944 |
| Db | 5875 | GACCGCTGTCTGCCATCACCATGCCAGGTGTGGCTCGCCACACCATGCGAGACCATCCGA | 5934 |
| QY | 5945 | TCAGTGGCTACTACAGAAACATCTATCAGCCCCCTCAGGGCAATGCTCAGTCAATACAG | 6004 |
| Db | 5935 | TCCATTTGGCTACTACCGCAACATATACACCCCCCGGAAGCAACGCTTCATCATCAG | 5994 |
| QY | 6005 | GACTTCACTGAGGATGGGCACTCTCTTACACACTTCTACCTGGGCACTGGCCGCGGGTG | 6064 |
| Db | 5995 | GACTACACGAGGAAGGCTGCTTCTACAAACAGCTTCTTTGGGTACAAGTCGAGGGGTG | 6054 |
| QY | 6065 | ATATACAAGTATGGCAAACTGTCAAAAGTGCAGAGAGCGTCTATGACACCAACAGGTC | 6124 |
| Db | 6055 | TTATTTCAAATACAGAAAGCAGACTAGGCTCTCAGAAATTTTATATGATAGACAAAGATC | 6114 |
| QY | 6125 | AGTTTCACCTATGACGAGCGGAGCATGCTGAAGACCATCAACCTTACAGAATGAGGGC | 6184 |
| Db | 6115 | AGTTTTACTATGATGAACACGAGGAGTCTCTAAAGACAGTAAACCTCCAGAGTATGGT | 6174 |
| QY | 6185 | TTCACTGCACCATCCGCTACCGTCAGATTTGGGCCCCCTGATTGACCGACAGATCTCCGC | 6244 |
| Db | 6175 | TTTATTTGCAACATTAGATACAGGCAATTTGTTCCCTGATTGACAGCGAGATTTCCGC | 6234 |
| QY | 6245 | TTCTACTGAGGAAGGATGGTCAACGCCCGCTTTGACTTACAACTATGACAAACAGCTCCGG | 6304 |
| Db | 6235 | TTTAGTGAAGATGGATGGTAAATGCAAGATTTGACTATAGCTATGACAAACAGCTTTTCCA | 6294 |
| QY | 6305 | GTGACCATGTCAGGCTGTGATCAACGAGACCCCATGCGCCATTTGATCTCTATCGCTAT | 6364 |
| Db | 6295 | GTGACCATGTCAGGCTGTGATCAATGAACCGGCATGCGCTATTTGATCTGTATCAGTTT | 6354 |
| QY | 6365 | GATGATGTCTCAGGCAACACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATT | 6424 |
| Db | 6355 | GATGACATTTCTGGCAAGTTGAGCAGTTTGGAAAGTTTGGAGTTATATATATGATATT | 6414 |
| QY | 6425 | AACCATGATCATCAACACAGCTGTCTATGACCCACCAACCAAGCAATTTTGTATGCAATGGCAGG | 6484 |
| Db | 6415 | AACCATGATCATTTCTACAGCTGTATGATACCTATACGAAGCACTTTGTATGCTCATGGCGGT | 6474 |

Db 7540 CAGCAGTGGGATGATATACCGCCCATCTTCGGAGTCCAGCAGCAAGTGGCGCGCAGGCC 7599
QY 7625 AAGGCTTTGTACCTTAGAACGGTTGACCAAGTCTATGCTTCCACATCACCAGCTGC 7684
Db 7600 AAGGCTTCTGTGCTGGGGAAGATGGCGAGGTGACAGTGAGCGCGCGCGCGCGG 7659
QY 7685 CAGCAGGCTCAAAGACCAAGAAAGTTTGCACTCAGCGGCTCAGTCTTTGGCAAGGGGTC 7744
Db 7660 ---GGCGGAGTCTGGCTGTGTTGCGCACGGTCAAGTCCGTGATCGGCAGAGGGCTC 7716
QY 7745 AAGTTTGCTTGAAGATGCGGAGTGACACAGACATCATAGTGTGGCCAAATGAGGAT 7804
Db 7717 ATGCTGCGCTCAGCCAGGCGCGTGCAGACCAACGTTGCTCAACATCGCCAAACGAGGAC 7776
QY 7805 GGGGGAAGGTTGCTGCCATCTTGNACCATGCCCCACTACTAGAACCTGCACTTCCACC 7864
Db 7777 TGCAATCAAGGTGGCGCGGCTCAACACGCTTTTACCTGGAGAACCTTGCACCTTCAACC 7836
QY 7865 ATTGATGGGTGGATACCCATTACTTTGTGAACACAGGACCTTTCAGAAAGGTGACCTGGCC 7924
Db 7837 ATCGAGGGCAAGACACGCACTACTTTCATCAACACCAACGCGCCGAGAGCGACCTGGGC 7896
QY 7925 ATCTGCGCTCAGTGGGCGCGCGAACCTTGAGAAATGGGTCAACGCTCACTGTGTCC 7984
Db 7897 ACGTCTGCGTTGACCAAGCGCGCGCAAGGCGCTGGAGAACGCGCATCAACGTTGACGGTGTG 7956
QY 7985 CAGATCAACACAGTACTTAATGCGAGGACTAGACGCTACACAGACATCCAGCTCCAGTAC 8044
Db 7957 CAGTCCACCAAGTGTGTGAACCGCAGGACGCGCAGGTTTCGCGGACGTGGAGATGCAAGTTC 8016
QY 8045 GGGGCACTGTGTTGAACACACGCTACGGGACAAAGTTTGTGATCAGAGAGAGGCAAGGTC 8104
Db 8017 GGGCGCTGCGCTGCAAGTGTGCGCTACCGCATGACCTTGAAGAGAGAGGCGCGCATC 8076
QY 8105 CTGAGCTGCGCGCGCAGAGAGCGCTGCGCAAGCGTGGCGCGCGCAGCAGCAGACTG 8164
Db 8077 CTGAGCAGCGCGCGCAGCGCGCTGCGCGCGCGCTGGCGCGCGCAGCAGCAGCGCTG 8136
QY 8165 CGGGAAGGGAGAGAGCGCTGCGGCGCTGCAAGAGGGGAGAGCAGCAGGTTGCTGAGC 8224
Db 8137 CGGACGCGGAGAGGCGCGCGCTTGGACGAGGCGGAGAGCGCGCAGCTGCTGAGC 8196
QY 8225 ACAGGCGGTGCAAGCTACGAGCGCTTTTCGTGATCTCTGTCGAGCAGTACCCAGAA 8284
Db 8197 GCGGCAAGGTGAGGGCTACGAGCGGTACTACTCTCGTGGAGCAGTACCCCGAG 8256
QY 8285 CTGTCAGACAGCGCCCAACATCCACTTCATGAGACAGCGAGATGGCGCGGAGTGA 8344
Db 8257 CTGCGGACAGCGCCCAACATCCAGTTCTTGGCGCAGAGCGAGATCGGCAGGAGTAA 8316
QY 8345 C 8345
Db 8317 C 8317

RESULT 10

ADH41968
ID ADH41968 standard; DNA; 8645 BP.

XX

AC ADH41968;

XX

DT 25-MAR-2004 (first entry)

XX

DE Novel human nucleic acid NOVA0s.

XX

KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;
KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;
KW neotropic; antiparkinsonian; antiasthmatic; antifertility;
KW cardiomypathy; atherosclerosis; hypertension; cancer; obesity; diabetes;
KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX OS Homo sapiens.
XX WO2003102159-A2.
XX PD 11-DEC-2003.
XX
XX 04-JUN-2003; 2003WO-US017573.
XX
XX 04-JUN-2002; 2002US-0385490P.
XX 04-JUN-2002; 2002US-0385615P.
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XX 06-JUN-2002; 2002US-0386355P.
XX 06-JUN-2002; 2002US-0386357P.
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XX 06-JUN-2002; 2002US-0386459P.
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XX 06-JUN-2002; 2002US-0386864P.
XX 07-JUN-2002; 2002US-0386701P.
XX 07-JUN-2002; 2002US-0386796P.
XX 07-JUN-2002; 2002US-0386931P.
XX 07-JUN-2002; 2002US-0387078P.
XX 07-JUN-2002; 2002US-0387081P.
XX 07-JUN-2002; 2002US-0387083P.
XX 10-JUN-2002; 2002US-0387429P.
XX 10-JUN-2002; 2002US-0387540P.
XX 10-JUN-2002; 2002US-0387866P.
XX 11-JUN-2002; 2002US-0387606P.
XX 11-JUN-2002; 2002US-0387610P.
XX 11-JUN-2002; 2002US-0387659P.
XX 11-JUN-2002; 2002US-0387668P.
XX 11-JUN-2002; 2002US-0387696P.
XX 11-JUN-2002; 2002US-0387859P.
XX 12-JUN-2002; 2002US-0387934P.
XX 12-JUN-2002; 2002US-0387960P.
XX 12-JUN-2002; 2002US-0388022P.
XX 12-JUN-2002; 2002US-0388096P.
XX 12-JUN-2002; 2002US-0388432P.
XX 12-JUN-2002; 2002US-0388479P.
XX 13-JUN-2002; 2002US-0389123P.
XX 14-JUN-2002; 2002US-0389120P.
XX 14-JUN-2002; 2002US-0389146P.
XX 17-JUN-2002; 2002US-0389742P.
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XX 19-JUN-2002; 2002US-0390006P.
XX 19-JUN-2002; 2002US-0390144P.
XX 19-JUN-2002; 2002US-0390209P.
XX 25-JUN-2002; 2002US-0391726P.
XX 06-AUG-2002; 2002US-0401628P.
XX 09-AUG-2002; 2002US-0402268P.
XX 12-AUG-2002; 2002US-0402822P.
XX 13-AUG-2002; 2002US-0403458P.
XX 15-AUG-2002; 2002US-0403617P.
XX 15-AUG-2002; 2002US-0403732P.
XX 26-AUG-2002; 2002US-0406182P.
XX 12-SEP-2002; 2002US-0410085P.
XX 13-SEP-2002; 2002US-0410505P.
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XX 30-SEP-2002; 2002US-0415195P.
XX 23-OCT-2002; 2002US-0420627P.
XX 23-OCT-2002; 2002US-0420718P.
XX 24-OCT-2002; 2002US-0420852P.
XX 31-OCT-2002; 2002US-0422705P.
XX 01-NOV-2002; 2002US-0423095P.
XX 05-NOV-2002; 2002US-0423748P.

(CURA-) CURAGEN CORP.

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Alsbrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;

| | | | | | | | |
|----|------|--|------|----|------|---|------|
| Db | 1618 | ATCTGGCATCTGGCTTTTATTAATGATGGGAAAAATGACAGCAGGTGTCTTTTAATACC | 1677 | Db | 2698 | AAATCCTTTTATGATCGAATCAGTTTCCTTATATAGGATCTGATAGACCCCATGTTATACCT | 2757 |
| Qy | 1706 | ACTGCCATTGAGTCGGTGGATACCTGCCCAGCAACTGCTATGGCAATGCTGACTGCATC | 1765 | Qy | 2768 | GGGGAGAACCCCTTTTATGATGGAGGCGATCTGTGTGTTATTTCTGGGCCCAAGTGATGACATCA | 2827 |
| Db | 1678 | ATTGTTATAGAGTCTGTGGTGGAAATGTCGCCGAAATGGCAATGGAAATGCGGT | 1737 | Db | 2758 | GGAGAAAGTCTCTTCAATAAGAGCCTTGCATCTGTTCATCAGAGGCCCAAGTACTGACTGCT | 2817 |
| Qy | 1766 | TCTGGACCTGCCACTGCTTCTCTGGGTTTCTCGGCCCCGACCTGTGGCAGAGCCTCTGTC | 1825 | Qy | 2828 | GATGGAAACCCCTCGTGTGGTGTGAACATCAGTTTTTGTGCAATAAACCCCTCTCTTTGGANAT | 2887 |
| Db | 1738 | TCTGGAACTTGCCATTGTTTCCAGGATTTCTGGGTCCGATTTGTTCAAGAGCCGCTGT | 1797 | Db | 2818 | GATGGAACTCCACTTATTGGAGTAAATGTCTCGTTTTTCCATTACCCAGAAATATGGATAT | 2877 |
| Qy | 1826 | CCCGTGTCTGTAGCGGAAATGGCCAAATACATGAAGGCGAGATGCTGTGTGCCACAGTGGC | 1885 | Qy | 2888 | ACAATCAGCAGCGCAGATGGCAGCTTTGACTTTGGTCACAAATGGCGGCATCTCCATCATC | 2947 |
| Db | 1798 | CCAGTGTATGTAGTGGCAACGGCGAGTACTCCAAGGGCGCTGCTGTGTTTCAGCGGC | 1857 | Db | 2878 | ACTATTACCGCCGACGACCGGAATGTTTGACTTTGGTGGCAATGGTGGGGCTCTCTAACT | 2937 |
| Qy | 1886 | TGGAAGGCCCTGAGTGCAGTGTGCCACCAACCAAGTGATTCGATGTGGCCTGCACCAAC | 1945 | Qy | 2948 | CTGCGGTTCCAGCGGCGACCTTTTCATCACACAGGAGCACACCCCTGTGGCTGCCATGGGAT | 3007 |
| Db | 1858 | TGGAAGGCCACCGAGTGTGATGTGCCGACTTACCAGTGTATTCACCCACAGTGTGGGGT | 1917 | Db | 2938 | TTGGTATTTGAAGCATCCCATTTCTCACTCAGTATCATATCTGTGTGGATTCATCGAAT | 2997 |
| Qy | 1946 | CATGGCACCTGCATCAGCGGCACCTGCATCTGCAACCCCTGGCTACAAAGGCGGAGAGCTGT | 2005 | Qy | 3008 | CGCTTCTTTGTCAATGAAACCATCATCATGAGACATGAGGAGAAATGAGATTTCCAGCTGT | 3067 |
| Db | 1918 | CGTGGGATTTGATCATGGGCTCTGTGCTTGAGCTCAGATACAAAGGAGAAATGTTGT | 1977 | Db | 2998 | GTCTTTTATGTGATGATACCCCTAGTCAATGGAGAAAGAGAAATGACATTTCCAGCTGT | 3057 |
| Qy | 2006 | GAGGAAGTGACTGCAATGGAACCCCAACATGTTCAAGGCCGGGTGTCTGCTGAGAGCGAA | 2065 | Qy | 3068 | GACCTGAGCAATTTTGCCTGCCCCCAACCCAGTCTCTCTCCATCCCACTGACGTCTCTTC | 3127 |
| Db | 1978 | GAAGAGCTGACTGTATAGACCTCGGGTGTCTTAATCATGGTGTGTATCCACGGGAA | 2037 | Db | 3058 | GATCTGAGTGGATTCGTGAGGCCAAATCCCATCAITTTGTGTCTTATCCACTTTTATCCACTTT | 3117 |
| Qy | 2066 | TGCCATGCTTTTGGGATGGGAGGACCAACTGCGGAGACCCCGGGGCCACATGCTTA | 2125 | Qy | 3128 | GCAGCTCTCTGTGCAGAGAAAGGCCCATTTGTGCCGGAATTCAGAGCTTTTGCAGGAGGAA | 3187 |
| Db | 2038 | TGTCACTGCACTCCAGGATGGGAGGTAGCAATTTGTGAATACTGAAGACCATGTGTCCA | 2097 | Db | 3118 | TTCAGATCTTCTCTGAGACAGTCCCATCTTCCCGAAACACAGGTACTTCCACGACGAA | 3177 |
| Qy | 2126 | GACCAAGTTCAGGCCAGCAACTCTCCCGACACCGGGCTTTGACACTGTGACCCA | 2185 | Qy | 3188 | ATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACTCTGAGCAGCGGACCCCTGGGTAC | 3247 |
| Db | 2098 | GACCAAGTCTCCGGCCACGGAACGTATCTTCAAGAAAGTGGCTCTGCACTGTGACCTT | 2157 | Db | 3178 | ACTACAATTTCCAGGAACAGATTTTGAACACTCTCTACTTGTAGTTCCAGAGCTGCAGGGTAT | 3237 |
| Qy | 2186 | AGCTGGACTGGACACGACTGTTCTATCGAGATCTGTCTCCGACTGTGTGGTGCCTATGGC | 2245 | Qy | 3248 | AAATCTGTCTGAGGATGAGCTCACCCACCCGACCATCCCTTTCACCTCATGAAAGTG | 3307 |
| Db | 2158 | AACTGGACTGGCCAGACTGCTCAACGAAATATGTTCTGTGGACTGTGGCTCACACGGC | 2217 | Db | 3238 | AAAGTCAGTTCTCAAGATCACCATGACCCAGTCTATTATTTCATTTAATGAAGGTT | 3297 |
| Qy | 2246 | GTGTGCTAGGGGCACCTCGCTGCGAGGATGGCTGGATGGGGGAGAGCCTGGACCAAG | 2305 | Qy | 3308 | CACCTCATGTAGCGGTGGAGGCCGCTCTTCAGGAAGTGGTTCGCTGCAGGCCCCAGAC | 3367 |
| Db | 2218 | GTTTGCATGGGGGGAGCTGTGCTGTGAAGAGGCTGGAGCGGGCCAGCTGTAAATCAG | 2277 | Db | 3298 | CATCTTATGTAGTGTAGTAGGAAGACTCTTCCAAAGTGGTTCCTGCTCACCAAC | 3357 |
| Qy | 2306 | CGSGCTGCCACCGCGCTGTGCCGACATGGGACCTGCCCGACGCAAGTGGAGTGC | 2365 | Qy | 3368 | CTGTCTTATTTATTTTGGGAACAAGACAGCGTCTACAACCAAGAGGTGTTTGGGCTT | 3427 |
| Db | 2278 | AGAGCTTGCCACCCCTGTGCGGACACGGGACCTTCAAGATGGCAAGTGTGAATGC | 2337 | Db | 3358 | TTGGCTATACTTTTCATATGGGATAAAACAGATGCATATAATCAGAAAGTCTATGGTCTA | 3417 |
| Qy | 2366 | AGCCCTGGCTGGAATGGCGAACACTGCACCATCGCTCACTATCTGGATAGGGTAGT--- | 2421 | Qy | 3428 | TCAGAACCTTTGTCTTCGTGGTATGAATATGAATCCTGCCAGATCTAACTCTGTGG | 3487 |
| Db | 2338 | AGCCAGGCTGGAATGGAGAGCACTGCACATCGCTCACTATTTGGATAAGATGTTAA | 2397 | Db | 3418 | TCTGAAGCTGTTGTGTGAGTGGATATGATGAGTCTGTTGGACCTGACTCTGTGG | 3477 |
| Qy | 2422 | -----TAAAGAGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTACC | 2467 | Qy | 3488 | GAAAAAGAACACAGTGTGACGGGCTATGAAATTTGACCGTCCAAGCTTGGAGGATGG | 3547 |
| Db | 2398 | GACAAGATAGGATATAAAGAGGTTGTCTGGTCTGTGCAACAGCAATGGAAGATGTACC | 2457 | Db | 3478 | GAAAGAGGACTGCCAATCTGCAGGGCTATGAATTTGGATGCGTCCAAACATGGGTGGCTGG | 3537 |
| Qy | 2468 | TTAGACCTGAATGTTGGCACTGCTGCCAGCTGGCTGGAGAGAGCTGGCTGTGAC | 2527 | Qy | 3548 | AGCTTAGACAAACATCATGCTTCAACATTTCAAGTGGTATCTCTGCACAAAGGGAATGGG | 3607 |
| Db | 2458 | CTGACCAAAATGGCGACATTTGTGTGCCAGCTTGGATGGAGAGGAGCAGGCTGTGAC | 2517 | Db | 3538 | ACATTAGATAAACATCACGTGCTGGATGTACAGAACGGTATACTGTACAGGGAACCGG | 3597 |
| Qy | 2528 | ACTTCCATGGAGACTGCTCGGTGACAGCAAAAGACAAATGATGAGATGGCTTGGTGGAC | 2587 | Qy | 3608 | GAGAACAGTGTGTCTCAGCAGCCTCTGTCTTGTGGGAGCATCATGGGCAATGGGCGC | 3667 |
| Db | 2518 | GTAGCCATGGAGACTCTTTGCACAGATAGCAAGGACAAATGAAGGGATGGACTCATTTGAC | 2577 | Db | 3598 | GAAACACGATTCTATCTCCAGCAGCCTCCAGTGTGAGTAGCATCATGGGCAATGGGCGA | 3657 |
| Qy | 2588 | TGATGACCTGTGCTGCTCCAGCCCTGTGCCATATCAACCCGCTGTGCTTGGC | 2647 | Qy | 3668 | CGGAGAGCATCTCTGCGCCCGCTGCAACGGGCTTGTCTGACGCGCAACAGCTCTCGGCC | 3727 |
| Db | 2578 | TGCATGGATCCGATTTGCTGCTACAGATTTCTGCGCAGAAATCAGCCCTATTGTGCGGGA | 2637 | Db | 3658 | AGCGGAGCATTTCTGCGCCCGCTGCAATGGTCAAGCTGATGGTAAAGTACTTACTGGCC | 3717 |
| Qy | 2648 | TCCCTAACCTCTGGACATCATCCAGGACACAGTCCCTGTGTTCACAGCAGAACCTA | 2707 | Qy | 3728 | CCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAACTACATT | 3787 |
| Db | 2638 | CTGCCGATCTCTAGGACATCATTTAGCAAGCCCTTCAATGCGCTTCTCAGCAGCTGCC | 2697 | Db | 3718 | CCAGTGGCGCTAGCTTGTGGGATCGATGGCAGTCTGTACGTAGGCGATTTCAACTACGTG | 3777 |
| Qy | 2708 | CACCTCTTATGACCGCATCAAGTCTCTGTGGGAGGGACAGCAGCAGCAATAATCCCC | 2767 | Qy | 3788 | AGAAGGATCTTCCCTCTGGAAATGTCAACCAATCTCTAGAGCTGAGGAATAAGATTTC | 3847 |
| Db | | | | Db | 3778 | CGGCGGATATTCCCTTCTGGAATGTAAACAGTGTCTTAGAACCTAAGAAATAAGATTTT | 3837 |

| | | | | | | | |
|----|------|--|------|----|------|--|------|
| Qy | 3848 | AGACATAGTCACATGTCAGACACACAAATACCTACCTGGCCACAGACCCCATAGTGGGGCC | 3907 | Qy | 4928 | CGCGAGACTCTACTGGGATGCCCTCTGGCTGGTGTGCCAGATGCCAGGTACTACTGG | 4987 |
| Db | 3838 | AGACATAGCAGCAACCCAGCTCATAGATACCTTGCACCGATCCAGTCACGGAGAT | 3897 | Db | 4915 | AGACGGGACCCAAATCGCATGCCAGTTCGAGTGGTGTCTCTGTATAACCAAGTGATATGG | 4974 |
| Qy | 3908 | GTCTTCTCTTCTGACAGCAACAGCGGGGGTCTTTAAATCAAGTCCACTGTGGTGTG | 3967 | Qy | 4988 | GTGACCAATGGGACCAACAGTCGACCTCAAGAGTGTGACCAACAGACACAGAGTGGCC | 5047 |
| Db | 3898 | CTGTACGTTTCTGACACAAACCCCGCAGAAATTTATCGCCCAAGTCACTTACGGGGCA | 3957 | Db | 4975 | TTGACAAATAGGAACAAATGATGTTTGAAGGATGACTGTCTCAAGGACTGGAAATAGTT | 5034 |
| Qy | 3968 | AAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGACAGGTGACCAAGTCCCTCCCTTT | 4027 | Qy | 5048 | ATGATGACATACCATGGCAATTCGGGCTTCTGSCAACCAAAAGCAATGAAAACGGATGG | 5107 |
| Db | 3958 | AAAGACTTGAATAAAATGCAAGAGTCTGTCGAGGACAGGGAGCAATGCTTCCGTTT | 4017 | Db | 5035 | TTGTTTACTTACCATGGCAATATGAGGCTTTTACGCACTAAAGTGTAACTTGGATGG | 5094 |
| Qy | 4028 | GATGACATCTCGTGGGGGATGTGGGAAGGCCACAGAACCACTCACCAATCCGAG | 4087 | Qy | 5108 | ACAACTTTTATAGTACGACAGCTTTGGCGCTCGTCAAAATGTGACCTTCCCTACTGGC | 5167 |
| Db | 4018 | GACGAGCGAGATGTGGGGATGGAGGAAGCCCGTGGAAAGCCACACTCATGAGTCCCAA | 4077 | Db | 5095 | ACAACTTTTGTGACTATGACAGTGAAGTCTGTGACAAATGTTACGTTTCCAACTGGA | 5154 |
| Qy | 4088 | GGTATTACAGTGGACAAAGTTTGGGCTGATCTACTTCTGGTGGATGGCACCATGATCAGACG | 4147 | Qy | 5168 | CAGGTGAGCAGTTTCCGAAATGATACAGACAGTTTCACTGATGTCCTCAGGTAGACCTCC | 5227 |
| Db | 4078 | GGAAATGGCAGTTGATAAGAAATGGATTATCTACTTTGTTGATGGAACTGATAGGAA | 4137 | Db | 5155 | GTGGTCAAAACCTGCTATGGGACATGGAACAGGCTATCACAGTGGACATTTGAGTCACT | 5214 |
| Qy | 4148 | ATCGATCAGAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCACATCAGCCGG | 4207 | Qy | 5228 | AGC---NAGGATGATGTCAACCAACCAACCTGTCTGCCTCAGGCGCTTCTACACA | 5284 |
| Db | 4138 | GTGACCAAAATGGAATCATATCACTCTCTGGGCTCTAAGATTTGACTTCAGCCAGA | 4197 | Db | 5215 | AGCCGAGAAGAATGTGAGATCACTTCAAAATCTGTCTCGATCGATTTCTTTTACACC | 5274 |
| Qy | 4208 | CCACTCAGCTGTGATCTGTCATGGAATTTCCCGAGTAAAGTGAAGTGGAGTGGCCACAGAC | 4267 | Qy | 5285 | CTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCGGATGGCTCTTGGCGTG | 5344 |
| Db | 4198 | CTTTAACTTGTGACACCAAGTGCATCAGCCAGGTACGTCTGGAAATGGCCCACTGAC | 4257 | Db | 5275 | ATGTTTCAAGATCAGTTAAAGAACAGCTACAGATTTGGTTATGACGGCTCCTCAGAATT | 5334 |
| Qy | 4268 | TTAGCCATCAACCAATGGCAACTCACTTTATGTCTCGACAACAATGTGGTCTCTGCA | 4327 | Qy | 5345 | CTGCTGGCCAAACGGCATGGAGGTGGCGCTGAGACTGAGCCCACTTGTCTGGCTGGCACC | 5404 |
| Db | 4258 | CTAGCCATTAAACCTATGGATTAATCTCAATTTATGTCTGGATTAATATGATGATTTACAG | 4317 | Db | 5335 | ATCTAGCCAGTGGCTTGGACTCACTACTCAAAACAGAGCGCGACGTCTTGGCTGGCACC | 5394 |
| Qy | 4328 | ATCTCTGAAAACCAACAGGTGGCAATGTGCGCGGAGGCCCATGCACTGCCAGTCCCT | 4387 | Qy | 5405 | GTCAACCCCAACCGTGGCAAGAGGAATGTCACTGCTGCCCTCGACCAACGGCTCAACCTG | 5464 |
| Db | 4318 | ATCACTGAAAATCGTCAAGTTGCGATTGTGTGAGCGGCCCATGCACTGTCAAGTCCC | 4377 | Db | 5395 | GCTAATCCGACGGTTGCCAAAAGAAACAATGACTTTGCTGGCGAGAACGTTCAAACTTG | 5454 |
| Qy | 4388 | GGCATGACCACTTCTCTGTAAGCAAGTGGCCATCCAGCAACCTGGAGTCAGCCACC | 4447 | Qy | 5465 | GTGAGTGGGGCCAGCGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGGCGCGG | 5524 |
| Db | 4378 | GGAGTGG---AATATCTGTGGGGAAGCACGCGGTGCAGAACACTGGAAATCAGCCACT | 4434 | Db | 5455 | GTGGAATGGAGATTCGGAAGAGAGCAAGCCCAAGGAAAGTCAATGTCTTTGGCGGCAAG | 5514 |
| Qy | 4448 | GCTTTGGCTGTTTACACAATGGGGTCTGTATATTTGTGAGACTGATGAGAAAAGATC | 4507 | Qy | 5525 | CTGCGGTGCAACCCGAAATCTCTATCTCTGACATTTGATCGGTTACAGCACAGAG | 5584 |
| Db | 4435 | GCCATTGTGTCTCTACAGTGGGGTCTGTACATTTCTGAACTGATGAGAGAAAT | 4494 | Db | 5515 | CTCAGGGTTAATGCGAGAAACCTCTTTTCAGTTTGTATCGAACCAACAAAGACAGAA | 5574 |
| Qy | 4508 | AACCGCATCAGCAGGTCAACCATAGTGGAGAGATCTCACTGTTGTGGGGCCCCAGT | 4567 | Qy | 5585 | AAGATCTATGATGACACCGCAAGTTCACCTCTCGGATTTCTGTACGACAGCGCGGGCGG | 5644 |
| Db | 4495 | AACCGGATAAGGCAGGTCAACACAGATGGAGAAATCTCTTAGTGGCGGAATACCTTCA | 4554 | Db | 5575 | AAGATCTATGACGACCACTCGTAATTTCTAGGAGTGGCTACGACACGCTCTGGGCAC | 5634 |
| Qy | 4568 | GGCTGTGACTGTAAAATGATGCCAACTGCTGATTTGTTTCTGGAGACGATGGTTATGCC | 4627 | Qy | 5645 | CCCAGCTCTGGTCAACCCAGCAGCAGGTGAATGGTGTCAACGTTGACATCTCCCTGGG | 5704 |
| Db | 4555 | GAGTGTGACTGCAAAAATGATGCCAACTGTGACTGTATACCAAGTGGAGATGGCTACGCC | 4614 | Db | 5635 | CCGACTCTCTGGCTGCCAAGCAGCAAGCTGATGCGGTCAATGTCACTATTTCCACACA | 5694 |
| Qy | 4628 | AAGGATGCAAGTAAATACCCCATCTTCTTGGCTGTGTGCTGTGATGGGGAGCTCTAC | 4687 | Qy | 5705 | GGTTACATTTGCTGGATCCAGAGGGGATCATGTCTGAAAGAAATGGAATAGACACGGCG | 5764 |
| Db | 4615 | AAGGATGCCAACTCAGTGGCCCATCTCTCCCTGGCTGTCTTCCAGATGGTACATGTAT | 4674 | Db | 5695 | GGTCAAAATGGCAGCATCCAGCGAGGCCACCTAGCGAGAAAGTAGATTATGACGGACAG | 5754 |
| Qy | 4688 | GTGGCGGACCTTTGGGAACATCCGAATTCGGTTTATCCGGAGAAACAAAGCTTTCTCAAC | 4747 | Qy | 5765 | GGCCGCTACATCCAGSATCTTCTGATGGGAAGACATGGAGCTACACATCTATTAGAG | 5824 |
| Db | 4675 | ATTGCAGATCTAGGGAATATCCGGATCCGGGCTGTGTCAAGAAATAAGCCTTTACTTAAC | 4734 | Db | 5755 | GGGAGGATCGGTCTCGGGTCTTTGCTGATGGTAAACATGGAGTTACACATATTAGAA | 5814 |
| Qy | 4748 | ACCCAGAACATGATGAGCTGTCTTCAACCAATTTGACGAGGACTCTATCTGTTGATACC | 4807 | Qy | 5825 | AAGTCCATGTGCTGCTACTACACAGCCAGAGGAGTATATCTTTTGGAGTTCGACAAAGAT | 5884 |
| Db | 4735 | TCTATGAATCTTATGAAGTTGCGTCTCCAACTGATCAAGAACTCTACATCTTTGACATC | 4794 | Db | 5815 | AAGTCCATGGTCTTCTGCTTCATAGCCAGCGGAGTACATCTTTCGAATACGATATGTTG | 5874 |
| Qy | 4808 | ACCGCAAGCACCTGTACACCCAAAGCCCTGCCACAGGAGACTACTGTACAACTTCACC | 4867 | Qy | 5885 | GACCGCTCTCTTCTGTGACGATGCCCAACGTGGGGCGGACAGACTAGAGACCATCCGC | 5944 |
| Db | 4795 | AATGGTACTCACCAATATACTGTAGTTTAGTCACTGTGTGATTAATCTTACAAATTTAGC | 4854 | Db | 5875 | GACCGCTCTCTGCGCATCACCATGCCAGTGGCTCGCCACACCATCGACACCATCCGA | 5934 |
| Qy | 4868 | TACACTGGGGCGGCGACATCACTCATACAGACAAACAAATGGCAACATGTTAAATGTC | 4927 | Qy | 5945 | TCAGTGGGCTACTACAGAAACATCTATCAGCCCTCTGAGGGCAATGCTCAGTCTATACAG | 6004 |
| Db | 4855 | TACAGCAATGCAATGATATTACTGCTGTGACAGACAGCAATGGCAACACCCCTTAGAATT | 4914 | Db | 5935 | TCCATTTGGCTACTACCGCAACATATACAAACCCCGGAAAGCAAGCCCTCCATCATCAG | 5994 |
| | | | | Qy | 6005 | GACTTCTAGGATGGGCACCTCTTTCACACCTTTCTACCTGGGCACTGGCGCGAGGGTG | 6064 |

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|----------------------------------|---|---------------------|--|------|
| QY | 8225 | ACAGGGCGGGTGC | AAAGCGTACGACGGGTTTTTCGTGATCTCTGTCGAGCAGTACCCAGAA | 8284 |
| DB | 8197 | GCGGCAAGGTG | CAGGCTACGACGGGTACTACGTACTCTCGGTGGAGCAGTACCCCGAG | 8256 |
| QY | 8285 | CTGTCAGACAGCGCCCAAC | CAATCCACTTCATGAGACAGACGAGATGGGCCCGAGGTGA | 8344 |
| DB | 8257 | CTGGCCGACAGCGCCCAAC | ATCCAGTTCCTGCGGCAGAGCGAGATCGGCAGGAGTAA | 8316 |
| QY | 8345 | C | 8345 | |
| DB | 8317 | C | 8317 | |
| RESULT 11 | | | | |
| ADH41972 | | | | |
| ADH41972 standard; DNA; 8204 BP. | | | | |
| XX | ADH41972; | | | |
| XX | 25-MAR-2004 | (first entry) | | |
| XX | Novel human nucleic acid NOV40u. | | | |
| XX | ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; | | | |
| XX | anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; | | | |
| XX | neurotropic; antiparkinsonian; antiasthmatic; antiinfertility; | | | |
| XX | cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; | | | |
| XX | AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease; | | | |
| XX | Parkinson's disease; asthma; fertility disorder; chromosome mapping; | | | |
| XX | tissue typing; preventive medicine; pharmacogenomic; vaccine. | | | |
| OS | Homo sapiens. | | | |
| XX | WO2003102159-A2. | | | |
| XX | 11-DEC-2003. | | | |
| XX | 04-JUN-2003; 2003WO-US017573. | | | |
| XX | 04-JUN-2002; 2002US-0385490P. | | | |
| PR | 04-JUN-2002; 2002US-0385615P. | | | |
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| PR | 05-JUN-2002; 2002US-0386041P. | | | |
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| PR | 10-JUN-2002; 2002US-0387423P. | | | |
| PR | 10-JUN-2002; 2002US-0387540P. | | | |
| PR | 10-JUN-2002; 2002US-0387866P. | | | |
| PR | 11-JUN-2002; 2002US-0387606P. | | | |
| PR | 11-JUN-2002; 2002US-0387610P. | | | |
| PR | 11-JUN-2002; 2002US-0387659P. | | | |
| PR | 11-JUN-2002; 2002US-0387668P. | | | |
| PR | 11-JUN-2002; 2002US-0387696P. | | | |
| PR | 11-JUN-2002; 2002US-0387859P. | | | |
| PR | 12-JUN-2002; 2002US-0387934P. | | | |
| PR | 12-JUN-2002; 2002US-0387960P. | | | |
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| PR | 12-JUN-2002; 2002US-0388432P. | | | |
| PR | 12-JUN-2002; 2002US-0388479P. | | | |
| PR | 13-JUN-2002; 2002US-0389123P. | | | |
| PR | 14-JUN-2002; 2002US-0389120P. | | | |

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|----|------|--|------|----|------|---|------|
| Db | 64 | CGCGCTACACAAATTCCTCCGACAGCAATGAGGAGTGC GGGTACCCACACAGAAAGTCC | 123 | Db | 1039 | GACACATTTGAGA-----ATGGAAAAAGTGAATTCGTATACATGCCAACAAACACTGTG | 1092 |
| Qy | 149 | TACAGCTCCAGCGAGACCCCTGAAGGCTAGACACAGGA---CGCCGCGCTAGCCTATGGC | 205 | Qy | 1226 | CTATACCCCTCAGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAGAACCAACA | 1285 |
| Db | 124 | TACAGTTCCAGCGAGACATTTGAAGGCTTTTGTATCATGATTCCTCGCGGCTGCTTTACGGC | 183 | Db | 1093 | TCATTTACCTTTCTGGAGACA----- | 1111 |
| Qy | 206 | AGCGCGTCAAGGACATTTGCGCGAGGAGGCGAGGAATTCGCGCGACAGGTGCCAAC | 265 | Qy | 1286 | GAAGGAAAGCCAGTAGTTTCTTCCAGAGGACAGTTTTCATAGATTTCTGGAGAAATTTGAT | 1345 |
| Db | 184 | AACAGATGAGATTTGGTTTACAGAGAAGCAGACGATTTCTAGACAGGACAGAAAT | 243 | Db | 1112 | -ATGGAAAAATTAGTGGATTTACGCAAGAAAAATAACCATAGATTTCCGGAGAACTTGAT | 1170 |
| Qy | 266 | TTCAACCTCGCGGAGCTGGGGCTGGGAAGATTAACGCCCCCTTCAACGGGACCTGTATCCGG | 325 | Qy | 1346 | GTGGGAAGCGAGCCCTCCAGAGATTTCTCTGGCACCTTTCTGGAGATCTCAAGTGTTC | 1405 |
| Db | 244 | TTTACCCTAAGGCAGTTAGGAGTTTGTGAACAGCAACTCGAAGAGGACTGGCAATTTGT | 303 | Db | 1171 | ATTGGCCGAAGAGCAATTCAGAGATTTCTCCGGGATCTTCTGGAGATTCACAGCTCTTC | 1230 |
| Qy | 326 | ACAGACATTTGGCCTGCCCAATGGGCTACTCATGGGGCTGGCTGTATGCCGACATG | 385 | Qy | 1406 | ATAGACCAATCCTGTGTCATCTGAAATTCATATGTGTCTCTGGGAAAGGACGCCCTGTGTGC | 1465 |
| Db | 304 | GCGGAAATGGGCTCCCTCACAGAGGTTACTCTATCAGTGCAGGGGTGATGCTGATACT | 363 | Db | 1231 | ATTGATCAGCACAGTTTCTTAATTCATATCTCTCTCAGAGGATGCAITGATTGGA | 1290 |
| Qy | 386 | GAGGCTGACACGGTGTCTCCCTGAGACCCCGTGGTCTGTGGGGCGGAGCACACGG | 445 | Qy | 1466 | ATTTATGGCAGAAAAAGGCTCCTCTCTTCCACATA-----CACAGTTTGACTTT | 1513 |
| Db | 364 | GAATATGAAGCATGATGTCCCGAGAGCATGCCATGAGACTTTGGGGCAGGGGGTCAAA | 423 | Db | 1291 | GTATATGGCCGGAAGAGTTACCGCTTCCCATACTCAGTCTCTCCCGCCAGTATGACTTC | 1350 |
| Qy | 446 | TCAGGCGCAGCTCTGCTGTCCAGCGGGGCCAATTTCCAATCTCACACTCACCGACCC | 505 | Qy | 1514 | GTGAGCTCTCGATGGCAGGAGGCTCTAAACCAGGAGCGCGGAGCCTTAGAGGGACC | 1573 |
| Db | 424 | TCAGGCGCAGCTCTGCTGTCCAGTCCGTCCCACTCAGCCCTCAGCCCTGACAGATACG | 483 | Db | 1351 | GTGAGCTCTCGATGGCAGGAGGCTGATTCAGAGAGCAGCGGAGCCTGCTTGAGACG | 1410 |
| Qy | 506 | GAGCATGAAGAACTGAGACTGATCATCCGGGGCGGCTGAGAACACAGCGGGCTCCGG | 565 | Qy | 1574 | CGCGCAGTCTCGGGAACTGTGCCCCCTCCAGCATGAGACAGGCTTCATCCAGTAT | 1633 |
| Db | 484 | GAGCAGGAAACAGTCCGACAGTGAATGAGCAACCTGCAAGCAATCAAGGCCAGTCT | 543 | Db | 1411 | GAGAGAGCGGGCGGAGGAGATCCGTACAGCTTCATGAGGCGGCTTATTCAGTAC | 1470 |
| Qy | 566 | ACGCGCGCGCGCTCTCGACGCCCAACACCCCAACAGCAGCACCGCGGCTCCATT | 625 | Qy | 1634 | TTGGATTCAGGAATCTGGCACTTGGCTTTTTCATAGCGGAAAGAGTCAGAACTGGTT | 1693 |
| Db | 544 | ACCTCGAGCGCTTCCGCTTCCATAGACGACTCTGCAAGCATCATCATCATC | 603 | Db | 1471 | TTGGATTCAGGAATCTGGCACTTGGCTTTTTCATAGTGGGAAAAATGCGAGCAGGTG | 1530 |
| Qy | 626 | AACTCCTGAACCGGGGCACTTCAGCGCGAGGAGCAACCCAGCGCGGCCCCACAGGAC | 685 | Qy | 1694 | TCTTTTCTCACCACTGCCATTCAGTCGGTGGATTAAGTCCCGAGCACTGCTATGSCAAT | 1753 |
| Db | 604 | ACTTCTCTCAAGAACTCCCTGACCAATAGAAGGAACAGAGTCGGCGCCCGCGCT | 663 | Db | 1531 | TCTTTTAATACCATTTGTTATAGAGTCTGTGGTGGAAATGTCCCGAAATTGCCATGAAAT | 1590 |
| Qy | 686 | CATCGCTCTCGGAGAGCCCTTCCGGCGGCGCCAGAGAGCTGCGCCAGCGCCAGGAG | 745 | Qy | 1754 | GGTACTGATCTCTGGGACCTGCCACTGCTCTCTGGGTTTCTGGGCGCCGACTGTGGC | 1813 |
| Db | 664 | GCTTTGCCCGCGAGTGCAAAC-----CACACCCGAGTCCGTCCAGCTGCGAGGAC | 714 | Db | 1591 | GGAGATGCGTTTCTGGAACTTGCCATTTGTTTCCAGGATTTCTGGGTCCGATTTGTTCA | 1650 |
| Qy | 746 | AACTGGCTCTCAACAGCAATCCCTCGAGACCCAGGAACTTAGGCAAGCAGCCATTC | 805 | Qy | 1814 | AGAGCCTCTGCCCCGTGCTCTGTAGCGGAAATGCGCAATATAGAAAGCAGATGCTTG | 1873 |
| Db | 715 | AGCTGGGTCTTGCGAGTAATGATACCACTGGAAAGCAGGCAATTT----- | 758 | Db | 1651 | AGAGCGCTGTCCAGTGTATGTAGTGGCAACGGGCACTACTCCAAGGCGCGCTGCCCTG | 1710 |
| Qy | 806 | CTAGGGACATTCAGGAGCAACCTCATTTAGATGGACATTTCTCGCGCGCTCCCGCCATGAT | 865 | Qy | 1874 | TGCCACAGTGGCTGGAAAGCGCTGATGCGATGTCGCCACCAACAGTGTATCGATGTG | 1933 |
| Db | 759 | ----- | 758 | Db | 1711 | TGTTTCAGCGGCTGGAAAGGCGCACCGAGTGTGATGTGCGGACTACCCAGTGTATTTGACCCA | 1770 |
| Qy | 866 | GGGGCTTACAGTGAAGGCACTTCTCTTCAAGCTGGAGGCACTTCCCGCTCTTCTGTCG | 925 | Qy | 1934 | GCCTGCAGCAACCATGSCACCTGCATCAGGGCACCTGCATCTGCAACCTCGGCTACAAG | 1993 |
| Db | 759 | -----CCTATTCAAAAACAGGAACAGGTACAAACGCGCACTGTTCACT | 798 | Db | 1771 | CAGTGTGGGGTGTGGGATTTGTATCATGGGCTCTGTGCTTGCAGCTCAGGATACAA | 1830 |
| Qy | 926 | ACCACATCAGCGGTACCACTGAGCTGCAGCACAGTGTACTCTCTCGCGCCCGACCC | 985 | Qy | 1994 | GGCGAGAGTGTGAGGAAGTGGATGTCATGGACCCCAATGTTTCAGGCCGGGTGTCTGC | 2053 |
| Db | 799 | ACTGCAACCCAGGATACAAATGGCATCTGGCTCTGTTTATTCACCACCCTACTCGGCCA | 858 | Db | 1831 | GGAGAAAGTTGTGAAGAGCTGACTATAGACCCCTGGGTGTTCTTAATCATGCTGTGTGT | 1890 |
| Qy | 986 | CTGCGCGCAGCACCTTTCGCGCGCGGCTTTAACTCAAGAAAGCCCTCCAAAGTACTGT | 1045 | Qy | 2054 | GTGAGAGGCAATGCGCAITGCTTTTGGGATGGGAGGACCAACTGCGAGACCCCGAGG | 2113 |
| Db | 859 | CTACCTAGAAACACCTTATCAAGAGTCTTTTAATTCAGAAAGTCTTCAAGTACTGT | 918 | Db | 1891 | ATCCACGGGAAATGTCACTGCAGTCCAGGATGGGAGGTAGCAATTTGTGAAATACTGAAG | 1950 |
| Qy | 1046 | AACTGGAAGTGCAGCCCTGAGCGGCATCTGTCATCTCAGCCACTCTGTGTCTCTGCTG | 1105 | Qy | 2114 | GCCACATGCTTAGACAGTGTTCAGGCGCACGGAACCTTCTCTCCGGACACCGGGCTTTCG | 2173 |
| Db | 919 | AGCTGGAATGCACTGCACTGTGTGCGGTAGGGGTCTCGGTGTCTCTGGCAATACTCCTG | 978 | Db | 1951 | ACCATGTGTCAGACAGTGTCTCCGGCCACGGAAACGATATCTTCAAGAAAGTGTCTCTGC | 2010 |
| Qy | 1106 | GCATCTTTTGGCCATGCACTTTTGGGCTTAACTGGCACTGACGCGATGAGGGGG | 1165 | Qy | 2174 | AGCTGTGACCCCAAGCTGGACCTGGACACGACTGTCTTCTATCGAGATCTGTCTGCCGACTGT | 2233 |
| Db | 979 | TCTTATTTTATAGCAATGCACTCTTTTGGGCTTCACTGGCAGCTTACAGCAGACTGAAAT | 1038 | Db | 2011 | ACGTGTGACCCCTAACCTGGACTGGCCCGAGACTGCTCAACGAAATATGTTCTGTGGACTGT | 2070 |
| Qy | 1166 | CAGATGTATGAGATCACGGAGGACACAGCGAGCATTTGGCTGTGTGCCAACCGGCTCTCC | 1225 | Qy | 2234 | GTGGCCATGTGGCGTGTGCGTAGGGGCGACCTGCGCGTGGAGGATGCGTGGATGGGGGCA | 2293 |
| Db | | | | Db | 2071 | GGCTCACACGGCGTTTTCATGCGGGGAGCGTGTGCTGTGGAAGAGCTGGACGGGCCCCA | 2130 |

| | | | | | | | |
|----|------|--|------|----|------|---|------|
| QY | 2294 | GCCTGCGACCGGGGCTGCCACCCGCGTGTGCCGAGATGGGACCTCCCGCGACGC | 2353 | QY | 3356 | GCAGCCCCAGACCTGTCTTATTATTCTTATTTGGGCAAGACAGACGCTCTCAACCCAGAAG | 3415 |
| Db | 2131 | GCCTGTAAATCAGAGAGCTGCCACCCCGCTGTGCCGAGCAAGGACCTGCAAGGATGGC | 2190 | Db | 3211 | GCTCACCACAACTTGGCCTATATCTTTTATATGGGATAAACAAGATGCATATATACAGAAA | 3270 |
| QY | 2354 | AAGTGCAGATGACGCCCTGGCTGGAATGGGGAACACTGCAACCATCGCTCACTATCTGGAT | 2413 | QY | 3416 | GTGTTTGGGCTTTTCAGAAAGCCTTTGTTCCGTGGGTATGAATATGAATCTCTGCCAGAT | 3475 |
| Db | 2191 | AAGTGTGAATCGACCCAGGGCTGGAATGGAGAGCACTGCATCTATCGCTCACTATTTGGAT | 2250 | Db | 3271 | GTCTATGCTCTATCTGAAGCTGTGTGTCAGTTGGATATGAGTATGAGTCGTGTGGAC | 3330 |
| QY | 2414 | AGGGTAGT-----TAAAGAGGGTTGGCCCTGGGTTGTGCAATGGCAAC | 2455 | QY | 3476 | CTAATCTGTGGGAAAAAAGAACACAGCTGTCAGGGCTATGAAATTGACCGCTCCAAG | 3535 |
| Db | 2251 | AAGATAGTTAAAGACAAGATAGGATATAAAGAGGGTTGTCTGTGCTGTGCAACAGCAAT | 2310 | Db | 3331 | CTGACTCTGTGGGAAAAGAGGACTGCCATTCTGACAGGGCTATGAAATTGATGGTCCAAC | 3390 |
| QY | 2456 | GGCAGATGATCTTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGAGAGGA | 2515 | QY | 3536 | CTTGGAGGATGGAGCCCTAGACAAACATCATGCCCTCAACATTCAAAAGTGGTATCTCTGCAC | 3595 |
| Db | 2311 | GGAAAGATGATCCCTGGACCAAAATGGCGGACATTTGTGTGTGCCAGCCCTGGATGGAGGA | 2370 | Db | 3391 | ATGGGTGGCTGGACATTAGATAAAACATCACGTGCTGGATGTACAGAAACGGTATACTGTAC | 3450 |
| QY | 2516 | GCTGGCTGTGACACTTCCATGGAGACTGCCCTGGGTGACAGCAAGACAATGATGGAGAT | 2575 | QY | 3596 | AAAGGAAATGGGGAGAAACCAAGTTTGTCTCAGCAGCCCTCTCTCAATTGGGAGCATCATG | 3655 |
| Db | 2371 | GCAGGCTGTGACGTAGCCATGGAGACTCTTTTGCAAGATAGCAAGGACAATGAAGGGAT | 2430 | Db | 3451 | AAGGAAAACGGGAAAAACCAAGTTTCATCTCCAGCAGCCTCCAGTCTGTGAGTAGCATCATG | 3510 |
| QY | 2576 | GGCTGTGTGACTGTGATGGACCTGACTGCTGCTCCCTCCAGCCCTGTGCCATPATCAACCCG | 2635 | QY | 3656 | GGCAATGGGGCGCGGAGAAAGCATCTCTGCCAGCTGCAACCGCCCTTGTCTGACGGCAAC | 3715 |
| Db | 2431 | GGACTCATGTGACTGATGATCCGATTCGATTTGCTGCTACAGAGTTCCTGCCGAATCAGGCC | 2490 | Db | 3511 | GGCAATGGGGGAAGGCGCAGCATTTCTGCCCCAGTTGCAATGGTCAAGCTGATGTTAAC | 3570 |
| QY | 2636 | CTGTGCCCTTGGCTCCCTTAACCCCTTGGAATCATTCAGAGGACACAGGTCCTCTGTGCA | 2695 | QY | 3716 | AAGCTCTCTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGAT | 3775 |
| Db | 2491 | TATTTGCGGGGACTGCCGGATCCTCAGGACATCATTTAGCCAAAGCCTTCAATCGCCTTCT | 2550 | Db | 3571 | AAGTTACTGGCCCCAGTGGCGCTAGCTTTGTGGGATCGATGGCAGTCTGTACGTAGGCGAT | 3630 |
| QY | 2696 | CAGCAGAACCTTACACTCTCTCTATGACCGCATCAAGTTCCCTGCTGGGCGAGGACAGCAGC | 2755 | QY | 3776 | TTCAACTACATTAGAGGATCTTCCCTCTGGAAATGTCAACCAACATCTCTAGAGCTGAGG | 3835 |
| Db | 2551 | CAGCAAGTGGCAATTCCTTTATGATCGAATCAGTTTCCCTTATAGGATCTGATAGCACC | 2610 | Db | 3631 | TTCAACTACGTGGCGCGGATATTTCCCTTTCTGGAAATGTAAACAAGTGTCTTAGAACTAAGA | 3690 |
| QY | 2756 | CACATAATCCCCGGGGAGAACCCCTTTGATGGAGGGCATGCTGTGTTATTTCTGTGGCCAA | 2815 | QY | 3836 | AATAAAGATTTACAGACATAGTCAAGTCCAGACACACAAATACTACCTGGCCACAGACCCC | 3895 |
| Db | 2611 | CATGTTATACCTGGAGAAAGTCTTTCAATAAGAGCCTTGCATCTGTATCAGAGGGCCAA | 2670 | Db | 3691 | AATAAAGATTTTAGACATACAGCAGCAACCCAGCTCATAGATACTACCTTGCACCGATCCA | 3750 |
| QY | 2816 | GTGATGACATCAGATGGAAACCCCTTGGTTGGTGTGAACATCAGTTTGTCAATAACCCCT | 2875 | QY | 3896 | ATGAGTGGGGCCGCTTCTCTCTTGACAGCAACAGCGCGGGCTTTTAAATCAAGTCC | 3955 |
| Db | 2671 | GTACTGACTGTGTGATGGAACTCCACTTATTTGGAGTAAATGTCTCGTTTTTCCATTACCCA | 2730 | Db | 3751 | GTACGGGAGATCTGTACGTTTCTTGACACAAACACCCCGCAGAAATTTATCGCCCCAAAGTCA | 3810 |
| QY | 2876 | CTCTTTGGATATACAAATCAGCAGGCAAGATGGCAGCTTTTGACTTGGTGACAAATGGCGGC | 2935 | QY | 3956 | ACTGTGTGTGTGAGGACCTTGTCAAGAACTCTGAGGTGTTGGCGGACAGAGTGCACAG | 4015 |
| Db | 2731 | GAATATGGATATACTATTACCGCCAGGACGGAATGTTTGACTTGGTGGCAAAATGGTGGG | 2790 | Db | 3811 | CTTACGGGGGCAAAAGACTTGAACATAAATGCAAGAGTCTGTCGAGGACAGGGGAGCAA | 3870 |
| QY | 2936 | ATCTCCATCATCCTCGGTTTCAGCGGGCACTTTTCATCACAACAGGAGCACCCCTGTGG | 2995 | QY | 4016 | TGCCTCCCTCTTGATGACACTCGCTCGGGGATGGTGGGAAGGCCACAGAAAGCCACACTC | 4075 |
| Db | 2791 | GCCTCTCTAACTTTGGTATTTGAAGGATCCCAATTCCTCACTCAGTATCATACTGTGTGG | 2850 | Db | 3871 | TGCTTCCGTTTGACAGGCGAGATGTGGGATGGAGGGAAGGCCGTGGAAAGCCACACTC | 3930 |
| QY | 2996 | CTGCCATGGGATCGCTTCTTCTGTCATGGAACCATCATCATGAGACATGAGGAGATGAG | 3055 | QY | 4076 | ACCAATCCAGGGGTATTAACAGTGGACAAGTTTGGGCTGATCTACTTCTGATGGGACCC | 4135 |
| Db | 2851 | ATTCCATGGAATGTCTTTTATGTGATGGATACCTAGTCAATGGAGAAAGAGAGATGAC | 2910 | Db | 3931 | ATGAGTCCCAAGGAATGGCAGTTGATAAGAAATGGAATTAATCTACTTTTGTGTGAGAAC | 3990 |
| QY | 3056 | ATTCCAGCTGTGACCTGAGCAATTTTGGCCGCCCAACCCCAAGTCGTCTCTCCATCCCA | 3115 | QY | 4136 | ATGATCAGACGATCGATCAGAAATGGGATCATCTCCACCCCTGCTCGGCTCTTAATGATCTC | 4195 |
| Db | 2911 | ATTCCAGCTGTGATCTGAGTGGATTCGTTGAGGCCAAATCCCATCATTTGTGTCACTGCT | 2970 | Db | 3991 | ATGATTTAGGAAGTTGACCAAAATGGAAATCATATCAACTCTTCTGGGCTCTTAACGATTTG | 4050 |
| QY | 3116 | CTGACGCTCTCGCAGCTCTGTGACAGAAAGGCCCAATTTGGCCGGAATTCAGGCT | 3175 | QY | 4196 | ACATCAGCCCGGCCACTCAGCTGTGATTTCTGTCAATGATATTTCCAGGTGAAGTGGAG | 4255 |
| Db | 2971 | TTATCCACCTTTTTCAGATCTTCTCTGTAAGACAGTCCCATCATTTCCCGAAAAACAGGTA | 3030 | Db | 4051 | ACTTCAGCCAGACCTTTAACTTTGTGACACCAGCATGCAATCATCAGCCAGGTACGCTTGAA | 4110 |
| QY | 3176 | TTGCGAGGGAATCTCTATCTCTGCTGCAAGATGAGGCTGAGCTTACCTGAGAGCCGG | 3235 | QY | 4256 | TGGCCCAACAGACTTAGCCATCAACCAATGGAACACTCACTTTATGTCTCTCGAACAAAT | 4315 |
| Db | 3031 | CTCCAGAGGAATCTAATTTCCAGGAACAGATTTGAAACTCTCTACTTGTAGTTCCAGA | 3090 | Db | 4111 | TGGCCCACTGACCTAGCCATTAAACCTATGATTAATCTCCATTTATGTCTCTGATTAAT | 4170 |
| QY | 3236 | ACCCCTGGCTACAAATCTGTCTGAGGATCAGCCTCAACCCAGCCAGCAATCCCTTTCAAC | 3295 | QY | 4316 | GTGTGCTGTGCAAAATCTCTGAAAAACCAACAGGTGGGCAATTTGCGGGGAGGCCCATGAC | 4375 |
| Db | 3091 | GCTGCAAGGATTAAGTCAGTTCTCAAGATCACCATGACCCAGTCTATTATTCATTTAAT | 3150 | Db | 4171 | GTAGTTTACAGATCACTGAAATCGTCAAGTTCGCAATTTGCTGTGACGGGCCCATGAC | 4230 |
| QY | 3296 | CTCATGAGTGCACCTCATGTGAGGCTGGAGGGCCGCTCTTTCAGGAAGTGGTTCGCT | 3355 | QY | 4376 | TGCCAGGTCCCTGGCATTTGACCACTTCTCTGTGAAGAGGTGGCCATCCACGCAACCTG | 4435 |
| Db | 3151 | TTAATGAAGGTTTCATCTTATGGTAGTGTAGTAGGAAGACTCTTCCAAAAAGTGGTTCT | 3210 | Db | 4231 | TGTCAGGTTCGCGGAGTGG---AATAATCTGTGGGGAAGCAGCGGTCAGACAACTG | 4287 |
| QY | | | | QY | 4436 | GAGTCAGCCACCGCTTTTGGCTGTTTTCACACAAATGGGGTCTCTGTATATTTGCTGAGACTGAT | 4495 |

| | | | | | | | |
|----|------|--|------|----|------|---|------|
| Db | 4288 | GAATCAGCCACTGCCATTCGTGTCTCCTACAGTGGGGTCTCTGTACATTAATCTGAAACTGAT | 4347 | Db | 5368 | TTTGGCCGCAAGCTCAGGGTTAATGGCAGAAACCTCCTCTTTCAGTTGACTTTTGATCGAACA | 5427 |
| Qy | 4496 | GAGAAAAGATCAACCGCATCAGCAGGTCCACACTAGTAGGGAGAGATCTCACTCGTTGCT | 4555 | Qy | 5573 | ACACCCACAGAGAAGATCTATGATGACCAACCGCAAGTTTACCCCTTCGGATTCCTGTACGAC | 5632 |
| Db | 4348 | GAGAAGAAATTAACCGGATAGCGGATAGGAGGTCCACACAGATGGAGAAATCTCCTTAGTGGCC | 4407 | Db | 5428 | ACAAAGACAGAAAAGATCTATGACGACCAACCGTAATTTCTACTGAGGATCGCCTACGAC | 5487 |
| Qy | 4556 | GGGGCCCCAGTGGCTGTACTGTAAAAATGATGCCAACTGTGATTTGTTTTCTGAGAC | 4615 | Qy | 5633 | CAGGCGGGCGGCCAGCGCTCTGTGTACCCAGCAGCAGCTGAATGGTGTCAACGTGACA | 5692 |
| Db | 4408 | GGATACCTTCAGAGTGTGACTGCAAAATGATGCCAACTGTGATTTGTTTTCTGAGAC | 4467 | Db | 5488 | ACGTCGTGGCACCCGACTCTCTGGCTGCCAAGCAGCAAGCTGATGGCCGTCAATGTCACC | 5547 |
| Qy | 4616 | GATGGTTATGCCAAGATGCAAAAGTTAAATACCCCATCTTCCTTGCTGTGTGTGCTGAT | 4675 | Qy | 5693 | TACTCCCTGGGGTTTACATTTCTGCTGCATCCAGAGGGGCATCATGCTGTAAGAAATGGA | 5752 |
| Db | 4468 | GATGGCTAGCCCAAGATGCCAACTCAGTGCCCCATCTCCCTGGCTGCTTCTCCAGAT | 4527 | Db | 5548 | TATTCATCCACAGGTCAAAATGCCAGCATCCAGCAGGACCACCTAGCGAGAAAGTAGAT | 5607 |
| Qy | 4676 | GGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTATCCGGAGAACAG | 4735 | Qy | 5753 | TACGACACAGGGCGGCATCATCTCCAGGATCTTCGTGTATGGGAAGACATGGAGCTAC | 5812 |
| Db | 4528 | GGTACACTGTATATTGCAGATCTAGGGAATATCCGGATCCGGCTGTGTCAAGAATAAG | 4587 | Db | 5608 | TATGACGACAGGGGNGATCGTGTCTCGGGTCTTTGCTGATGGTAAACATGGAGTTAC | 5667 |
| Qy | 4736 | CTTTTCTCAACCCAGAACATGTATAGCTGTCTTCACCAATTCACAGGAGCTCTAT | 4795 | Qy | 5813 | ACATCTTAGAAGTTCATGTGTCTGTACTACACAGCAGGAGGAGTATATCTTTGAG | 5872 |
| Db | 4588 | CTTTTACTTAATCTATGAATCTTATGAAGTTGGCTCTCCAACTGATCAAGNACTCTAC | 4647 | Db | 5668 | ACATATTTAGAAAAGTCCATGGTCTTCTGTCTTATAGCCAGCGCAGTACATCTTCGAA | 5727 |
| Qy | 4796 | CTGTTTGATACACCGCAGACCTGTATACCCAAAGCCTGCCACAGAGACTACCTG | 4855 | Qy | 5873 | TTTGACAAGAATGACCGCTCTCTTCTGTGACGATGCCCAACGTGGCGCGGACACACTA | 5932 |
| Db | 4648 | ATCTTTGACATCAATGGTACTACCAATATACTGTAAAGTTTAGTCACTGCTGATTACCTT | 4707 | Db | 5728 | TACGATATGTGGGACCGCTGTCTGCCATCACCATGCCCAGTGTGGCTCGCCACCACTG | 5787 |
| Qy | 4856 | TACAATCTACACTGCGGAGCGGGACATCACTCATACACAGAACAAATGCGAAC | 4915 | Qy | 5933 | GAGACATCCGCTCAGTGGCTACTACAGAAAACATCTATCAGCCCTCAGGGCAATGCC | 5992 |
| Db | 4708 | TACAAATTTAGCTACAGCAATGCAATGATTAATCTGCTGTGACAGACGAATGGCAAC | 4767 | Db | 5788 | CAGACATCCGATTCATTTGGCTACTACCGCAACATATACAAACCCCGGAAAGCAACGCC | 5847 |
| Qy | 4916 | ATGGTAAATGTCGCGAGACTCTACTGGGATGCCCTCTGGCTGTGGTCCAGATGGC | 4975 | Qy | 5993 | TCAGTCTACACAGACTTCACTGAGATGGGCACCTCTTCTCAACCTTCTACCTGGGCAC | 6052 |
| Db | 4768 | ACCTTTAGAAATAGACGGGACCAATCGCATGCCAGTTCGAGTGTGTCTCTGTATAC | 4827 | Db | 5848 | TCCATCATCAGGACTACAAACGAGGAAGGCTGCTCTACAAACAGCTTTCTTTGGGTACA | 5907 |
| Qy | 4976 | CAGGTGACTGGGTGACCATGGGCACCAACAGTGCACTCAAGAGTGTGACCAACAAGGA | 5035 | Qy | 6053 | GGCCGAGGCTGATATACAGATATGGCAACCTGTCAAAGCTGGCAGAGCGCTCTATGAC | 6112 |
| Db | 4828 | CAAGTATATGGTTGACATAGGAACAAATGGATTTTGAAGGCACTGCTCAAGGA | 4887 | Db | 5908 | AGTCGGAGGCTTTATTTCAATACAGAGGCGAGCTAGGCTCTCAGAAATTTTATATGAT | 5967 |
| Qy | 5036 | CACAGTTGGCCATGATGACATACATAGGCAATTCGGCCCTTCGGCAACCAAAAGCAAT | 5095 | Qy | 6113 | ACCACCAAGTCTCAGTTTCACTTACCTATGACGAGACGGCAGGATGCTGAAGACCACTCAACCTA | 6172 |
| Db | 4888 | CTGGAATTAGTTTGTGTTTACTTACCATGGCAATAGTGGCCCTTTTAGCCACTAAAGTGAT | 4947 | Db | 5968 | AGCAAGATCAGTTTTTACCTATGATGAAACAGCAGGAGTCTTAAAGACAGTAAACCTC | 6027 |
| Qy | 5096 | GAAACGGATGGACAACTTTATGATGACGACAGCTTTGGCCGCTGACAAATGTGACC | 5155 | Qy | 6173 | CAGAAATGAGGGCTTCACTGCAACCATCCGCTACCGTCAAGTTGGGCCCTGTATGACCGA | 6232 |
| Db | 4948 | GAAACTGGATGGACAACTTTTGTACTATGACAGTGAAGTCTCTGACAAATGTTACG | 5007 | Db | 6028 | CAGAGTGTGTTTATTTGTCACCATTAGATACAGGCAAAATTTGGTCCCTGATGACAGG | 6087 |
| Qy | 5156 | TTCCCTACTGGCCAGGTGACAGTTTCCGAAGTGATAACAGAGTTCAAGTGCAATGCCAG | 5215 | Qy | 6233 | CAGATCTCCGCTTCACTGAGGAAGCATGGTCAAGCCCGTTTTCAGCTACACTATGAC | 6292 |
| Db | 5008 | TTTCCAACTGGATGGTCAAAACCTGCATGGGGACATGGCAAGGCTATCAGATGGAC | 5067 | Db | 6088 | CAGATTTTCCGCTTTAGTGAAGATGGGATGGTAAATGCAAGATTTTGACTATAGCTATGAC | 6147 |
| Qy | 5216 | GTAGAGACTCCAGC---AAGGATGATGTCAACATACCAACCAACCTGTCTGCTCAGGC | 5272 | Qy | 6293 | AACAGCTTCCGGGTGACACAGCATGAGGCTGTGATCAACGAGACCCCACTGCCCATTTGAT | 6352 |
| Db | 5068 | ATTGAGTCACTAGCCGAGAAGAAGATGTGAGCATCACTTCAAAATCTGTCTCGATCGAT | 5127 | Db | 6148 | AACAGCTTTTCGAGTGACCAAGCATGAGGCTGTGATCAATGAAACGCACTGCTCATTTGAT | 6207 |
| Qy | 5273 | GCCTTCTACACTGCTGCAAGCAAGTCCGGACAGCTACTACATCGGGCCGATGGC | 5332 | Qy | 6353 | CTCTATCGCTATGATGATGTGTGAGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAAT | 6412 |
| Db | 5128 | TCCTTCTACACCACTAGCCGAGAAAGATGTGAGCACTCACTTCAAAATCTGTCTCGATCGAT | 5187 | Db | 6208 | CTGTATCAGTTTGTATGACATTTCTGGCAAGTTTGGACAGTTTGGAAAGTTTGGAGTTATA | 6267 |
| Qy | 5333 | TCCTTGGGCTGTCTGCGCAACCGCATGAGGTGGCGCTGACAGACTGAGCCCACTTG | 5392 | Qy | 6413 | TACTATGACATTAACACAGATCATCACCAAGCTGTATGACCCACACCAAGCATTTTGTAT | 6472 |
| Db | 5188 | TCCTCAGAAATTAATCTAGCCAGTGGCTGCACTCACTACCAACAGAGCCGACGTT | 5247 | Db | 6268 | TATTATGATTAACACAGATCATTTCTACAGCTGTAATGACCTATACGAGCACTTTGAT | 6327 |
| Qy | 5393 | CTGGCTGGACCGCTCAACCCCAACCGTGGGCAAGAGAAATGTCAAGCTGCCCATTCGACAAC | 5452 | Qy | 6473 | GCATATGGCAGGATGAAGGAAGTGCAGTATGATCTTCCGCTCGCTCATGTACTGGATG | 6532 |
| Db | 5248 | CTGGCTGGCACCGCTAATCCGACGGTTGCGAAGAAACATGACTTTTGCCTGGCGAGAAC | 5307 | Db | 6328 | GCTCATGGCCGATCAAGGAGATTTCAATATGAGATATTCAAGTCCGCTCATGTACTGGATT | 6387 |
| Qy | 5453 | GGCTCAACTGGTGGAGTGGCCGACGCAAGAGCAGCTCGGGCCAGGTCACGTGC | 5512 | Qy | 6533 | ACCGTCCAGTATGATAACATGGGGCGAGTAGTGAAGAGAGCTGAAGTAGGACCCCTAC | 6592 |
| Db | 5308 | GGTCAAAACTTGGTGGAAATGGAGATTCGGAAGAGCAAGCCCAAGGGAAGTCAATGTC | 5367 | Db | 6388 | ACAAATTCAGTATGATAACATGGGTGGGTAAACCAAGAGAGAGATTAAATAGGGCCCTTT | 6447 |
| Qy | 5513 | TTTGGGCGCGGCTGCGGTTGCAACCCGAAATCTCCTATCTCTGGAATTTGATCGCGTA | 5572 | Qy | 6593 | GCCAAATACCACTCGCTACTCTCTATGATGATGATGTGACGGCCAGCTGCAGACAGTCTCC | 6652 |
| Db | | | | Db | 6448 | GCCAAACACCAACCAATATGCTTATGAATATGATGTTGATGGAGAGCTCCAAACAGTTTAC | 6507 |

Qy 746 AACTGGCTCTCAACAGCAACATCCCTCTGGAGACCAGAACCTTAGGCAAGCAGCCATT 805
Db |||||
Qy 862 AGCTGGGTCCTTGGCAGTAATGTACCACTGGAAAGCAGGCAATT----- 905
Db |||||
Qy 806 CTAGGGACATTTGCAGGACAACTCATTTAGATGGACATTTCTCGCGCCTCCCGCCATGAT 865
Db |||||
Qy 906 ----- 905
Db |||||
Qy 866 GGGGTTACAGTGACGGGCACTTCTCTTCAAGCCTTGAGGCACCTCCCGCTCTTCTGC 925
Db |||||
Qy 906 -----CCTATTCAAAACAGGAACAGGTACAAAGCCTTCTTCAAGTACTGT 945
Db |||||
Qy 926 ACCACATCACCAGGGTACCCACTGACGTCAGACAGTGTACTCTCTCGCCGCCGACCC 985
Db |||||
Qy 946 ACTGCAACCCAGGATACACAATGGCATCTGGCTCTGTGTTATTACACACCTACTCGGCCA 1005
Db |||||
Qy 986 CTGCCCCCAGCACCTTCGCCCGCGCGCTTTAACTCTCAAGAGCCCTCCAAGTACTGT 1045
Db |||||
Qy 1006 CTACCTAGAAACACCTTATCAAGAAGTCTTTTAAATTCAGAAGTCTTCAAGTACTGT 1065
Db |||||
Qy 1046 AACTGGAAGTGGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCACTCTGCTG 1105
Db |||||
Qy 1066 AGCTGGAATGCACTGCACTGTGTGCCGTAGGGGTCTCGTGTCTCTGGCAATATCTCTG 1125
Db |||||
Qy 1106 GCATACTTTGTGGCATGCACCTGTTTGGCCTTAACTGGCACCTCGACCGCATGGAGGG 1165
Db |||||
Qy 1126 TCTTATTTATAGCAATGCATCTCTTTGGCCTCACTGGCAGCTACAGACACTGAAAT 1185
Db |||||
Qy 1166 CAGATGTATGAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCGAGTCTCC 1225
Db |||||
Qy 1186 GACACATTTGAGA-----ATGGAAAAGTGAATCTGTATACCATGCCAACAAACACTGTG 1239
Db |||||
Qy 1226 CTATACCCCTCAGGGGCACTGGCTTAGAGACCCCTGACAGAAAGGCAAGGAACACACA 1285
Db |||||
Qy 1240 TCATTACCTCTGGAGACA----- 1258
Db |||||
Qy 1286 GAAGAAAGCCAGTAGTCTTTTCCAGAGACAGTCTTATAGATTCTGGAGAAATGTAT 1345
Db |||||
Qy 1259 -ATGGAANAATTAGTGGTAATTTACGCAAGAAATAACACCATAGATTCCGGAGAACTGTAT 1317
Db |||||
Qy 1346 GTGGGAAGCGCAGCCTCCAGAAAGATTCTCTCGGCACCTTTCTGGAGATCTCAAGTGTTC 1405
Db |||||
Qy 1318 ATTGSCCAGAGCAATTTCAAGAGATTCTCCCGGGATCTTCTGGAGATCACAGTCTTC 1377
Db |||||
Qy 1406 ATAGACCAATCTGTGTCATCTGAATTTCAATGTGTCTCTGGAAAGGACGCTGTTGGC 1465
Db |||||
Qy 1378 ATTGATCAGCCACAGTCTTTCTTAAATTCAAATATCTCTCTCAAGAGGATGCAATTGATGA 1437
Db |||||
Qy 1466 ATTTATGCGAGAAAGGCTCCCTCCTTACATA-----CACAGTTTGACTTT 1513
Db |||||
Qy 1438 GTATATGCGCGAGAAAGTACCGCTTCCCATACTCAGTCTCCCCCAGTATGACTTC 1497
Db |||||
Qy 1514 GTGGAGCTGCTGGATGGCAGGAGCTCTTAACCCAGGAGCGCGAGCCTTAGAGGGACC 1573
Db |||||
Qy 1498 GTGGAGCTCTGGATGGCAGCAGGCTGATGCGCAGAGAGCAGCGAGCTGCTTGAGACG 1557
Db |||||
Qy 1574 CCGGCCAGTCTCGGGGAACTGTGCCCCCTCCAGCCATGAGACAGGCTTATCCAGTAT 1633
Db |||||
Qy 1558 GAGAGAGCGCGCGCAGCGAGATCCCGTCAAGCTTTCATGAGCGCGGCTTTATCCAGTAC 1617
Db |||||
Qy 1634 TTGGATTCAAGGAATCTGGCACTTGGCTTTTACATGACGGAAGGAGTCAGAGTGTGT 1693
Db |||||
Qy 1618 TTGGATTCTGGAAATCTGGCACTGGCTTTTATAATGATGGGAAATGCGAGCAGGTG 1677
Db |||||
Qy 1694 TCTTTCTCACCACTGCCATTTAGTTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAAT 1753
Db |||||
Qy 1678 TCTTTTAATACCATTTGTTATAGAGTCTGTGGTGGAAATGTCCCGGAAATGGCCATGGAAT 1737
Db |||||
Qy 1754 GGTGACTGATCTCTGGGACCTGCCACTGCTTCTCGGGTTTCTGGGCCCCGACTGTGGC 1813
Db |||||
Qy 1738 GGAGAAATGCGTTCTTGGAACTTGGCAATTTGTTTTCAGGATTTCTGGGTCGGGATTTGTTCA 1797
Db |||||

Qy 1814 AGAGCCCTCTGCCCTCGTCTCTGTAGCGGAAATGGCCAAATACATGAAAGCAGATGCTTG 1873
Db |||||
Qy 1798 AGAGCGCTGTCTCAGTGTATTGTAGTGGCAACGGGCAGTACTCCAAAGGCGCGCTGCTG 1857
Db |||||
Qy 1874 TGCCACAGTGGCTGGAAAGCGCTGAGTGGATGTGCCACCAACAGTGTATCGATGTG 1933
Db |||||
Qy 1858 TGTTCAGCGGCTGGAAAGGCAACCGAGTGTGTGCCGACTACCCAGTGTATTGACCCA 1917
Db |||||
Qy 1934 GCCTGAGCAACCATGSCACTGCATCACGGGCACTGTCACTCTGCAACCCCTGGCTACAAG 1993
Db |||||
Qy 1918 CAGTGTGGGGTCTGGGATTTGTATCATGGCTCTCTGTCTTGCAGCTCAGGATACAA 1977
Db |||||
Qy 1994 GGGAGAGCTGTGAGGAAGTGGACTGCATGGAACCCACATGTTTCAGCGCGGGGTGTCTGC 2053
Db |||||
Qy 1978 GGAGAAAGTTGTGAAGAAGCTGACTGTATAGACCTCTGGGTGTTCTAATCATGTGTGTGT 2037
Db |||||
Qy 2054 GTGAGAGGCAANTGCCATTTGCTTTGTGGGATGGGAGGACCACTCTGGAGACCCCGAG 2113
Db |||||
Qy 2038 ATCCACGGGGAATGTCTACCTGAGTCCAGGATGGGAGGTAGCAATTTGTGAATACTGAAG 2097
Db |||||
Qy 2114 GCCACATGCTTAGACCACTGTTTTCAGGCCACGGAACTTCTCTCCGGACACCGGGCTTTGC 2173
Db |||||
Qy 2098 ACCATGTGTCCAGACCACTGCTCGGCCACGGAACTGATCTTCAAGAAAGTGGCTCTGC 2157
Db |||||
Qy 2174 AGCTGTGAACCAAGCTGGACTGGACACAGACTGTTTCTATCGAGATCTGTGTGCCGACTGT 2233
Db |||||
Qy 2158 ACGTGTGACCTTAACCTGGACTGGCCACAGACTGTCTCAACGAAATATGTTCTGTGGACTGT 2217
Db |||||
Qy 2234 GGTGGCCATGGCTGTGCTAGGGGACCTTCCGCTCGCGGATGCTGTGATGGGGGCA 2293
Db |||||
Qy 2218 GGCTCACACGCGCTTTCATGGGGGGACGTGTGCTGTGAAGAAAGCTGCACGGGCCCA 2277
Db |||||
Qy 2294 GCCTGCGACACAGCGGGCTGCCACCCGCTGTGCCAGCATGGGACCTGCCGCGACGGC 2353
Db |||||
Qy 2278 GCCTGTAACTCAGAGAGCTGCCACCCCGCTGTGCCAGCACGGGACCTGCAAGATGGC 2337
Db |||||
Qy 2354 AAGTGGAGTGCACGCCCTGCTGGAATGGGAAACATGTCACCATCGCTCACTATCTGGAT 2413
Db |||||
Qy 2338 AAGTGTGAATGCAAGCCAGGCTGGAAATGGAGAGCACTGCACATATCGCTCACTATTGGAT 2397
Db |||||
Qy 2414 AGGTAGT-----TAAAGGGTTTGCCTGGTGTGCAATGGCAAC 2455
Db |||||
Qy 2398 AAGATGTTTAAAGCAAGATAGGATATAAAGAGGGTTGTCTCTGTCTGTGCAAGCAAT 2457
Db |||||
Qy 2456 GGCAAGATGTAACCTTAGACCTGAATGTTGGCACTGCGCTCTGCCAGCTGGGCTGGAGAGA 2515
Db |||||
Qy 2458 GGAAGATGTAACCTGGACCAAAATGGCGGACATTTGTGTGCCAGCTGGATGGAGAGA 2517
Db |||||
Qy 2516 GCTGGCTGTGACACTTCCATGGAGACTGCTCTGCGGTGACAGCAAGAAACAATGATGGAGAT 2575
Db |||||
Qy 2518 GCAGGCTGTGACGTAGCATGGAGACTCTTTTGCA CAGATAGCAAGGCAATGSAAGGGAT 2577
Db |||||
Qy 2576 GGCCTGTGAGTGCATGGACCTGACTGCTGCTCCAGCCCTCTGCCATATCAACCCG 2635
Db |||||
Qy 2578 GGACTCAATTGACTGCATGGATTCGGATTTGCTGCTACAGAGTTCCTGCCAGATCAGCCC 2637
Db |||||
Qy 2636 CTGTGCTTGGCTCCCTTAACCTCTGGAATCATCTCAGAGAGACACAGGTCCTCTGTGTCA 2695
Db |||||
Qy 2638 TATTGTGGGAGCTGCCGGATCTCTCAGACATCATTAGCCAAAGCCTTCAATCGCTTCT 2697
Db |||||
Qy 2696 CAGCAGAACCTTACACTCTTCTATGACCGCATCAAGTTCTCTGTTGGGAGGAGCAGACG 2755
Db |||||
Qy 2698 CAGCAAGCTGCCAAATCCTTTTATGATCGAATCAGTTTCTCTTATAGGATCTGATAGACC 2757
Db |||||
Qy 2756 CACATAATCCCGGGGAGAACCCCTTTGATGGAGGATGCTTGTGTTATTCTGTGGCCAA 2815
Db |||||
Qy 2758 CATGTTATCTGCTGAGAAAGTCTTCAATAAGAGCCTTGTGATCTGTGATCAGAGGCCAA 2817
Db |||||
Qy 2816 GTGATGATCATCAGATGGAACCCCTGTTGGTGTGAAACATCAGTTTTTGTCAATAACCT 2875
Db |||||
Qy 2818 GTACTGACTGCTGATGGAACCTCCACTTATGGAGTAAATGTCTCGTTTTTCCATTACCCA 2877
Db |||||
Qy 2876 CTCTTTGGATATACAATCAGAGGCAAGATGGCAGCTTTTGACTTGGTGACAAATGGCGGC 2935
Db |||||

Db 2878 GAATATGGATATACTATTACCGCCAGAGCGGAATGTTTGACTTGTGTGCAAAATGTTGGG 2937
Qy 2936 ATCTCCATCATCTCGGGTTCGAGCGGGACCTTTTCATCACACAGAGACACACCTTGTGG 2995
Db 2938 GCCTCTTAACCTTTGGTATTTGAACGATCCCCATTCCTCACTCAGTATCATATGTTGG 2997
Qy 2996 CTGCCATGGATCGCTTTCTTTGTATGGAACCATCATCATGACATCAGGAGAAATGAG 3055
Db 2998 ATTCCATGGAATGCTCTTTATGATGATGATACCTAGTATGAGGAAAGAGAGATGAC 3057
Qy 3056 ATTCCAGCTGTGACCTGAGCAATTTTGGCCGCCCCCAACCCAGTCTGCTCTCCATCCCCA 3115
Db 3058 ATTCCAGCTGTGATCTGAGTGGATTCTGAGGCCAAATCCCATCATTTGTTGTCATCACCT 3117
Qy 3116 CTGACGCTCTTCCAGCTCTCTGTGCAGAGAAAGGCCCATTTGTGCGGGAATTCAGGCT 3175
Db 3118 TTATCCACCTTTTTCAGATCTTCTCTGGAACAGTCCCATCATTCCTCCGAAACACAGGTA 3177
Qy 3176 TTGCAGGAGAAATCTCTATCTCTGGCTGCAAGATGAGCTGAGCTACCTGAGCAGCCGG 3235
Db 3178 CTCACGAGGAAACTCAATTCAGGAACAGATTTGAAACTCTCTACTTGTAGTTCACAG 3237
Qy 3236 ACCCTCGGCTACAAATCTGTCTGAGGATCAGGCTCACCCACCCGACCATCCCTTTCAAC 3295
Db 3238 GCTGAGGGTATTAAGTCAGTTCTCAAGATCACCATGACCCAGTCTATTATTCATTTAAT 3297
Qy 3296 CTCAATGAAGGTGACCTCATGATGAGGTAGCGGTGGAGGGCCGCTCTTACGGAAGTGGTTCG 3355
Db 3298 TTAATGAAGGTTTCATCTTATGGTAGCTGTAGTAGGAAGACTCTTCCAAAGTGGTTTCCT 3357
Qy 3356 GCAGCCCCGACCTGTCTATTATTTTCATTTGGGCAAGACAGACGCTCTACACACAGAAG 3415
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Qy 3416 GTGTTTGGGCTTTCAGAAGCTTTGTTTCCGTGGGTATGAATATGAATCTCTCCCGAGAT 3475
Db 3418 GTCTATGGTCTATCTGAAGCTGTGTCTCAGTTGGATATGAGTATGAGTCGTGTTGGAC 3477
Qy 3476 CTAATCTGTGGGAAAAAGAAACAAACAGTCTCGAGGCTATGAATTTGACGGTCCAAG 3535
Db 3478 CTGACTCTGTGGGAAAAAGAGACTGCGCATTTCTCAGGGCTATGAATTTGGATGCTGCCAAC 3537
Qy 3536 CTTGGAGATGGAGCTTAGACAACATCATGCCCTCAACATTCAAAGTGATATCTTCGCAC 3595
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Qy 3596 AAAGGGAATGGGAGAACCACTTTGTCTCAGCAGCCTCTCTGTCATTTGGGAGCATCATG 3655
Db 3598 AAGGGAACCGGGGAAACCAAGTTCACTCCAGCAGCCTCCAGTCGTGAGTAGCATCATG 3657
Qy 3656 GGCAATGGGCGCGGAGAACATCTCTGCCCCAGCTGCAACCGCCTTGTGACGGCAAC 3715
Db 3658 GGCAATGGGCGAAGGCGCAGCATTTCTGCCCCAGATTGCAATGTCGAAGCTGATGTTAAC 3717
Qy 3716 AAGCTCTGCCCCAGTGGCCCTCACTGTGGCTCTGACGGGAGCCTCTATGTGGGTGAT 3775
Db 3718 AAGTTACTGCCCCAGTGGCGCTAGCTTGTGGGATCGATGGCAGTCTGTACGTAGGCGAT 3777
Qy 3776 TTAACCTACATTTAGAAAGATCTTCCCCTCTGGAAATGTACCAACATCTCTAGAGCTGAGG 3835
Db 3778 TTCACTACTGCGGGGATATTTCCCTTCTGGAAATGTAACAAGTCTCTTAGAACTAAGA 3837
Qy 3836 AATAAAGATTTACACATAGTCAACGTCCAGCAACAAATATCTACTGGCCACAGACCCC 3895
Db 3838 AATAAAGATTTAGACATAGCAGCAACCCAGCTCATAGATACCTTTCGCAACGGATCCA 3897
Qy 3896 ATGATGGGCGCTCTTCTCTTCTGACAGCAACAGCCGGCGGTCTTTAAATTCAGTCC 3955
Db 3898 GTACGGGAGATCTGTACGTTCTGTACACAAACCCCGCAGAAATTTATCCGCCCAAGTCA 3957
Qy 3956 ACTGTGTGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTGTGGGGACAGGTGACCAG 4015

Db 3958 CTTACGGGGGCAAAAAGACTTGACTAAAAATGCAGAAGTCTGTCGACGGGACAGGGGAGCAA 4017
Qy 4016 TGCCTCCCTTTTGATGACACTCGCTGCGGGATGTTGGGAAGGCCACACAGGCCACACTC 4075
Db 4018 TGCCCTTCGTTTGACGAGCGGAGATGTGGGATGAGGGAAGGCCGTGGAAGCCACACTC 4077
Qy 4076 ACCAATCCACAGGGTATTACAGTGACCAAGTTTGGGCTGATCTACTCTCTGTGATGCCACC 4135
Db 4078 ATGAGTCCCAAGGAATGGCAGTTGATAAGAAATGGATTAACTACTCTTCTGTGATGAACC 4137
Qy 4136 ATGATCAGACGATCGATCAGAAATGGGATCATCTCCACCCTGCTGGCTCTAATGATCTC 4195
Db 4138 ATGATTAGGAAGTTGACCCAAATGGAATCATATCAACTCTTCTGCGCTCTAACGATTG 4197
Qy 4196 ACATCAGCCCGCCACTCAGCTGTGATTCTGTCAATGATATTTCCAGGTAAAGACTGGAG 4255
Db 4198 ACTTCAGCCAGACCTTTAACTTTGTGACACACAGATGACATCAGCCAGGTACGTCTGGAA 4257
Qy 4256 TGGCCACACAGACTTAGCCATCAACCCAAATGGCAACTCACTATTATGTCTCGACAACAAT 4315
Db 4258 TGGCCCACTGACTAGCCATTAACTATGGATAACTCCATTTATGTCTCTGGATAATAAT 4317
Qy 4316 GTGGTCTCGCAATCTCTGAAAACACACAGGTGGCAATTTGTCGCGGAGGCCATGCAC 4375
Db 4318 GTAGTTTACAGATCACTGAAAATCGTCAAGTTTCGCAATTTGCTGAGCGGCCATGCAC 4377
Qy 4376 TGGCAGGTCCCTGGCAATTGACCACTTCTGTCAAGCAAGTGGCCATCCACGCAACCCCTG 4435
Db 4378 TGTCAAGTTCCCGAGTGG---AATATCTGTGGGGAAGCAGCGGTGCAGACAACTG 4434
Qy 4436 GAGTCAGCCACCGCTTTGGCTGTTCACAAATGGGGTCTCTATATATGCTGAGACTGAT 4495
Db 4435 GAATCAGCCACTGCCATTCTGTCTCTACAGTGGGGTCTCTGTACATTAATCTGAAACTGAT 4494
Qy 4496 GAGAAAAAGATCAACCGCATCAGGCAAGTCCACCATAGTGGAGAGATCTCACTCGTTC 4555
Db 4495 GAGAAAGAAATTAACCGGATAAGGCAGGTCAACAAGATGGAGAAATCTCTTAGTGGCC 4554
Qy 4556 GGGGCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTTGTTTCTCGAGAC 4615
Db 4555 GGAATACCTTCAGAGTGTGACTGCAAAAATGATGCCAACTGTGACTGTTACCAAGATGGA 4614
Qy 4616 GATGTTATGCCAAGGATGCAAAAGTTAAATACCCCACTTCTCTTGGCTGTGTGTGCTGAT 4675
Db 4615 GATGGCTACGCCAAGGATGCCAACTCAGTGGCCCCATCTCCCTGGCTGCTCTCCAGAT 4674
Qy 4676 GGGGAGCTCTAGTGGGCCACCTTGGGAAACATCCGAATTCGGTTTATCCGGAAGAACAG 4735
Db 4675 GSTACACTGTATATTGACATCTAGGGAATATCCGGATCCGGCTGTGTCAAAAGAAATAG 4734
Qy 4736 CCTTTCTCAACACCCAGAACATGTATGAGCTGTCTTCCAAATTCACAGGAGCTCTAT 4795
Db 4735 CCTTTACTTAATCTTATGAATCTTATGAAGTTGCGCTCTCCAACTGATCAAGAACTCTAC 4794
Qy 4796 CTGTTTGATACCAACCCGCAAGCACCTGTACACCCAAAGCCTTGCCCAAGAGACTACCTG 4855
Db 4795 ATCTTTGACATCAATGCTACTCAACCAATATACTGTAAAGTTTAGTCACTGGTGTACCTT 4854
Qy 4856 TCAACTTCACCTTACACTGCGGAGCGGACATCACAATCATCAACAGAAACAATGGCAAC 4915
Db 4855 TACAAATTTAGCTACAGCAATGACAAATGATATTTACTGCTGTGACAGACGAATGGCAAC 4914
Qy 4916 ATGGTAAATGTCCGCGAGACTCTACTGGGATGCCCTCTGGCTGTGGTCCAGATGGC 4975
Db 4915 ACCCTTAGAATTAGACGGGACCCAAATCGCATGCCAGTTTCAGTGGTGTCTCTCTGATAAC 4974
Qy 4976 CAGGTGTACTGGGTGACCATGGGCACCAACAGTGCACCTCAAGAGTGTGACCAACAGGA 5035
Db 4975 CAAAGTATGTTGGTGTGACAAATAGGAACAATGGATGTTTGAAGGCATGACTGCTCAAGGA 5034
Qy 5036 CACGAGTTGGCCATGATGACATACCATGGCAATTCGGGCTTCTGGCAACCAAAAGCAAT 5095
Db 5035 CTGGAATTAGTTTGTATTACTTACCATTGCAATAGTGGCCTTTTAGCCACTAAAAAGTAT 5094

[illegible]

Db 8317 GCACGAGGTAAC 8329

RESULT 13

ADH41932

ID ADH41932 standard; DNA; 8657 BP.

XX AC ADH41932;

XX

DT 25-MAR-2004 (first entry)

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XX Novel human nucleic acid NOV40a.

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XX ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; neurotic; antiparkinsonian; antiasthmatic; antiinfertility; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease; Parkinson's disease; asthma; fertility disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; vaccine.

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XX Homo sapiens.

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XX WQ2003102159-A2.

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XX 11-DEC-2003.

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XX 04-JUN-2003; 2003WO-US017573.

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XX 04-JUN-2002; 2002US-0385490P.

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XX 04-JUN-2002; 2002US-0385615P.

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XX 04-JUN-2002; 2002US-0385755P.

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XX 05-JUN-2002; 2002US-0386041P.

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XX 06-JUN-2002; 2002US-0386355P.

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XX 06-JUN-2002; 2002US-0386357P.

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XX 06-JUN-2002; 2002US-0386447P.

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XX 06-JUN-2002; 2002US-0386459P.

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XX 06-JUN-2002; 2002US-0386465P.

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XX 06-JUN-2002; 2002US-0386864P.

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XX 07-JUN-2002; 2002US-0386701P.

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XX 07-JUN-2002; 2002US-0386796P.

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XX 07-JUN-2002; 2002US-0386931P.

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XX 07-JUN-2002; 2002US-0387087P.

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XX 07-JUN-2002; 2002US-0387081P.

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XX 07-JUN-2002; 2002US-0387083P.

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XX 10-JUN-2002; 2002US-0387429P.

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XX 10-JUN-2002; 2002US-0387540P.

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XX 10-JUN-2002; 2002US-0387866P.

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XX 11-JUN-2002; 2002US-0387608P.

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XX 11-JUN-2002; 2002US-0387610P.

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XX 11-JUN-2002; 2002US-0387659P.

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XX 11-JUN-2002; 2002US-0387668P.

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XX 11-JUN-2002; 2002US-0387696P.

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XX 11-JUN-2002; 2002US-0387859P.

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XX 12-JUN-2002; 2002US-0387934P.

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XX 12-JUN-2002; 2002US-0387960P.

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XX 12-JUN-2002; 2002US-0388022P.

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XX 12-JUN-2002; 2002US-0388096P.

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XX 12-JUN-2002; 2002US-0388432P.

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XX 12-JUN-2002; 2002US-0388479P.

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XX 13-JUN-2002; 2002US-0389123P.

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XX 14-JUN-2002; 2002US-0389120P.

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XX 14-JUN-2002; 2002US-0389146P.

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XX 17-JUN-2002; 2002US-0389743P.

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XX 18-JUN-2002; 2002US-0389604P.

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XX 18-JUN-2002; 2002US-0389884P.

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XX 19-JUN-2002; 2002US-0390006P.

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XX 19-JUN-2002; 2002US-0390144P.

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XX 19-JUN-2002; 2002US-0390209P.

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XX 25-JUN-2002; 2002US-0391726P.

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XX 06-AUG-2002; 2002US-0401628P.

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XX 09-AUG-2002; 2002US-040268P.

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XX 12-AUG-2002; 2002US-0402822P.

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|----|---|------------------|----|------|---|------|
| PR | 13-AUG-2002; | 2002US-0403458P. | QY | 266 | TTTACCCCTGGGAGCTGGGGCTGGAAGTAACGCCCCCTTCAACGGGACCCCTGTATCCGG | 325 |
| PR | 15-AUG-2002; | 2002US-0403617P. | Db | 391 | TTTACCCCTAAGGACAGTTAGGAGTTTGTGAACAGCAACTCGAAGAGGACTGGCATTTTGT | 450 |
| PR | 26-AUG-2002; | 2002US-0406182P. | QY | 326 | ACAGACATTGGGCTGCCCCCAATGCGGCTACTTCCATGGGGGCTGGCTCTGATGCGGACATG | 385 |
| PR | 12-SEP-2002; | 2002US-0410085P. | Db | 451 | GCGGAATGGGGCTCCCTCACAGAGTTTACTTATCAGTGCAGGGGTGAGATGCTGATACT | 510 |
| PR | 13-SEP-2002; | 2002US-0410505P. | QY | 386 | GAGGCTGACACGGTGTCTCCCTGAGCACCCCGTGTCTGTGGGGCGGAGACACACGG | 445 |
| PR | 30-SEP-2002; | 2002US-0415195P. | Db | 511 | GAAATGAAGCAGTGAATGTCCTCCAGAGCATGCCATGAGACTTTTGGGGCAGGGGGTCAAA | 570 |
| PR | 23-OCT-2002; | 2002US-0420627P. | QY | 446 | TCAGGGCGCAGCTCTCTGCTGTCCAGCGGGGCAATTTCCAACTCTCACTCAACGACAC | 505 |
| PR | 24-OCT-2002; | 2002US-0420852P. | Db | 571 | TCAGGGCGCAGCTCTCTGCTGTCCAGCGGGGCAATTTCCAACTCTCACTCAACGACAC | 630 |
| PR | 31-OCT-2002; | 2002US-0422750P. | QY | 506 | GAGCATGAAAAACACTGAGACTGATCATCCGGGGGCTGCGAGAACACGCGGCTCCGG | 565 |
| PR | 01-NOV-2002; | 2002US-0423095P. | Db | 631 | GAGCAGAAAAACAAGTCCGACAGTGAGAAATGAGCAACCTGCAAGCAATCAAGGCGAGTCT | 690 |
| PR | 05-NOV-2002; | 2002US-0423748P. | QY | 566 | ACGCGCGCGCGCGCTCTCGCACGCCACACACCCCAACAGCACACCGCGGCTCCATT | 625 |
| XX | (CURA-) CURAGEN CORP. | | Db | 691 | ACCTTGAGCGCTTTCGCGCTTCCATAGCAGACTCTGCACAGCATCATCTCCATC | 750 |
| XX | Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL; | | QY | 626 | AACCTCCCTGAACCGGGGCAACTTTCAGCCGAGAGCAACCCCGCGCGGCCCCACCGAC | 685 |
| XX | Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR; | | Db | 751 | ACTTCTCTCAACAGAAACTCCCTGAGCCAAATAGAAGGAACAGAGTCCGCGCGCGGCT | 810 |
| XX | Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L; | | QY | 686 | CATCGCTCTCCGAGAGCGCCCTGCGGGCGGCCAGGAGGCTGCCACGCCAGCAG | 745 |
| XX | Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R; | | Db | 811 | GCTTTGCCCGCGAGCTGCAAAC-----CACACCGAGTCCGTCAGCTGCGAGC | 861 |
| XX | Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR; | | QY | 746 | AACCTGGCTCTCAACAGCAACATCCCTCGAGACCAAGAAACCTTAGGCAAGACCCATT | 805 |
| XX | MacLachlan T, Malvankar UM, Mcqueeney K, Mezick AJ, Miller CE; | | Db | 862 | AGCTGGGTCTTGGCAGTAATGATACCACTGAGAAAGCAGGCACTT----- | 905 |
| XX | Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L; | | QY | 806 | CTAGGACATTGCGAGCAACCTCATTTAGATGGACATTTCTGGCGGCTCCCGCCATGAT | 865 |
| XX | Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G; | | Db | 906 | ----- | 905 |
| XX | Spytek KA, Stone DU, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ; | | QY | 866 | GGGCTTACAGTACGAGGCACTTCTTCAAGCCTGGAGGCACTTCCCGCTCTTCTGC | 925 |
| XX | Wolenc AR, Zhong M, Zhong H; | | Db | 906 | -----CCTATTCAAAACAGGAACAGGTACAAGCCACTGTTTCTAGT | 945 |
| XX | WPI; 2004-053467/05. | | QY | 926 | ACCACATCACAGGATACCACTGACCTCCAGCAGCAGTGTACTCTCTCCGCCCGGACCC | 985 |
| XX | P-PSDB; ADH41933. | | Db | 946 | ACTGCAACCCAGATACAAATGGCATCTGGCTCTGTTTATTCACCACTACTCTCGGCA | 1005 |
| XX | New NOVX polypeptides and nucleic acid molecules useful for preventing or | | QY | 986 | CTGCCCCGAGCAGCTTTCGCGCGCGGCTTTAACTCAAGAGCCCTTCAAGTACTGT | 1045 |
| XX | treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, | | Db | 1006 | CTACCTAGAAACACCCCTATCAAGAAAGTGCTTTTAAATTCAGAAAGTCTTCAAGAGTACTGT | 1065 |
| XX | atherosclerosis or diabetes, in chromosome mapping, tissue typing or in | | QY | 1046 | AACCTGGAAGTGGCAGCGCTGAGCGCATCTCATCTCAGCCACTCTGGTCTATCTGCTG | 1105 |
| XX | pharmacogenomics. | | Db | 1066 | AGCTGGAATAGCATGTCACACTGTGTCCGTAGGGGTCTCGGTGCTCTGGCAATACTCTG | 1125 |
| XX | Claim 20; SEQ ID NO 485; 1503pp; English. | | QY | 1106 | GCATACCTTTGGGCATGCACTCTTTGGCCTAAACTGGCACCTGCGACCCGATGGAGGG | 1165 |
| XX | The invention relates to 566 new isolated human polypeptides and their | | Db | 1126 | TCATTATTTATAGCAATGTCATCTCTTTGGCCTCACTGGCAGCTACAGCAGCTGAAAT | 1185 |
| XX | encoding genes, sequences that are at least 95% identical to these or | | QY | 1166 | CAGATGATAGATACAGGAGGACACAGCCAGAGTGGGCTGTGCCAACCGAGCTCTCC | 1225 |
| XX | sequences comprising one or more conservative substitutions in these. The | | Db | 1186 | GACACATTTGAGA-----ATGGAAGAGTGAATTTCTGATACCATGCCAACAACTGTG | 1239 |
| XX | polypeptide, polynucleotide and antibodies against the polypeptides are | | QY | 1226 | CTATACCCCTCAGGGGCACTGGCTTAGAGACCCCTGACAGAAAGGCAAGGAAAGGAAACCA | 1285 |
| XX | useful in diagnosing, treating or preventing NOVX-associated disorders, | | Db | 1240 | TCATTACCTCTTGAGACA----- | 1258 |
| XX | e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, | | QY | 1286 | GAAAGAAAGCCAGTAGTCTTTTCCAGAGGACAGTTCATAGATTTCTGGAGAAATTTGAT | 1345 |
| XX | diabetes, AIDS, multiple sclerosis, graft-versus-host disease, | | Db | 1259 | -ATGGAATTTAGTGGATTTACGCAAGAAATAACACCATAGATTTCCGAGAACTTGT | 1317 |
| XX | Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders. | | QY | 1346 | GTGGGAGGCGAGCCTCCAGAAAGATTCTCTCGCACTTTCTGAGATCTCAAGTGTTC | 1405 |
| XX | The nucleic acids are further used as hybridization probes, in chromosome | | XX | | | |
| XX | mapping, tissue typing, preventive medicine, and pharmacogenomics. The | | XX | | | |
| XX | polypeptides are also useful as vaccines. This sequence represents an | | XX | | | |
| XX | example of the nucleic acid sequence of the invention. | | XX | | | |
| XX | Sequence 8657 BP; 2345 A; 2069 C; 2201 G; 2042 T; 0 U; 0 Other; | | XX | | | |
| XX | Query Match 41.6%; Score 3473.8; DB 12; Length 8657; | | XX | | | |
| XX | Best Local Similarity 65.2%; Pred. No. 0; | | XX | | | |
| XX | Matches 5445; Conservative 0; Mismatches 2692; Indels 216; Gaps 14; | | XX | | | |
| QY | 35 ATGGACGTGAAGGAGGAGGAGCTTACCGCTCGCTGACCCGCGC---CGCGACCCGAG | 91 | | | | |
| Db | 151 ATGGATGTGAAGAACGCGAGGCTTACTGCTCCCTGACCAAGAGCAGACGAGAAAGGAA | 210 | | | | |
| QY | 92 CCGCGCTACACGAGCTCGTCCGGGACAGCAGGAGGGGCAAG---CCCGCAGAAATCG | 148 | | | | |
| Db | 211 CCGCGCTACACAAATTCCTCCGAGACAAATGAGGATGCGGGTATCCACAGAAATGCC | 270 | | | | |
| QY | 149 TACAGCTCCAGCGAGACCTGTAAGGCTTACGACCCAGGA---CGCCGCTAGCTATGCC | 205 | | | | |
| Db | 271 TACAGTTCAGCGAGACATTGAAGCTTTTGATCATGATTTCTCGCGGCTGTTTACGCG | 330 | | | | |
| QY | 206 AGCCGCTCAAGACATTGTGCGGCGAGGAGCGGAGGAATTTCTGCGCAGAGTGGCCAC | 265 | | | | |
| Db | 331 AACAGAGTGAAGGATTTGGTTTACAGAGAAGCAGACGAGTTCCTACTAGACAAGGACAGA | 390 | | | | |

Db 1318 ATTGGCCGAAGACCAATTCAAGAGATTCTCCCGGATCTTCTGGAGATCAAGCTCTTC 1377
QY 1406 ATAGACCATCTGTGATCTGAAATCAATGTGTCTCTGGGAAAGGCAGCCCTGTTGGC 1465
Db 1378 ATTGATCAGCCACAGTTTCTTAAATCAATATCTCTTTCAAGAGATGTCATTGATGGA 1437
QY 1466 ATTTATGGCAGAAAGGCGCTCCCTCTCTCCACATA-----CACAGTTTCACTTT 1513
Db 1438 GTATATGGCCGAAGAGTTACCGCTTCCCATCTCAGTCTCTCCCCAGTATGACTTC 1497
QY 1514 GTGGAGCTCTGGATGGCAGGAGGCTCTTAACCCAGAGGCGCGAGCCCTAGAGGGACC 1573
Db 1498 GTGGAGCTCTGGATGGCAGAGGCTGATTGCGAGAGACGCGAGCCCTGCTTGAGACG 1557
QY 1574 CGCGCCAGTCTCGGGGAATCTGCGCCCTCCAGCCATGACAGGCTTTCATCCAGTAT 1633
Db 1558 GAGAGAGCGCGGCGGAGCGAGATCCGTGAGCTTTATGAGCGCGCTTTATCCAGTAC 1617
QY 1634 TTGGATTCAAGGAATCTGGCACTTGGCTTTTAAATGACGGAAAGAGTCAGAGTGT 1693
Db 1618 TTGGATTCTGGAAATCTGGCATCTGGCTTTTATATGATGGGAAATTCAGAGCAGGTG 1677
QY 1694 TCTTTTCTCACCACCTGCCATTGAGTCGTCGTGATACTGCCAGCAACTGCTATGSCAAT 1753
Db 1678 TCTTTTAAATACCATGTTATAGATCTGTGGTGGATGTCCCGAAATTTGCCATGGAAT 1737
QY 1754 GTGACTGATCTCTGGGACCTGCGCACTGCTGCTCTGGGTTTCTTGGGCCCGCACTGTGGC 1813
Db 1738 GGAGAATGCGTTTCTGGAACTTGCCATTGTTTCCAGGATTTCTGGGTCCGGATTGTTC 1797
QY 1814 AGAGCTCTGCCCCGCTCTGTAGCGGAATGGCCATACATGAAGAGCAGATGCTTG 1873
Db 1798 AGAGCGCTGTCCAGTGTATGTAGTGGCAACGGGCGAGTACTCCAAAGGGCGCTGCTG 1857
QY 1874 TGCCACAGTGGCTGGAAAGCGCTGAGTCGATGTGCCCAACCACTGATTCGATGTG 1933
Db 1858 TGTTTCAGCGGCTGGAAAGGCGACCGAGTGTGATGTGCCGACTACCCAGTATTTGACCCA 1917
QY 1934 GCTTGAGCAACCATGGCACTGTCATCAGCGGCACTGTCATCTGCAACCTCTGCTACAAG 1993
Db 1918 CAGTGTGGGGTCTGTGGGATTTGTATCATGGGCTCTGTGCTTGCAAGCTCAGGATACAA 1977
QY 1994 GCGCAGAGCTGTAGGAAGTGAAGTCACTGATGGACCCACATGTTTCAGCGCGGGTGTCTG 2053
Db 1978 GGAGAAGTGTGAAGAAGCTGACTGTATAGACCTTGGGTGTTCTAATCATGTGTGTGT 2037
QY 2054 GTGAGAGCGGAATGCCAATGTCTTGTGGATGGGAGGCAACCACTGCGAGACCCCGAG 2113
Db 2038 ATCCAGCGGGAATGTCACTGCAGTCCAGGATGGGAGGTAGCAATTTGTGAATACTGAAG 2097
QY 2114 GCACATGCTTAGACAGTGTTCAGGCGACAGGAACCTTCTCCCGGACACCGGGCTTTGC 2173
Db 2098 ACCATGTGTCCAGACAGTGTCTCCGCGCACCGAACTATCTTCAAGAAAGTGGCTCTCTG 2157
QY 2174 AGCTGTGACCCAGCTGGACTGACAGACTGTCTTATCGAGATCTGTGCTGCCGACTGT 2233
Db 2158 ACSTGTGACCCCTAACTGGACTGGCCAGACTGCTCAACGGAATATGTTCTGTGGACTGT 2217
QY 2234 GTTGGCCATGGCGTGTGCGTAGGGGCACTCTGCGGCTGCGAGGATGGCTGGATGGGGCA 2293
Db 2218 GGCTCACACGGCGTTTGCAATGGGGGGAAGTGTGCTGTGGAAGAAGCTGGACGGGCCA 2277
QY 2294 GCTTCGACACAGCGGCGCTGCCACCCGCTGTGCGGAGATGGGACCTGCCCGCAGCGG 2353
Db 2278 GCCTGTAATCAGAGAGCTGCCACCCCGCTGTGCGGAGCACGGGACCTGCAAGGATGCG 2337
QY 2354 AAGTGGAGTGCAGCCCTGGCTGGAATGGCGACACTGCAACCATCGCTCACTATCTGGAT 2413
Db 2338 AAGTGTGAATGTCAGCGCAGGGCTGGAATGGAGAGCACTGCACTATCGCTCACTATTTGGAT 2397
QY 2414 AGGGTAGT-----TAAAGAGGGTTCGCTTGGCTTGTGCAATGGCAAC 2455

Db 2398 AAGATAGTTAAAGACAAGATAGGATATAAAGAGGGTGTCTCTGGTCTGTGTCAACAGCAAT 2457
QY 2456 GGCAGATGTACTTAGACTGAATGGTTGGCACTCGCTCTGCAGCTGGCTGGAGAGGA 2515
Db 2458 GGAAGATGTACCTGGACCAAAATGGCGGACATTTGTGTGCCAGCTGGATGGAGAGA 2517
QY 2516 GCTGGCTGTGACACTTCCATGGAGACTGCTGCGGTGACAGCAAAAGACAATGATGAGAT 2575
Db 2518 GCAGGCTGTGAGTAGCCTAGGACTCTTTGACAGATAGCAAGGACAAATGAAGGGAT 2577
QY 2576 GGCCTGTGGAGTGCATGGACCTGACTGCTGCTCCAGCCCTCTGCCATATCAACCG 2635
Db 2578 GGCATCATTTGATGTGATGGATCCCGATTTGCTGCTACAGAGTTCCTGGCAGAAATCAGCCC 2637
QY 2636 CTGTGCTTGGCTCCCTTAAACCTCTGGACATCATCCAGAGACACAGGTCTCTGTGTCA 2695
Db 2638 TATTGTGGGAGTCTCCGATCTCTCAGACATCATTTAGCCAAAGCCTTCAATCGCTTCT 2697
QY 2696 CAGCAGAACTTACACTCTCTTATGACCCGATCAAGTTCTCTGTGGGCGAGGACAGCAG 2755
Db 2698 CAGCAAGCTGCCAAATCTTTTATGATCGAATCAGTTTCTTATAGGATCTGATAGCAC 2757
QY 2756 CACATAATCCCGGGGAGAACCCCTTTGATGGAGGCGATGCTTGTGTTATTCTGTGCCAA 2815
Db 2758 CATGTTATACCTGGAGAAAGTCTTTCAATAAGAGCCTTGCATCTGTCAATCAGAGCCAA 2817
QY 2816 GTGATGACATCAGATGGAAACCCCTGTTGGTGTGAAACATCAGTTTGTCTCAATAACCT 2875
Db 2818 GTACTGACTGTGATGGAACTCCACTTATTTGAGTAAATGTCTCGTTTTTCCATTACCCA 2877
QY 2876 CTCTTTGGATATPACATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGTGACAAATGGCGG 2935
Db 2878 GAATATGATATACTATTACC CGCAGGACGGAAATGTTGACTTGGTGGCAATGGTGG 2937
QY 2936 ATCTCATCATCTCGGGTTTCAGCGGGCACTTTTCATCACACAGGAGCACACCTGTGG 2995
Db 2938 GCCTCTCTAACTTTGGTATTTGAAACGATCCCAATTTCTCAGTATCATCTGTGTGG 2997
QY 2996 CTGCCATGGATCGCTTCTTCTGATGGAACCATCATCATGAGACATCAGGAGAAATGAG 3055
Db 2998 ATTCCATGAATGTCTTTTATGATGGATACCTTAGTCAATGGAGAAAGAGAGATGAC 3057
QY 3056 ATTTCCAGCTGTGACTGAGCAATTTTGGCCGCCCAACCCAGTCTCTCTCATCCCCA 3115
Db 3058 ATTTCCAGCTGTGATCTGAGTGGATTTCTGTAGGCGCAAAATCCCATCATTTGTGTCTAC 3117
QY 3116 CTGAGCTCTTCGCCAGCTCTCTGTCAGAGAAAGCCCCCATTTGTGCGGGAATTCAGGCT 3175
Db 3118 TTATCCACCTTTTTCAGATCTTTCTCTGAAGACAGTCCCATCATTTCCGAAACACAGGTA 3177
QY 3176 TTGCGAGGAGAAATCTCTATCTCTGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGG 3235
Db 3178 CTCCAGAGGAAACTTACAATTCAGGAACAGATTTTGAAACTCTCTCTACTTTGATTTCCAGA 3237
QY 3236 ACCCTTGGCTACAAATCTGTCTGAGGATCAGCTCACCCACCGACCACTCCCTTTCAAC 3295
Db 3238 GCTGAGGGTATAAGTCACTCTCAAGATCACCATGACCCAGTCTATTATTCATTTAAT 3297
QY 3296 CTCATGAAGGTGCACCTCATGTTAGCGGTGGAGGGCGGCTCTTTCAGGAAGTGGTTCGT 3355
Db 3298 TTAATGAAGTTTCATCTTATGTTAGTGTAGTGAAGAGACTCTTCCAAAAGTGGTTTCCT 3357
QY 3356 GCAGCCCCAGAGCTGTCTTATTTTCAATTTGGGCAAGACAGACGCTCTACACACAGAA 3415
Db 3358 GCTCACCAAACTTGGCTTATCTTTTATATGGGATAAACAGATGCAATATATCAGAAA 3417
QY 3416 GTGTTTGGCTTTTCAAGAGCTTTTGTTCCTGGGTATTAATAATGAATCTCTGCCAGAT 3475
Db 3418 GTCTATGGTCTATCTGAAGCTGTGTGTGATGGATATGATGATGAGTCTGCTGTTGGAC 3477
QY 3476 CTAATCTCTGGGAAAAAGAAACAACAGTGTGCGAGGCTATGAAATTCAGCGGTCCAAG 3535
Db 3478 CTGACTCTCTGGGAAAAGAGGACTGCTCAATTTCTGAGGGCTATGAATTTGATGCTCCAAC 3537

| | | | |
|----|------|---|------|
| Qy | 3536 | CTTGGAGGATGGAGCCCTAGACAAACATCATGCCCCTCAACATTCAAAGTGGTATCTCTGCAC | 3595 |
| Db | 3538 | ATGGTGGCTGGACATTTAGATAAAACATCACGTCCTGGATGTACAGAACGGTATACTGTATC | 3597 |
| Qy | 3596 | AAAGGGAATGGGAGAACCAATTTGTGTCTCAGCAGCCTCTGTCTATTTGGGAGCATCATG | 3655 |
| Db | 3598 | AAGGGAACGGGGAAACCAAGTTTCATCTCCACAGCCTCCAGTCGTGTAGTAGCATCATG | 3657 |
| Qy | 3656 | GGCAATGGGCGCCGGAGAACATCTCTGTCGCCAGCTGCAACGGCCCTTGCTGACGGCAAC | 3715 |
| Db | 3658 | GGCAATGGGCGAAGGCGACATTTCTGTCGCCAGTTGCAATGGTCAAGCTGATGGTAAC | 3717 |
| Qy | 3716 | AAGCTCTGGCCCCAGTGGCCCTCACTGTGGCTCTGACGGGAGCCTCTATGTGGGTGAT | 3775 |
| Db | 3718 | AAGTTACTGGCCCCAGTGGCGCTAGCTTTGTGGATCGATGGCAGTCTGTACGTAGCGGAT | 3777 |
| Qy | 3776 | TTCAACTACATTTAGAAGGATCTTCCCCTCTGGAAATGTCAACCAACATCTTAGAGCTGAGG | 3835 |
| Db | 3778 | TTCAACTACGTGGCGGATATTCCCCTCTCGAAATGTAAACAAGTGTCTTAGAACCTAAGA | 3837 |
| Qy | 3836 | AATAAAGATTTACACATAGTACAGTCCAGCACACAATACTACTCTGGCCACAGACCCC | 3895 |
| Db | 3838 | AATAAAGATTTTAGACATAGCAGCAACCCAGCTCATAGATACTACCTTGCACGGATCCA | 3897 |
| Qy | 3896 | ATGAGTGGGCGGTCTTCTTTCTGACAGCAACAGCCGGCGGTCTTTAAATCAAGTCC | 3955 |
| Db | 3898 | GTACGGGAGATCTGTACGTTTCTGCACAAACACCCCGCAGAAATTTATGCCCAAAGTCA | 3957 |
| Qy | 3956 | ACTGTGGTGTGAAGACCTTGTCAAGATCTCTGAGTGGTTTGGGGACAGAGTACCAG | 4015 |
| Db | 3958 | CTTAGGGGGCAAAAGACTTGACTTAAATATGCAGAACTCGTCGCAGGGACAGGGAGCAA | 4017 |
| Qy | 4016 | TGCTCTCCCTTTGTATGACACTCGCTCGGGGATGGTGGGAAGGCCACAGAAAGCCACATC | 4075 |
| Db | 4018 | TGCCTTCGTTTGACGAGGCGAGATGTGGGATGAGGGAAGGCCGTGGGAAGCCACACTC | 4077 |
| Qy | 4076 | ACCAATCCAGGGGTATTACGTGGACAAAGTTTGGGCTGATCTACTCTGTGGATGGCAAC | 4135 |
| Db | 4078 | ATGAGTCCCAAAGGAATGGCAGTTGATAAAGATGGATTAATCTACTTTGTGTGATGGAAAC | 4137 |
| Qy | 4136 | ATGATTCAGACGCATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTC | 4195 |
| Db | 4138 | ATGATTAGAAAGTTGACCAAAATGGAATCATATCAACTCTTCTGGGCTCTAACGATTTG | 4197 |
| Qy | 4196 | ACATCAGCCCGGCCACTCAGCTGTGATTTCTGTATGATATTTTCCAGGTAAAGACTGGAG | 4255 |
| Db | 4198 | ACTTCAGCCAGACCTTTAACTTTGTGACACCAAGCATGACATCAGCCAGGTACGTCTGGAA | 4257 |
| Qy | 4256 | TGGCCCAAGACTTAGCCATCAACCAATGGACAACCTCAGTTTATGCTCGACAAACAAT | 4315 |
| Db | 4258 | TGGCCCACTGACTAGCCATTTAACCTATGATTAATCTCAATTTATGCTCTGGATTAATAAT | 4317 |
| Qy | 4316 | GTGGTCTCTGCAATCTCTGAATAACCAAGGTGGCGATTTGCGCGGAGGCCCATGGAC | 4375 |
| Db | 4318 | GTAGTTTTACAGATCACTGMAAATCGTCAAGTTGCGATTGCTGTGGACGGCCCATGCAC | 4377 |
| Qy | 4376 | TGCCAGTCCCTGGCATTTGACCACTTCTGCTTAGCAGAAGTGGCCATCCACGCAACCTGT | 4435 |
| Db | 4378 | TGTGAGTTTCCGGAGTGG---AATATCTGTGGGAAGCAGCGGTGTCAGACAAACTGT | 4434 |
| Qy | 4436 | GAGTCAGCCACCGCTTTGGCTGTTTTACACAATGGGGTCTGTATATTGCTGTGAGACTGAT | 4495 |
| Db | 4435 | GAATCAGCCACTGCCATTTGCTGTGCTTACAGTGGGGTCTGTATCAATTTACTGAAACTGAT | 4494 |
| Qy | 4496 | GAGAAAAGATCAACCGCATAGGCAGGTTCACCACTAGTGAGAGATCTCACTGTGTGCT | 4555 |
| Db | 4495 | GAGAAAGAAATTTAACCGGATAAGCAGGTTCACACAGATGGAGAAATCTCTTAGTGGCC | 4554 |
| Qy | 4556 | GGGGCCCCAGTGGGTGTGACTGTAAAAATGATGCCAACTGTGATTTGTTTTCTGGAGAC | 4615 |
| Db | 4555 | GGAAATACCTTCAGAGTGTGACTGCAAAAATGATGCCAACTGTGACTGTATTACAGAGTGG | 4614 |

Db 5695 TATTATCATCACAGGTCAAATTCGACGATCCAGGAGGCACCACTAGCGAGAAAGTAGAT 5754
Qy 5753 TAGCACCAGGCGGCGCATCATCAGGATCTTCGCTGATGGGAGAGACATGGAGCTAC 5812
Db 5755 TATGACGGACAGGGAGGATCGTGTCTCGGGTCTTTGCTGATGGTAAACCATGGAGTTAC 5814
Qy 5813 ACATACTTAGAAGATCCATGGTGTCTTACTACAGACGAGAGGAGTATATCTTTGAG 5872
Db 5815 ACATATTTAGAAAAGTCCATGGTCTTCTGCTTCATAGCCAGGAGTACATCTTCGAA 5874
Qy 5873 TTTCGAAGAATACCGCCTCTCTTCTGTGACGATGCCCAACGTTGGCGGCGAGACACTA 5932
Db 5875 TAGCATATGTGGACCGCTGTCTGCCATCACCATGCCAGTGTGGCTGCCACACCATG 5934
Qy 5933 GAGACCATCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCGCTGAGGCGCATGCC 5992
Db 5935 CAGACCATCCGATCCATTTGGCTACTACCGCAACATATACAACCCCGCGAAAGCAACGCC 5994
Qy 5993 TCAGTCATACAGACTTCACTGAGGATGGCACCTCTCTTCAACACTTCTACCTGGGCACT 6052
Db 5995 TCCATCATCAGGACCTACAAAGGAGGCTGCTTCTACAAACAGCTTCTTGGGTACA 6054
Qy 6053 GGCAGGAGGTGATATACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGAC 6112
Db 6055 AGTCGGAGGCTCTTATTCAAATACAGAAGCGAGACTAGGCTCTCAGAAATTTTATATGAT 6114
Qy 6113 ACCACCAAGGCTGTTTACCTATGACGAGACGGGAGGACATGCTGAAGACCATCAACCTA 6172
Db 6115 AGCACAAAGATCAGTGTATTTACCTATGATGAACAGCAGGAGTCCCTAAAGACAGTAAACCTC 6174
Qy 6173 CAGAAATGAGGCTTCACTGCAACCTCCGCTACCGTCAGATTTGGGCCCTGTGATGACGA 6232
Db 6175 CAGAGTGATGTTTTATTGACCACTTAGATACAGGCAAAATGGTCCCTGATGACAGG 6234
Qy 6233 CAGATCTCCCGCTTCACTGAGGAAGGCATGGTCAACCGCCGTTTGAACCTCAACCTATGAC 6292
Db 6235 CAGATTTCCCGCTTTAGTGAAGATGGATGGTAAATGCAAGATTTGACTATAGCTATGAC 6294
Qy 6293 AACAGCTTCGGGTGACAGCATGAGGCTGTGATCAACGAGACCCCACTGCCCATGAT 6352
Db 6295 AACAGCTTTGAGTGACAGCATGACAGGCTGTGATCAATGAACCGCACTGCCCTATTGAT 6354
Qy 6353 CTCTATCGCTATGATCATGTGTCAGGCAAGACAGACAGTGTGGGAAGTTTGGTGCACT 6412
Db 6355 CTGTATCAGTTTGATGACATTTCTGGCAAAGTTGACAGGTTTGGAAAAGTTTGAGATTATA 6414
Qy 6413 TACTATGACATTAACAGATCATCACAGCTGTGATGACCCACCAACCAAGCATTTTGAT 6472
Db 6415 TATTATGATATTAAACAGATCATTTCTACAGCTGTAATGACCTATACGAAGCACATTTGAT 6474
Qy 6473 GCATATGGCAGGATGAAGAGTGCAGTATGAGATCTTCGGCTCGCTCATGTACTGGATG 6532
Db 6475 GCTCATGGCGGTATCAAGGAGATTCAATATGAGATATTAGGTTCGCTCATGTACTGGATT 6534
Qy 6533 ACCGTCCAGTATGATTAACATGGGCGAGTAGTCAAGAGAGCTGAAGTAGGACCCCTAC 6592
Db 6535 ACAATTCAGTATGATTAACATGGGTGCGGTAAACAGAGAGAGATTAAATATAGGGCCCTTT 6594
Qy 6593 GCCAATACCACCTCGCTACTCTATGATGATGCTGACGGCCAGCTGCAGACAGTCTCC 6652
Db 6595 GCCAACCACCAAAATATGCTTATGATATGATGTTGATGGACAGCTCCAAACAGTTTAC 6654
Qy 6653 ATCAATGAACAGCACTCTGGCGCTACAGCTACGACCTCAATGGGAACTGCACTTACTG 6712
Db 6655 CTCAATGAAGATAATATGGCGGTACAACTACGATCTGAATGGAACCTCCATTTACTG 6714
Qy 6713 AGCCCTGGNAACAGTGCACGGCTCACCACTACGCTATGACATCGCGACCGCATCACT 6772
Db 6715 AACCCAAGTAACAGTGGCGGTCTGACACCCCTTTCGCTATGACCTGCGAGACAGATCACT 6774
Qy 6773 CGGCTGGGTGACGTGCAATACAAGATGGATGAGGATGGCTTCTTGAAGCAGCGGCGGT 6832

Db 6775 CGACTGGGTGATGTTCAATATATCGGTTGGATGAAGATGGTTTCTTACGTCAAAAGGGGACAG 6834
Qy 6833 GATATCTTTTGTAGTACAACTCAGCTGGCTGTCTCATCAAGGCGCTCAAAACGGGCTGGCAGC 6892
Db 6835 GAAATCTTTTGTATATAGTCTCAAGGGGCTTCTTAACCTCGAGTTTACATGAAGGAGTGGC 6894
Qy 6893 TGGAGTGTCAAGTACCGCTTACGATGGCTGGGCGCGCGTGTCTCAGCAAGAGAGACCCAC 6952
Db 6895 TGGACAGTGAATCTACCGTTATGACGGCTGGGAAGGCGGTGTTCTAGCAAAACCAAGTCTA 6954
Qy 6953 AGCCACCACTGCGAGTCTTCTATCGAGACCTGACCAACCCCGACCAAGGTCAACCCACTG 7012
Db 6955 GGACAGCACCTGACGATTTTTTATGCTGACTTAACTTATCCCACTAGGATTAATCTCATGTC 7014
Qy 7013 TACAACCACTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGAAGGACACCTCTCTT 7072
Db 7015 TACAACCACTTCGAGTTAGAAATTAACCTCCCTGTATTAATGATCTCCAAGGACATCTTTT 7074
Qy 7073 GCCATGGAGCTGAGCAGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 7132
Db 7075 GCCATGGAAATCAGCAGTGGGATGAATTTCTATATTGATCGGATAACACAGGACACCA 7134
Qy 7133 CTGTGCTGTCTTTAGTGGAAACAGTGTGATGATCAAGCAAAATCCTGTACACAGCTATGG 7192
Db 7135 CTGGCTGTGTTCAGTAGCAATGGGCTTATGCTGAAACAGATTCAGTACACTGCATATGG 7194
Qy 7193 GAGATCTACATGATACCAACCCCAACTTTTCAAGATCATCATAGGCTTACCATGTTGGCTC 7252
Db 7195 GAAATCTATTTTGTACTCTAATATGACTTTTCACTGTTTGAATTTGATTTTCACTGGTGG 7254
Qy 7253 TATGATCCCACTCAACAGCTGTGTCCACATGGGCGCGGAGATTATGATGTGTGGCCGA 7312
Db 7255 TATGACCCACTCACCAAAATTAATCCATTTTGGAGAAAGAGATTATGACATTTTGGCAG 7314
Qy 7313 CGCTGGAATAGCCACAGACCAAGCTGTGGAAAGCACTTAGTAGCAGCAAGCTATGCCCT 7372
Db 7315 CGTGGACAAACCTGACATAGAAATCTGGA---AAAGAAATTTGGGAAGGACCCAGCTCCT 7371
Qy 7373 TTTAATCTCTATATGTTCAAAAACCAACCCCATCAGCAACTCCAGGACATCAAGTGC 7432
Db 7372 TTTAATCTGTACATGTTTAGGAATTAACAACTTCGACGCAAAATTCATGACGTGAAGAT 7431
Qy 7433 TTTCAAGACAGATGTTAAACAGCTGGCTGCTCACCTTTTGGATTTCCAGCTACAAACGTGATC 7492
Db 7432 TACATCACAGATGTTAAACAGCTGGCTGGTGACATTTGGTTTCCATCTGCACAAATGCTATT 7491
Qy 7493 CTTGGTTATCCAAACAGACATGATGCCATGGAACCCCTCTACGAGCTCATCCACACA 7552
Db 7492 CTTGGATTCCTGTTTCCCAAATTTGATTTAACAGAACTTCTTACGA-----A 7539
Qy 7553 CAGATGMAAACCGCAGAGTGGGACAAACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTA 7612
Db 7540 CTTGTGAAGAGTGCAGAGTGGGATGATATACGCCCATCTTCGGAGTCCAGCAGCAAGTG 7599
Qy 7613 CAGAAAGCACTCAAGGCTTTTGTCACTTTAGAACGGTTTGAACAGCTCTATGCTCCACA 7672
Db 7600 GCGCGCAGCCCAAGGCTTCTGTGCTGGGGAAGATGCGCGAGGTGCGAGGTGAGCGCG 7659
Qy 7673 ATCAACAGTGCAGCAGGCTCCAAAGACCAAGAAAGTTTGCATTCAGCGGCTCAGTCTTT 7732
Db 7660 CGCGCGGCGCGG---GGCGCGCAGCTCTGGCTGTGGTTCCGCCACGGTCAAGTCTGATC 7716
Qy 7733 GGCNAGGGGTCAAGTTTTCCTTGAAGATGCGCGAGTCACACAGACATCATCACTGTG 7792
Db 7717 GGCNAGGGGTGATGCTGGCCCTCAGCCAGGGCGCGTGCAGACCAACGTGTCAACATC 7776
Qy 7793 GCCAATGAGGATGGGCGAAGGTTGCTGCCATCTTTGAACCATGCCCCACTACCTAGAGAAC 7852
Db 7777 GCCAAGGAGTGCATCAAGGTGGGCGCGTCTCAACAAACGCTTCTTACCTGGAGAAC 7836
Qy 7853 CTGCACTTCCATTTGATGGGTGATACCCATTAATTTGTTGAAACAGGACCTTCAGAA 7912
Db 7837 CTGCACTTCCATTCAGGGCAAGGACACGCACTACTTCTTCAAGACCAACCGCGCGAG 7896

| | | | |
|-----------|--|--|------|
| QY | 7913 | GGTGACCTGGCCATCTCTGGCCCTCAGTGGGGGGCGGCGAAACCTCTGGAGAAATGGGGTCAAC | 7972 |
| Db | 7897 | AGCGACCTGGGCAACGCTCGGTTGACCAAGCGCGCGAAGGGCTGGAGAACGGCATCAAC | 7956 |
| QY | 7973 | GTCACTGTGTCCAGATCAACACAGTACTTAAATGGCAGGACTAGACGCTACACAGACATC | 8032 |
| Db | 7957 | GTGACGGTGTGCGAGTCCACCACGGTGTGAACGGCAGGACGCGCAGGTTCCGCGGACGTG | 8016 |
| QY | 8033 | CAGCTCCAGTACGGGGCACTGTGCTTGAACACACAGCTACGGGACAAAGTTGGATGAGGAG | 8092 |
| Db | 8017 | GAGATGTCAGTTTCGGCGCGCTGGCGCTGCACTGGCGCTACGGCATGACCTTGGACGAGGAG | 8076 |
| QY | 8093 | RAGGCACGGTCTCTGAGCTGGCCCGGCAGAGAGCGCGTGGCCCAAGCGTGGGGCCGCGAG | 8152 |
| Db | 8077 | AAGGCGCGCATCTCTGAGCAGCGCGGCGAGCGCGGCTCGCCGGGCTGGCGCGCGGAG | 8136 |
| QY | 8153 | CAGCAGAGACTCTGGGGAAGGGAGGAAGCGCTCGGGCTTGGACAGAGGGGGAGAGCAG | 8212 |
| Db | 8137 | CAGCAGCGGTGCGCGACGGCGAGGAGGCGCGGCGCTCTGGACGGAGGGCGAGAAACGG | 8196 |
| QY | 8213 | CAGGTGCTGAGCAGCAGGGCGGTGCAAGGCTTACGACGGCTTTTTCGTGATCTCTGTGCGAG | 8272 |
| Db | 8197 | CAGTGTCTGAGCGCGCGCAAGGTGAGGGCTACGACGGGTACTACGTACTCTCGGTGGAG | 8256 |
| QY | 8273 | CAGTACCCAGAACTGTGACAGAGCGCCCAACAACTCATTCTATGACACAGAGCGAGATG | 8332 |
| Db | 8257 | CAGTACCCGAGCTGGCGACAGCGCCCAACAACTCATTCTCTCGCGCAGAGCGAGATC | 8316 |
| QY | 8333 | GGCGGAGGTGAC | 8345 |
| Db | 8317 | GGCAGGAGGTAAC | 8329 |
| RESULT 14 | | | |
| ABQ82343 | | | |
| ID | ABQ82343 | standard; cDNA; 8675 BP. | |
| XX | AC | | |
| XX | ABQ82343; | | |
| DT | 17-DEC-2002 | (first entry) | |
| DE | Human NOV15a | encoding cDNA SEQ ID NO:35. | |
| KW | Human; NOVX; | cytostatic; neuroprotective; anticonvulsant; cardiovascular; | |
| KW | cerebroprotective; nootropic; antidiabetic; | antiinflammatory; fungicide; | |
| KW | antirheumatic; antiarthritic; immunosuppressive; | antiallergic; virucide; | |
| KW | antianaemic; antibacterial; protozoacide; | antihelminthic; gene therapy; | |
| KW | cancer; leukaemia; lymphoma; melanoma; | neurological disorder; epilepsy; | |
| KW | stroke; ischaemic cerebrovascular disease; | Alzheimer's disease; allergy; | |
| KW | Pick's disease; vesicular transport disease; | cystic fibrosis; goitre; | |
| KW | diabetes mellitus; Grave's disease; | gastrointestinal disorder; vaccine; | |
| KW | ulcerative colitis; gastric disorder; | duodenal disorder; infection; | |
| KW | autoimmune disease; allergic reaction; | autoimmune haemolytic anaemia; | |
| XX | rheumatoid arthritis; gene; chromosome 4; | ss. | |
| OS | Homo sapiens. | | |
| XX | | | |
| PH | Key | Location/Qualifiers | |
| CDS | 151..8328 | | |
| FT | /*tag= a | | |
| FT | /product= "NOV15a" | | |
| FT | /transl_except= (pos:1249..1251,aa:Ser) | | |
| XX | | | |
| PN | WO200262999-A2. | | |
| XX | | | |
| PD | 15-AUG-2002. | | |
| XX | | | |
| PF | 31-DEC-2001; 2001WO-US049976. | | |
| XX | | | |
| PR | 29-DEC-2000; 2000US-0258928P. | | |
| PR | 02-JAN-2001; 2001US-0259415P. | | |
| PR | 04-JAN-2001; 2001US-0259785P. | | |

| | | | |
|---|---|---|-----|
| PR | 20-FEB-2001; | 2001US-0269814P. | |
| PR | 09-MAR-2001; | 2001US-0279863P. | |
| PR | 29-MAR-2001; | 2001US-0279832P. | |
| PR | 13-MAR-2001; | 2001US-0279833P. | |
| PR | 18-APR-2001; | 2001US-0284447P. | |
| PR | 25-APR-2001; | 2001US-0286683P. | |
| PR | 29-MAY-2001; | 2001US-0294080P. | |
| PR | 16-AUG-2001; | 2001US-0312915P. | |
| PR | 17-AUG-2001; | 2001US-0313325P. | |
| PR | 17-SEP-2001; | 2001US-0322699P. | |
| PR | 26-NOV-2001; | 2001US-0333350P. | |
| XX | (CURA-) CURAGEN CORP. | | |
| PA | Spytek KA, Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X; | | |
| PI | Malyankar U, Shinkets RA, Tchiernev VT, Spaderna SK, Gorman L; | | |
| PI | Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S; | | |
| PI | Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K; | | |
| PI | Gunther E, Smithson G, Millet I, Macdougall JR; | | |
| XX | WPI; 2002-732706/79. | | |
| DR | P-PSDB; ABP53586. | | |
| XX | New NOVX polypeptides and polynucleotides useful for treating NOVX- | | |
| PT | associated disorders, such as cancers, neurological disorders, disorders | | |
| PT | of vesicular transport, gastrointestinal disorders, and autoimmune | | |
| PT | diseases. | | |
| XX | Claim 8; Page 110-112; 444pp; English. | | |
| PS | The present invention describes novel human proteins designated NOVX, | | |
| XX | where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, | | |
| CC | cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, | | |
| CC | antidiabetic, antiinflammatory, antirheumatic, antiarthritic, virucide, | | |
| CC | immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide, | | |
| CC | protozoacide and antihelminthic activities, and can be used in gene | | |
| CC | therapy. The NOVX proteins, nucleotides or antibodies can be used in the | | |
| CC | manufacture of a medicament for treating a syndrome associated with a | | |
| CC | human disease selected from NOVX-associated disorder, such as cancers | | |
| CC | (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, | | |
| CC | ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, | | |
| CC | ischaemic cerebrovascular disease, Alzheimer's disease or Pick's | | |
| CC | disease), disorders of vesicular transport (e.g. cystic fibrosis, | | |
| CC | diabetes mellitus, Grave's disease, or goitre), gastrointestinal | | |
| CC | disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), | | |
| CC | autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic | | |
| CC | anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic | | |
| CC | and protozoal infections. The NOVX proteins can be used as immunogens to | | |
| CC | produce antibodies and as vaccines. The NOVX nucleotide sequences may be | | |
| CC | used in chromosome mapping, identifying individuals from minute | | |
| CC | biological samples (tissue typing), and in forensic identification of a | | |
| CC | biological sample. The present sequence encodes human NOV15a, which is | | |
| CC | located on chromosome 4 | | |
| XX | | | |
| SQ | Sequence 8675 BP; 2362 A; 2067 C; 2201 G; 2041 T; 0 U; 4 Other; | | |
| Query Match | | | |
| Best Local Similarity 41.6%; Score 3472.6; DB 6; Length 8675; | | | |
| Matches 5442; Conservative 65.2%; Pred. No. 0; | | | |
| Mismatches 2693; Indels 216; Gaps 14; | | | |
| QY | 35 | ATGGACCTGAAGGAGAGAAAGCCTTACCGCTCGGTGACCGCGCGC---CGCAGCGCGAG | 91 |
| Db | 151 | ATGGATGTGAAGAAACGACGCGCCTTACTGCTCCCTGACCAAGACGACGAGAGAGAA | 210 |
| QY | 92 | CGCGCTACACCACTGTCGCGGACAGCGAGAGGGCAAG---CCCCGAGAAATCG | 148 |
| Db | 211 | CGCGCTACACCAATTTCTCCGACACATAGAGAGTGGCGGTACCCACACAGAGTCC | 270 |
| QY | 149 | TACAGCTCCAGCGAGACCCCTGAAGCCCTACGACAGGA---CGCCGCTAGCCTATGCG | 205 |
| Db | 271 | TACAGTTCCAGCGAGACATTGAAAGCTTTTGATCATGATTCCTCGCGGTGCTTTACGCG | 330 |

QY 206 AGCGCGTCAAGGACATTTGTGCGCAGAGGCGGAGGAATTTCTGCGCAGCAGGTGCCAAC 265
Db 331 AACAGAGTGAAGGATTTGGTTTCACAGAGAAGCAGACGAGTTCTACTAGACAAGGACAGAAT 330
QY 266 TTCACCTCGGGAGCTGGGGCTGGAAAGATGAACGCCGCCCTCACCGGACCCCTGTACCGG 325
Db 391 TTTACCTTAAGGAGTTAGGAGTTGTGTGAACCAAGCAACTCGAAAGAGGACTGGCAATTTTGT 450
QY 326 ACAGACATTTGGCTGCCCAATCGGCTACTTCCATGGGGCTGGCTGTGATGCCGACATG 385
Db 451 GCGGAATGGGGCTCCCTCACAGAGTTACTATCATGTGAGGGTCAGATGCTGATCT 510
QY 386 GAGGCTGCACAGGTGTGTCCTCCCTGCAGCACCCCGTGGCTGTGTGGGCGCGAGCACACCG 445
Db 511 GAAATGAAGCAGTGTGTCCTCCAGAGCATGCCATGAGACTTTTGGGCGAGGGGGTCAAA 570
QY 446 TCAGGGGCGAGCTCTGCTGTGTCAGCGGGCCAAATTCNAATCTCACACTCAGCAGACC 505
Db 571 TCAGGGCGCAGCTCTGCTGTCAAGTCGGTCCAACTCAGCCCTCACCTCGACAGATACG 630
QY 506 GAGCATGAAACACTGAGACTGATCATCCGGCGGCTGCAGAACCAAGCGGCTCCCG 565
Db 631 GAGCAGAAACAGTCCGACAGTGAGATGAGCAACTCTGCAAGCAATCAGGCCAGTCT 690
QY 566 ACGCCGCGCGCGCTCTCGCACGCGCCACACCCCAACAGCACCAAGCGGCTCCAT 625
Db 691 ACCCTGAGCCCTTGGCGCTTCCCATAGCAGCACTCTGCACAGCATCATCCATC 750
QY 626 AACTCCCTGAAACCGGGGCAACTTCACGCCGAGAGCAACCCCAAGCGGCGCCCAAGCAG 685
Db 751 ACTTCTCTCAACAGAACTCCCTGAGCAATAGAAAGGAACCAAGTCCGGCGCCCGCGGT 810
QY 686 CACTCGCTCTCGGAGAGCCCTGCGCGGCGCCAGAGGCTGCCACAGCCCGCAGGAG 745
Db 811 GCTTTGCCCGCCAGGTGCAAC-----CACACCCAGTCCGTCCAGTGCAGGAG 861
QY 746 AACTGGGTCTCAACAGCAACATCCCTCGAGACCAAGGAACCTAGGCAAGCAGCCATTC 805
Db 862 AGTGGGTCTTGGCAGTATGTACCACTGGAAGGAGGCAATTT----- 905
QY 806 CTAGGACATTTGAGGACAACTCATTTGAGATGGACATTTCTGGCGCTCCCGCCATGAT 865
Db 906 ----- 905
QY 866 GGGGCTTACAGTGACGGGCACTTCTCTTCAAGCTTGGAGGACCTCCCGCTCTTCTGC 925
Db 906 -----CCTATTCAAAACAGGAACAGGTATCAACGCGCACTGTTCAGT 945
QY 926 ACCACATCACAGGTTACCCACTGACGTCCAGCACAGTGTACTCTCTCCGCGCCGACCC 985
Db 946 ACTGCAACCCAGGATACACATGGCATCTGGCTCTGTTTATTCACCACTACTCAGGCCA 1005
QY 986 CTCGCCCGCAGCACTTTCGCCCGCGGCTTTAACTCAAGAGCCCTTCAAGTACTGT 1045
Db 1006 CTACCTAGAAACACCCCTATCAAGAAGTGTCTTTAAATTCAGAAGTCTTCAAAAGTACTGT 1065
QY 1046 AACTGGAAGTGCAGCGCTGAGGCGCATGTCATCTCAGCCTCTGCTGTCATCTGCTG 1105
Db 1066 AGCTGAAATGCACTGCACGTGTGCGGTAGGGGTCTCGGTGCTCTGCGCAATACTCCTG 1125
QY 1106 GCATACTTTTGGGCCATGACCTGTTTGGCTTAACTGGCACCCTGCAGCGGATGGAGGGG 1165
Db 1126 TCTTATTTATAGCAATGCATCTCTTTGGCTCAACTGGCAGCTACAGCAGCTGAAAT 1185
QY 1166 CAGATGTATGAGATCACGGAGGACACAGCCAGAGTTGGCTGTGCGCAACCGCAGCTCC 1225
Db 1186 GACACATTTTGA-----ATGGAAGTGAATTCATGATACCATGTCACAAACACTGTG 1239
QY 1226 CTATACCCCTCAGGGGCACTGCTTAGACCCCTGACAGGAAGCAAGGAACACACA 1285
Db 1240 TCATTACCTNNNTGGAGCA----- 1258
QY 1286 GAAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAGTTTTCATAGATTTCTGAGAAATGAT 1345

Db 1259 -ATGGAAATTAGTGGATTTTACGCAAGAAATAACACCATAGATTTCCGAGAACTTGAT 1317
QY 1346 GTGGGAAGCGGAGCCTCCAGAGATTTCTCTGGCAGCTTTCTGGAGATCTCAAGTGTTC 1405
Db 1318 ATTGGCCGAAGACAAATCAAGAGATTTCTCCGGGATCTTTCTGGAGATCACAGCTCTTC 1377
QY 1406 ATAGACCATCTGTGTCATCTGAAATCAATGTCTCTCGGAAAGGAGCAGCCCTGGTTGGC 1465
Db 1378 ATTGATCAGCACAGTTTCTTAAATCAATATCTCTTCAGAAAGGATGCAATGATTGA 1437
QY 1466 ATTTATGGCAGAAAGGCTCCCTCTCTTCACTA-----CACAGTTTGACTTT 1513
Db 1438 GTATATGGCGGAAGATTAAGCGCTTCCCATCTCAGTCTCTCCCGCAGTATGACTTC 1497
QY 1514 GTGGAGCTCTGATGGCAGGAGGCTCTAAACCCAGGAGCGCGGAGCCTTAGAGGGAGC 1573
Db 1498 GTGGAGCTCTGATGGCAGGAGGCTGATTTGCCAGAGAGGAGCGGAGCCTGCTTGAGAGC 1557
QY 1574 CCGCGCCAGTCTCGGGGAACTGTGCCCGCTCCAGCCATGAGACAGGCTTCATCCAGTAT 1633
Db 1558 GAGAGAGCCGGGCGGAGGAGATCCGTGAGCTTCATGAGCGCGCTTTATCCAGTAC 1617
QY 1634 TTGGATTCAAGGAATTTGGCACTTGGCTTTTACAATGACGGAAAGAGTCAGAAAGTGT 1693
Db 1618 TTGGATTCTGGAATCTGGCATCTGGCTTTTATAATGATGGGAAATAATGAGAGCAGGTG 1677
QY 1694 TCTTTCTCACACTGCCATTTGATCGGTGGATTAACCTGCCAGCACTGCTATGGCAAT 1753
Db 1678 TCTTTTAAATACCAATTTATAGAGTCTGTGGTGGAAATGTCCCGAAATTTGCCATGGAAT 1737
QY 1754 GGTGACTGATCTCTGGGACCTGCCACTGCTTCTGGGTTTCTGGCGCCCGCACTGTGGC 1813
Db 1738 GGAGAAATGGTTTCTGGAATTTGCCATTTGTTTCCAGGATTTCTGGGTCCGATTTGTTCA 1797
QY 1814 AGAGCTCTCTGCCCTGCTGTGTAGCGAAATTTGCGCAATATACATGAAGGACAGATGCTG 1873
Db 1798 AGAGCGCTGTCCAGTGTATGTAGTGGCAACGGGAGTACTTCAAGGCGCGCTGCTG 1857
QY 1874 TGCCACAGTGGCTGGAAAGGCGCTGAGTGGATGTGCCACCAACCACTGATTCGATGTG 1933
Db 1858 TGTTCACGGCTGGAAAGGCGACCGAGTGTGATGTGCCCACTACCCAGTGTATTTGACCCA 1917
QY 1934 GCCTGCAGCAACCATGGCACCTGCATCAGGGCACCTGCATCTGCAACCTGCTGTACAAG 1993
Db 1918 CAGTGTGGGGTCTGGGATTTGTATCATGAGGCTCTGTGCTTGCAGCTCAGGATACAAA 1977
QY 1994 GGCAGAGCTGTGAGGAAGTGGATGTCATGGAACCCCACTGTTTACGCCCGGGGTGTGTC 2053
Db 1978 GGAGAAAGTTGTGAAGAGCTGACTGTATAGACCTTGGGTGTTCTAATCATGCTGTGTGT 2037
QY 2054 GTGAGAGGCAATGCCATTTGTTGGATGGGAGGACCACTGCGGAGACCCCGCAGG 2113
Db 2038 ATCCAGGGGAAATGTCACTGCAGTCCAGGATGGGAGGTAGCAATTTGTGAATTACTGAAG 2097
QY 2114 GCCACATGCTTAGACAGTGTTCAGGCCACGGAACCTTCTCCCGGACACCGGGCTTTGC 2173
Db 2098 ACCATGTGTCCAGACCAAGTCTCCGSCCAAGGACGATATCTTCAAGAAAGTGGCTCCTGC 2157
QY 2174 AGCTGTGACCCCAAGCTGGAATGGACACGATGTTCTATCGAGATCTGTGCTGCCGACTGT 2233
Db 2158 ACCTGTGACCCCTAACTGGACTGGCCAGACTGTCTCAACGAAATATGTTCTGTGGACTGT 2217
QY 2234 GGTGGCCATGGGCTGTGCGTAGGGGCACTGCGCTGCGGAGGATGGCTGGATGGGGGCA 2293
Db 2218 GGCTCACACGGGCTTTGCATGGGGGGGACGTGTGCTGTGAAGAGGCTGGACGGGCCCCA 2277
QY 2294 GCCTGCGACAGGGGCTGCCACCGCGCTGTGCCGAGCATGGGACCTGCGCGCAGCGC 2353
Db 2278 GCTGTAAATCAGAGAGCCTTGCCACCCCGCTGTGCCGAGACCGGACCTGCAAGGATGGC 2337
QY 2354 AAGTGGAGTGCAGCGCTCGCTGGAAATGGCAACACTGCACCATCGCTCATCTATCTGGAT 2413

Db 2338 AAGTGTGAATGCAGCCAGGCGCTGGAATGGAGAGCATGCACTATCGCTCACTATTTGGAT 2397
Qy 2414 AGGTTAGT-----TAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAAC 2455
Db 2398 AAGATAGTTAAAGACAAGATAGGATAAAAGAGGGTTGTCTGTGCTGTGCAACAGCAAT 2457
Qy 2456 GGCAGATGTACCTTAGACCTGMAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGA 2515
Db 2458 GGAAGATGTACCTGGAGCAAAATGGCGGACATTTGTGTGCGCAGCTGTGATGGAGAGGA 2517
Qy 2516 GCTGGCTGTGACACTTCCATGGAGACTGCCCTGCGGTGACAGCAAGAACAATGATGGAGAT 2575
Db 2518 GCAGCTGTGAGCTAGCCATGGAGACTCTTTTGCAAGATAGCAAGGAGCAATGAAGGGAT 2577
Qy 2576 GGCCTGTGTGATCGATGGACCTGTGATGCTGCTCCAGCCCTGTCGCCATATCAACCCG 2635
Db 2578 GGACTCATTTACTGTCATGGATCCCGATTTGCTGCTACAGAGTTCTCTGCCAGAAATCAGCCC 2637
Qy 2636 CTGTGCCCTTGGCTCCCTTAACCTCTGACATCATCCAGGAGACACAGGTCCTGTGTCA 2695
Db 2638 TATTGTGGGGACTGCGCGGATCCCTCAGGACATCATTAGCCAAAGCCTTCAATGCCCTTCT 2697
Qy 2696 CAGCAGAACTTACACTCTCTATGACCGCATCAAGTTCTCTGTTGGGAGGAGCAGACG 2755
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Qy 2756 CACATAATCCCGGGGAGAACCTTTGATGGAGGGCATGCTGTGTATTTCTGTTGGCCAA 2815
Db 2758 CATGTTATACCTGGAGAAAGTCTTTCAATAAGAGCCCTTGCATCTCATCAGAGGCCAA 2817
Qy 2816 GTGATGACATCAGATGGAAACCCCTCTGTTGGTGTGAACATCATGTTTGTCAATAACCT 2875
Db 2818 GTACTGACTGCTGATGGAACTCCACTTATTGGAGTAATGTCTCGTTTTCATTACCCA 2877
Qy 2876 CTCTTTGGATATACAATCAGCAGGCAAGATGGAGCTTTTGACTTTGGTGACAAATGGCGG 2935
Db 2878 GAATATGGATATCTATTATCCCGCAGGACGGAATGTTTGACTTTGGTGCAAAATGGTGG 2937
Qy 2936 ATCTCCATCATCTCGCGGTTGAGGGGCACCTTTTCATCACAGGAGCACACCTGTGG 2995
Db 2938 GCCTCTCTAACTTTGGTATTTGAACGATCCCATCTCTCACTCAGTATCATCTGTGTGG 2997
Qy 2996 CTGCCATGGGATCGCTCTCTTGTGATGGAACCACTCATCATGAGACATGAGGAAATGAG 3055
Db 2998 ATTCATGGAATGTCTTTTATGTGATGATACCTTAGTCTATGGAGAAAGAGAGATGAC 3057
Qy 3056 ATTCACAGCTGTGACCTGAGCAATTTTCCCGCCCCAACCCAGTGTCTCTCCATCCCA 3115
Db 3058 ATTCACAGCTGTGATCTGAGTGGATTCTGAGGCCCCAATCCCATCATTTGTGTCTACCT 3117
Qy 3116 CTGAGCTCTTCCGAGCTCTGTGCGAGAAAGGCCCATTTGTGCCGGAATTCAGGCT 3175
Db 3118 TTATCCACTTTTTCAGATCTTCTCTGAAGACAGTCCCATCATTTCCGGAACACAGGTA 3177
Qy 3176 TTGCAGGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACTGAGCAGCGG 3235
Db 3178 CTCACAGGAGAACTACAAATTCAGGACAGATTTGAAACTCTCTACTTGTGTTCCAGA 3237
Qy 3236 ACCCTGGCTACAAATCTGTCTGAGGATCAGCTTCACCCACCCGACCATCCCTTTCAAC 3295
Db 3238 GCTGAGGGTATAAGTCAGTTCTCAAGATCACCATGACCCAGTCTATTATTTCATTTAAT 3297
Qy 3296 CTCATGAAGTGCACCTCATGGTAGCGGTGGAGGCCGCTCTTCAGGAAGTGGTTGCT 3355
Db 3298 TTAATGAAGTTTCATCTTATGGTAGCTGTAGTAGGAAGACTCTTCCAAAGTGGTTTCT 3357
Qy 3356 GCAGCCCCAGACCTGCTCTATTATTATTTGGGACAAGACAGAGCTCTACAAACAGAG 3415
Db 3358 GCCTCACCAACTTGGCTCTACTTTTATATGGGATAAACAAGATGCATATAATCAGAAA 3417
Qy 3416 GTGTTTGGCTTTCAGAGCCCTTGTTCGCGGGTTATGAATATGAATCTCGTCCAGAT 3475
Db 3418 GTCTATGCTATCTGAAAGCTTTGTGTGCTCAGTTTGGATATGAGTATGAGTCTGTGTTGGAC 3477

Qy 3476 CTAATCTCTGTGGAAAAAAGAACCAACAGATGCTGCAGGGCTATGAAATTTGACGGGTCCAAG 3535
Db 3478 CTGACTCTGTGGAAAAAGAGGACTGCCATTTCTGCAGGGCTATGAAATTTGATGCTGCAAC 3537
Qy 3536 CTTTGGAGGATGGAGCTAGACAAACATCATGCCCTCAAAATTTCAAAGTGTGTATCTCTGCAC 3595
Db 3538 ATGGGTGGCTGGACATTTAGATAAACATCAGTCTGGATGTACAGAACCGGTATATCTGTATC 3597
Qy 3596 AAAGGAAATGGGGAGAACCAAGTTTGTCTCAGCAGCTCTCTATTATGGGAGCATCATG 3655
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Db 3658 GGCAATGGGCGGAGGCGCAGCATTTCTGCCCCAGTTGCAATGGTCAAGCTGATGTTAAC 3717
Qy 3716 AAGCTCTCTGGCCCCCAGTGGCCCTCACTGTGGCTCTGACGGGAGCTCTATATGGGTGAT 3775
Db 3718 AAGTTACTGGCCCCAGTGGCGCTAGCTTTGTGGATCGATGGCAGTCTGTACGTAGGCGAT 3777
Qy 3776 TTCAACTACATTAGAAGGATCTTCCCTCTGGAAATGTACCAACATCTCTAGAGCTCAGG 3835
Db 3778 TTCAACTACGTGCGGGGATATTCCCTTTCTGGAAATGTAAACAAGTGTCTTAGACTAAGA 3837
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Qy 3896 ATGAGTGGGGCCCTTCTTCTTCTGACAGCAACAGCGCGCGGTCTTTAAATCAAGTCC 3955
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Qy 3956 ACTGTGTGTGAGGAGACCTTTGCAAGAACTCTGAGGTGTTGCGGGAGCAGGTGACAG 4015
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Qy 4016 TGCTCTCCCTTTGATGACACTCGCTCGGGGATGGTGGGAAGGCCACAGAGGCCACACTC 4075
Db 4018 TGCTCTCCGTTTGACGAGGCGAGATGTGGGGATGGAGGAAGGCGGTGGAAGCCACACTC 4077
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Qy 4136 ATGATCAGACGATCGGATCAGAAATGGGATCATCTCCACCTCTGCTCGGCTCTTAATGATCTC 4195
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Qy 4196 ACATCAGCCCGCCACTCAGCTGTGATTTGTGTCAATGATATTTCCAGGTTAAGACTGGAG 4255
Db 4198 ACTTCAGCCAGACCTTTTAACTTTGTGACACCAGCATGCACATCAGCCAGGTACGTCTGGAA 4257
Qy 4256 TGGCCACAGACTTTAGCCATCNAACCAATGGCAACTCCTTTATGTCTCGACAAACAAT 4315
Db 4258 TGGCCCACTGACCTAGCCATTTAACCCCTATGATAACTCCATTTATGTCTCTGGATAATAT 4317
Qy 4316 GTGTCTCTGAAAATCTCTGAAAACACACAGGTGCGCATTTGTGCGGGAGGCCATGAC 4375
Db 4318 GTAGTTTACAGATCATGAAATCGTCAAGTTGCGCATTTGCTGTGGACGCCCATGAC 4377
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Db 4378 TGTCAAGTTCCCGAGTGG---AATATCTCTGCGGGAAGCAACCGGTGCGACAAACACTG 4434
Qy 4436 GAGTCAGCCACCGCTTTGGCTGTTCACAAATGCGGTCTGTATATTGCTTGAGACTGAT 4495
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4556 GGGGGCCCCAGTGGCTGTGACTGTAAAAATGATGTCACAACTGTGATGTTTTTCTGGAGAC 4615
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4555 GGAATACCTTTCAGAGTGTGACTGCAAAATGATGCAACTGTGTACAGAGTGA 4614
|||
4616 GATGTTATGCCAAGATGCCAAAGTTAAATACCCCATCTTCTTGGCTGTGTGTGAT 4675
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4615 GATGGCTACGCCAAGATGCCAAACTCAGTGGCCCCATCTCCCTGGCTGTCTCCAGAT 4674
|||
4676 GGGGAGCTCTACGTGGCCGACCTCTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAG 4735
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4675 GGTACACTGTATATTGTGAGATCTTAGGGAATATCCGGATCCGGGCTGTGTCAAGAAATAG 4734
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4736 CTTTCTCTCAACACCCAGAACATGTATGAGCTGTCTTTCACCAATTTGACAGGAGCTTAT 4795
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4735 CTTTACTTAACTCTATGAACTTCTATGAAGTTGGCTCTCCAACATGATCAAGAACTTAC 4794
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4915 ACCCTTAGAATTTAGACGGGACCCNAATCGATGCCAGTTTCGAGTGGTCTCTGTATAC 4974
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4976 CAGGTGTACTGGGTGACCATGGGACCAACAGTGCATCAAGAGTGTGACCAACAAGGA 5035
|||
4975 CAAGTGATATGTTGACAAATAGGAACAAATGGATGTTTGAAGGCGATGCTGCTCAAGGA 5034
|||
5036 CACGAGTTGGCATGATGATACCATGCAATTCGGGCTTCTGGCAACCAAAAGCAAT 5095
|||
5035 CTGGAATTAAGTTTGTACTTACCATGGCAATAGTGGCCTTTTAGCCATAAAAGTGAT 5094
|||
5096 GAAACGGATGGACAACATTTTATGATAGTACGACAGCTTTGGCGCCTGACAAATGTGACC 5155
|||
5095 GAAACTGGATGACAACTGTTTGTGACTATGACAGTGAAGTGTCTGACNAATGTTAGC 5154
|||
5156 TTCCCTTACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGTGTGATGCCAG 5215
|||
5155 TTTCCAACTGGAGTGGTGCACAAACCTGCATGGGACATGGACAAGGCTATCACAGTGGAC 5214
|||
5216 GTAGAGACCTCAGC---NAGGATGATGTCACATPAACCAACCAACTGTCTCGCTCAGGC 5272
|||
5215 ATTGAGTCACTAGCCGGAAGAAGATGTGAGCATCACTTCAAAATCTGTCTCGATCGAT 5274
|||
5273 GCCTTCTACACACTGCTGCAAGACCAAGTCCGGACAGCTACTACATCGGGGCCGATGGC 5332
|||
5275 TCTTTCTACACCATGTTCAAGATCAGTTAAGAAACAGCTACAGATTGGTTATGACGGC 5334
|||
5333 TCCTTGGCGTGTGCTGGCCAAACCGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTG 5392
|||
5335 TCCTCAGAAATTACTACGCCAGTGGCCTGGACTCACACTCAAAACAGAGCCGACGTT 5394
|||
5393 CTGGCTGGCACCGTCAACCCCAACCGTGGGCAAGAGAAATGTACCGTGGCCATCGACAC 5452
|||
5395 CTGGCTGGCACCGCTAATCCGACGGTGGCCAAAGAAACATGACTTTTGGCTGGCGGAGAAC 5454
|||
5453 GGCTTCAACTGTGTGAGTGGGCCACGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTC 5512
|||
5455 GGTCAAAACTTGGTGGAAATGGAGATTCCGAAAGAGCAAGCCCAAGGAAAGTCAATGTC 5514
|||
5513 TTTGGCGCGCGTGGGGTGCACAAACCGAAATCTCTTATCTCTGGACTTTGATCCGCTA 5572
|||
5515 TTTGGCGCGAAGCTCAGGGTTAATGGCAGAAATCTCTTTTCAGTTGACTTTGATCGAAC 5574
|||
5573 ACACGACACAGAGAAATCTATGATGACACCGCAAGTTCACCCCTCGGATTTCTGTAGAC 5632
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5575 ACAAGACAGAAATCTATGACGACCCACCGTAAATTTTCTACTGAGGATCGCCTACGAC 5634
|||
5633 CAGGGGGGGCCCCAGCCTCTGGTCAACCCAGCAGCGCTGAATGGTGTCAACGTGACA 5692

5635 ACCTGTGGGCAACCCGACTCTCTGGCTGCCAAGCAGCAAGCTGATGGCCGTCAATGTCAACC 5694
|||
5693 TACTCCCTCGGGGTTACATTTGCTGCGCATCCAGAGGGGCATCATGCTCTGAAAAGAAATGGA 5752
|||
5695 TATTATCCACAGGTCAAAATTCGCCAGCATCCAGAGGACCACTAGCGGAAAGTAGAT 5754
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5753 TACGACCAAGGGCGGCATCACATCCAGGATCTTTCGCTGATGGGAAGACATGGAGCTAC 5812
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5755 TATGACGACAGGGGAGGATCGTGTCTCGGGTCTTTGCTGATGGTAAACATGGAGTTAC 5814
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5813 ACATCTTAGAAGTCCATGTGTGCTACTACACAGCCAGAGGAGTATATCTTTGAG 5872
|||
5815 ACATATTTAGAAAAGTCCATGGTCTTCTGCTTCTAGCCAGCGCAGTACATCTTCGAA 5874
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5873 TTCGACAAAGATGACCGCTCTCTTCTGTGACGATGCCCAAGCTGGCGGCGAGACACTA 5932
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5875 TACGATATGTGGGACCGCTGTCTGCCATCACCATGCCAGTGTGGCTGCCACACCATG 5934
|||
5933 GAGACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCC 5992
|||
5935 CAGACCATCCGATCCATTTGGCTACTACCGCAACATATACAACCCCGGAAAGCAACGCC 5994
|||
5993 TCAGTCATACAGGACTTCACTGAGGATGGGCACCTCTTCAACCTTCTACCTGGGCATC 6052
|||
5995 TCCATCATCACGAGCTACAAACGAGGAAGGGCTGCTTCTACAAACAGCTTCTTGGGTACA 6054
|||
6053 GGCCCGGGGTGATATACAGTATGGCAAACTGTCAAAGCTGGCAGAGCGCTCTATGAC 6112
|||
6055 AGTCGAGGGTCTTATTCANATACAGAAAGGCGAGATAGGCTCTCAGAAATTTTATATGAT 6114
|||
6113 ACCACCAAGGTCACTTTCACTATGACAGAGCGGAGCATGCTGAAAGACCATCAACCTTA 6172
|||
6115 ACCACAAGTCACTTTTACCTATGATGAACAGCAGGAGTCTTAAAGACAGTAAACCTC 6174
|||
6173 CAGAAATAGGGGCTTCACTGTCAACCATCCGCTACCGTACAGTTGGGCGCCCTGATGACCGA 6232
|||
6175 CAGAGTGTGTTTATTTTGGACCATTAGATACAGCAAAATTTGGTCCCTGATTTGACAGG 6234
|||
6233 CAGATCTTCCGCTTCACTGAGGAAGGCATGGTCAACGCCGCTTTTGCATCTACACTATGAC 6292
|||
6235 CAGATTTTCCGCTTTAGTGAAGTGGGATGGTAAATGCAAGATTTTGACTATAGCTATGAC 6294
|||
6293 AACAGCTTCCGGGTGACACAGCATGACAGGCTGTGATCAACGAGACCCCACTGCCCATTTGAT 6352
|||
6295 AACAGCTTTGAGTGAACAGCATGACAGGTTGATCAATGAAGAACGCCACTGCTCTATGAT 6354
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6353 CTCTATCGCTATGATGTGTGAGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAAT 6412
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6355 CTGTATCAGTTTGTATGACATTTCTGGCAAAAGTTGAGCAGTTTGGAAAGTTTGGAGTTATA 6414
|||
6413 TACTATGACATTAACAGATCATACCAGCTGTCTATGACCGCCAGCCACACAGCACTTTTGTAT 6472
|||
6415 TATTATGATATTAACCCAGATCACTTTTACAGCTGTAATGACCTATACGAAGCACTTTGAT 6474
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6473 GCATATGGCAGATGAAGGAAGTGCAGATATGAGATCTTCCGCTCGCTCATGTACTGGATG 6532
|||
6475 GCTCATGGCGTATCAGGAGATTCAATATGAGATATTTCAGGTCTGCTCATGTACTGGATT 6534
|||
6533 ACCGCTCAGTATGATAACATGGGGCGAGTGTGAAGAAAGAGCTGAAGTATGAGACCCCTAC 6592
|||
6535 ACAATTCAGTATGATAACATGGGTCCGGTTAACCAAGAGAGAGATTAAATAGAGGCCCTTT 6594
|||
6593 GCCAATACACTCCGCTACTCTCTATGAGTATGATGTGACGGCCAGCTGCGAGCAGTCTCC 6652
|||
6595 GCCAACACCCACCAATATGCTTATGAATATGATGTGATGSGACAGCTCCAAACAGTTTAC 6654
|||
6653 ATCAATGACAAAGCTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACTTACTG 6712
|||
6655 CTCAATGAAAGATTAATGTGGCGGTACAACACTAGATCTGAATGGAAACCTCCATTTACTG 6714
|||
6713 AGCCCTTGGGAAACAGTGCACGGCTCACCACTTACGGTATGACATCCGCGACCGCATCACT 6772
|||

| | | | |
|------|----|--|------|
| 6715 | Db | AACCCAAAGTAACAGTGGCGCTGTGAACACCCCTTCGCTATGACCTGCGAGACAGAATCACT | 6777 |
| 6773 | Qy | CGGCTGGGTGACGTGCAATACAAGATGGATGAGGATGGCTTCTCTGAGGACAGCGGGCGGT | 6832 |
| 6775 | Db | CGACTGGGTGATGTTCAATATCGTTGGATGAAGATGGTTTCTCTACGTCAAAGGGGGCAGC | 6834 |
| 6833 | Qy | GATATCTTTTGAGTACAACATCAGCTGGCTGCTCATCAAGCGCTTACAACCGGGCTGGCAGC | 6892 |
| 6835 | Db | GAATCTTTTGAATATAGCTCCAAGGGGCTTCTAACTCGAGTTTACAGTAAGAAGCGATGGC | 6894 |
| 6893 | Qy | TGGAGTGTCAAGTACCGCTACGATGGCTGGGGCGGCGGTGTCCAGCAAGACGACGCCAC | 6952 |
| 6895 | Db | TGGACAGTGATCTACCGTTATGACGGCTGGGAAGGGGTGTTTCTAGCAAAAACGAGTCTA | 6954 |
| 6953 | Qy | AGCACCACTCTGCAGTTCTTCTATGACAGACTGACCAACCCCAACCAAGGTCAACCCACCTG | 7012 |
| 6955 | Db | GGACAGCACCTCGCAGTTTTTTTATGTCTGACTTAACATTTATCCCACTAGGATTTACTCATGTC | 7014 |
| 7013 | Qy | TACAACCACTCCAGCTCTGAGATCACCTCCCTCTACTACGATTCAGCATTTGCAAGGACACTCTTT | 7072 |
| 7015 | Db | TACAACCTTTGAGTTCCAGAAATTACCTCCCTGTATTATGATCTCCCAAGACATCTTTTT | 7074 |
| 7073 | Qy | GCCATGGAGCTGAGCAGTGGTGATGAGTTTATACATAGCTTTGTGACAAACATCGGGACCCCT | 7132 |
| 7075 | Db | GCCATGAAATCAGCAGTGGGATGAATCTTATATTGCATCGGATATACACAGGGACACCA | 7134 |
| 7133 | Qy | CTTGCTGTCTTTAGTGGAAACAGTTTTCATGATCAAGCAAAATCTGTATACACAGCTATGGG | 7192 |
| 7135 | Db | CTGGCTGTGTTCAGTAGCAATGGGCTTATGCTGAACAGAGTTCAGTACACTGCATATGGG | 7194 |
| 7193 | Qy | GAGATCTACATGGATACCAACCCCAACTTTTCAGATCATATAGCTACCATGGTGGGCTC | 7252 |
| 7195 | Db | GAATCTATTTTGACTCTAATATTGACTTTTCACTGGTAAATTGGATTTCAATGGTGGCTG | 7254 |
| 7253 | Qy | TATGATCCACTCACCAAGCTTTGCCATATGGGCCGGCGAGATTATGATGTCTGGCCGGA | 7312 |
| 7255 | Db | TATGACCCACTCACCAAATTAATCCACTTTGGGAAGAAGAGATTATGACATTTTGGCAGGA | 7314 |
| 7313 | Qy | CGCTGGACTAGCCACAGACCGAGCTGTGGAAGCACCTTGTAGTAGCAACAACGTCATGCCCT | 7372 |
| 7315 | Db | CGGTGGACACAACCTGACATAGAAATCTGGA--AAAGAATTGGGAAGGACCCAGCTCCT | 7371 |
| 7373 | Qy | TTTAACTCTATATGTTTCAAAAAACAACCCCATCAGCAACTCCCAGGACATCAAGTGC | 7432 |
| 7372 | Db | TTTAACTGTACATGTTTAGGAATTAACAACCCCTGCAAGCAAAAATCCATGACGTGAAGAAT | 7431 |
| 7433 | Qy | TTCAATGACAGATGTTAACAGCTGGCTGCTCACCTTTTCGATTTCCAGCTTACACAAGCTGATC | 7492 |
| 7432 | Db | TACATCAAGATGTTAACAGCTGGCTGGTGACATTTTGTTTTCATCTGCAACATGCTATT | 7491 |
| 7493 | Qy | CCTGGTTATCCCAAAACAGACATGGATGCCATGGAACCCCTCTACGAGCTCATCCACACA | 7552 |
| 7492 | Db | CCTGGATTCCCTGTTCCCAAAATTTGATTAAACAGAACCTTCTTTACGA-----A | 7539 |
| 7553 | Qy | CAGATGAACCGAGGAGTGGGACACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTA | 7612 |
| 7540 | Db | CTTGTGAAGAGTCAAGCTGGGATGATATACCGGCCATCTTCGGAGTCCAGCAGCAAGTG | 7599 |
| 7613 | Qy | CAGAAGCAGCTCAAGGGCTTTGTCAACCTTTAGAACGGTTTGACCAAGCTCTATGGCTCCACA | 7672 |
| 7600 | Db | CGCGGCGAGGCCAAGGCTTCTCTGCTGCTGGGGAAGATGGCCGAGGTGCAGGTGAGCGGG | 7659 |
| 7673 | Qy | ATCACCAAGTCCACAGCGGTCCAAAGACCAAGAAGTTTGTGATCCAGGGGCTCAGTCTTTT | 7732 |
| 7660 | Db | CGCCGGGGCGGC--GGCGCGCAGTCTCTGGCTGTGGTTTGGCCACCGGTCAAGTCCGCTGATC | 7716 |
| 7733 | Qy | GGCAAGGGGTCAAGTTTGGCTTCAAGGATGGCCGAGTGACCAACAGACATCATCAGTGTG | 7792 |
| 7717 | Db | GGCAAGGGCGTTCATGCTGTGGCCGTGAGCCAGGGCCGGGTGCAGACCAAGCTGCTCAACATC | 7776 |
| 7793 | Qy | GCCAAATGAGGATGGGCGAAGGGTTTGCTGCCATCTTTGAACCATGCCCACTACTAGAGAAC | 7852 |
| 7777 | Db | GCCAAACAGGATCATCAAGTGGCGCGGTGCTCAACAAACGCTTCTACTCTGGAGAAC | 7836 |

| | | | |
|-----------|---|---|------|
| Qy | 7853 | CTGCATCTTACCAATATGATGGGGTGGATACCCATTACTTGTGTGAACACGAGCACTTCAGAA | 7916 |
| Db | 7837 | CTGCATCTTACCAATATGATGGGGTGGATACCCATTACTTGTGTGAACACGAGCACTTCAGAA | 7896 |
| Qy | 7913 | GGTACTCGTCCCATCTCTGGGCGCTCAGTGGGGGGCGGMAACCCCTGGAGAAATGGGGTCAAC | 7972 |
| Db | 7897 | AGCGACTCTGGGACGCTGCGGTTGACAGCGGCGGCAGGCGCTGGAGAACGGCATCAAC | 7956 |
| Qy | 7973 | GTCACTGTGTCCAGATCAACACAGTACTTAAATGGCAGGACTAGACGCTACACAGACATC | 8032 |
| Db | 7957 | GTGACGGTGTGCGAGTCCACACCGGTGGTGAACGGCAGGACGCGCAGGTTTCGGCGACGTG | 8016 |
| Qy | 8033 | CAGCTCCAGTACGGGGCAGCTGTCTTGAACACACAGCTACGGGACAAAGTTTGGATGAGGAG | 8092 |
| Db | 8017 | GAGATGCAGTTCGGCGCGCTTGGCGCTGCAGTGCCTACGGCATGACCTTGGACGAGGAG | 8076 |
| Qy | 8093 | AAGGCACGGGTCTCTGGAGCTGGCCCGGCAGAGACCGTTCGCCAAGCGTGGGCGCCGCGAG | 8152 |
| Db | 8077 | AAGCGCGCATCTTGAGCAGGCGCGGCAGCGCGCTCGCCCGGGCTTGGCGCGCGAG | 8136 |
| Qy | 8153 | CAGCAGAGACTGCGGGAGGGGAGGAAGCGCTCGGGCTTGGACAGAGGGGGAGAACGAG | 8212 |
| Db | 8137 | CAGCAGCGCTGCGGCACGCGCAGAGGAGGGCGCGCGCTCTTGGACGAGGGCGGAGACGG | 8196 |
| Qy | 8213 | CAGGTCTGACACACAGGCGGGTGCAGGCTACAGCGGCTTTTTCGTGATCTCTGTCTCGAG | 8272 |
| Db | 8197 | CAGCTGTGAGCGCCGCGCAAGGTGCAGGGCTACAGCGGTACTACGTACTCTCGTGGAG | 8256 |
| Qy | 8273 | CAGTACCCAGAACTGTTCAGACAGCGGCCAACCAACATCCACTTTCATGACAGAGCGAGATG | 8332 |
| Db | 8257 | CAGTACCCCGAGCTGGCCGACAGGCGCCAACCAATCCAGTTCTCTGGCGAGAGCGAGATC | 8316 |
| Qy | 8333 | GGCGGAGGTGAC | 8345 |
| Db | 8317 | GGCAGGAGGTAAC | 8329 |
| RESULT 15 | | | |
| ADH41998 | | | |
| ID | ADH41998 standard; DNA; 8636 BP. | | |
| XX | | | |
| AC | ADH41998; | | |
| XX | | | |
| DT | 25-MAR-2004 (first entry) | | |
| XX | | | |
| XX | Novel human nucleic acid NOV40h #2. | | |
| XX | | | |
| KW | ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; | | |
| KW | anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; | | |
| KW | nootropic; antiparkinsonian; antiaerthmatic; antiinfertility; | | |
| KW | cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; | | |
| KW | AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease; | | |
| KW | Parkinson's disease; asthma; fertility disorder; chromosome mapping; | | |
| KW | tissue typing; preventive medicine; pharmacogenomic; vaccine. | | |
| OS | Homo sapiens. | | |
| XX | | | |
| FN | WO2003102159-A2. | | |
| XX | | | |
| PD | 11-DEC-2003. | | |
| XX | | | |
| PF | 04-JUN-2003; 2003WO-US017573. | | |
| XX | | | |
| PR | 04-JUN-2002; 2002US-0385490P. | | |
| PR | 04-JUN-2002; 2002US-0385615P. | | |
| PR | 04-JUN-2002; 2002US-0385755P. | | |
| PR | 05-JUN-2002; 2002US-0386041P. | | |
| PR | 06-JUN-2002; 2002US-0386355P. | | |
| PR | 06-JUN-2002; 2002US-0386357P. | | |
| PR | 06-JUN-2002; 2002US-0386447P. | | |
| PR | 06-JUN-2002; 2002US-0386459P. | | |
| PR | 06-JUN-2002; 2002US-0386465P. | | |

PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0386701P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0387078P.
PR 07-JUN-2002; 2002US-0387081P.
PR 07-JUN-2002; 2002US-0387083P.
PR 10-JUN-2002; 2002US-0387429P.
PR 10-JUN-2002; 2002US-0387540P.
PR 10-JUN-2002; 2002US-0387866P.
PR 11-JUN-2002; 2002US-0387606P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387659P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 12-JUN-2002; 2002US-0388432P.
PR 12-JUN-2002; 2002US-0388479P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389604P.
PR 18-JUN-2002; 2002US-0389126P.
PR 09-AUG-2002; 2002US-0401628P.
PR 12-AUG-2002; 2002US-0402268P.
PR 13-AUG-2002; 2002US-0402822P.
PR 13-AUG-2002; 2002US-0403458P.
PR 15-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403732P.
PR 26-AUG-2002; 2002US-0406182P.
PR 12-SEP-2002; 2002US-0410085P.
PR 13-SEP-2002; 2002US-0410505P.
PR 23-SEP-2002; 2002US-0412955P.
PR 30-SEP-2002; 2002US-0415195P.
PR 23-OCT-2002; 2002US-0420627P.
PR 23-OCT-2002; 2002US-0420718P.
PR 24-OCT-2002; 2002US-0420852P.
PR 31-OCT-2002; 2002US-0422750P.
PR 01-NOV-2002; 2002US-0423095P.
PR 05-NOV-2002; 2002US-0423748P.
XX
PA (CURA-) CURAGEN CORP.
XX Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
PI Ellerman K, Ertterberg S, Gangolli EA, Gerlach VL, Gorman L;
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;
PI Khramtsov NV, Larocheille WJ, Li L, Liang H, Low K, Macdougall JR;
PI MacLachlan T, Maliyankar UM, McQueeney K, Mezick AJ, Miller CE;
PI Millet I, Padigar M, Patturajan M, Peyman JA, Qian X, Rastelli L;
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CM, Voss EZ;
PI Wolenc AR, Zhong M, Zhong H;
XX
XX WPI; 2004-053467/05.
DR P-PSDB; ADH41999.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.
XX
XX Claim 20; SEQ ID NO 551; 1503pp; English.

CC The invention relates to 566 new isolated human polypeptides and their
CC encoding genes, sequences that are at least 95% identical to these or
CC sequences comprising one or more conservative substitutions in these. The
CC polypeptide, polynucleotide and antibodies against the polypeptides are
CC useful in diagnosing, treating or preventing NOVX-associated disorders,
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
CC The nucleic acids are further used as hybridization probes, in chromosome
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
CC polypeptides are also useful as vaccines. This sequence represents an
CC example of the nucleic acid sequence of the invention.

XX
SQ Sequence 8636 BP; 2338 A; 2064 C; 2200 G; 2034 T; 0 U; 0 Other;

Query Match 41.6%; Score 3472.2; DB 12; Length 8636;

Best Local Similarity 65.2%; Pred. No. 0; Mismatches 2693; Indels 216; Gaps 14;
Matches 5444; Conservative 0;

QY 35 ATGACGCTGAAGGAGGAGGAGCCTTACCGCTCGCTGACCCCGCGC---CGCAGCCCGAG 91
DB 151 ATGGATGTGAAGAACGCGAGGCTTTACTGCTCCCTGACCAAGAGCAGAGAGAGGAA 210
QY 92 CGCCGCTACACAGCTCGTCCGCGACAGCGAGGAGGCAAG---CCCCGAGAAATCG 148
DB 211 CGCGCTACACAAATTCCTCCGACAAATGAGGAGTCCGGGTACCCACACAGAGTCC 270
QY 149 TACAGCTCCAGGAGACCTGAAGCCTACGACAGG---CGCCGCTAGCCTATGCG 205
DB 271 TACAGTTCCAGGAGACATTTGAAAGCTTTTGTATGATGATTCCTCGCGGTGCTTTACGGC 330
QY 206 AGCCGCTCAAGGACATTTGTCCGCGAGGAGGCGGAGGAAATTCGCGCAGAGTGCCAAAC 265
DB 331 AACAGTGAAGATTTGTTTACAGAGAGAGCAGAGGTTTCACTAGACAAGACAGAAAT 390
QY 266 TTCACCTTCGGGAGCTGGGCTGGAAGAAATGAAAGGTAAGCCCGCTTACCGGACCTGTACCGG 325
DB 391 TTTACCTTAAGGAGTAGGAGTTTGTGAACCCAGCAATCGAAGAGGAGTGGCATTTTGT 450
QY 326 ACAGACATTTGGCTGCTCCCAATGCGGTACTTCAATGGGGGTGGCTCTGATCCGACATG 385
DB 451 GCGGAAATGGGGTCTCCCTCACAGAGGTTACTTATCAGTGCAGGGTTCAGATGCTGATCT 510
QY 386 GAGGCTGACACGGTGTGTCCTCAGACACCCCGTCTGTGGGGCGGAGCACACACG 445
DB 511 GAAATGAAGAGTATGTTCCACAGAGCATGCGATGAGACTTTGGGCGAGGGGGTCAAA 570
QY 446 TCAGGGCGAGCTCCTGCTGTCCAGCGGGGCAATTCOAATCTCACACTCACCGACACC 505
DB 571 TCAGGGCGAGCTCCTGCTGTCAAGTCGTCCTCAACTCAGCCCTCACCTGCAGATACG 630
QY 506 GAGCATGAAACACTGAGACTGATCATCCGGGGGCGCTGCAGAACCCAGCGGGCTCCCG 565
DB 631 GAGCAGAAACAAAGTCCGACAGTGAATGAGCAACTGCAAGCAATCAAGCCAGTCT 690
QY 566 AGCGCGCGCGCGCTCTCGCACGCCACACCCCAACCCAGCAGCAGCAGCGGCTCCATT 625
DB 691 ACCCTGAGCCCTTGGCGCTTCCCAATAGCAGACTCTGCGACAGCATCATCATCATC 750
QY 626 AACTCCCTGAACCGGGCAATTTCAAGCGGAGAGCAACCCAGCGGCGGCGCCCGACGAC 685
DB 751 ACTTCTCTCAACAGAAATCTCCCTGACCAATAGAGGACAGAGTCCGCGCGCGCGGT 810
QY 686 CACTGCTCTCCGAGAGCCCCCTGCGGGGGCGGCGGAGGCTTCCCGCCAGGAG 745
DB 811 GCTTTTCCCGCGAGTGCAGAAC-----CACACCGGTCGCTCCAGTGCAGGAC 861
QY 746 AACTGCTGCTCAACAGCAACATCCCTCGGAGAGCCAGGAACCTAGGCAAGCAGCATTC 805
DB 862 AGCTGGTCTTGGCAGTAAATGTACACTGGAAGAGGAGCATTT----- 905
QY 806 CTAGGAGCATTTGCGAGCAACCTCATTTGAGATGGACATTTCTCGCGCGCTCCCGCCATGAT 865

Db 906 ----- 905
Qy 866 GGGGCTTACAGTACGGGCACTTCTCTTCAAGCCTGGAGGCACTTCCCGCTCTTCTGC 925
Db 906 -----CCTATTCAAAACAGGAACAGGTACAAACGCCACTGTTCAGT 945
Qy 926 ACACATACACAGGTTACCACTGACGTCCAGCACAGTGTACTCTCTCCGCCGCCGACCC 985
Db 946 ACTGCAACCCAGGATACACAATGGCATCTGGCTCTGTTTATTCAACCACCTACTCGGCCA 1005
Qy 986 CTGCCCGCAGCAGCTTTCGCCGCCGCCCTTTAAACCTCAAGAACGCCCTCCAAAGTACTGT 1045
Db 1006 CTACCTAGAACAACCTTCAAGNAGTGTCTTTAAATTCAGAGTCTTTCAAAGTACTGT 1065
Qy 1046 AACTGGAAGTGGCAGCCCTGAGGCCCATCGTCAATCTCAGCCACTCTGGTCTATCTGCTG 1105
Db 1066 AGCTGGAAATGCACTGCACTGTGTGGCGTAGGGGTCTCGGTGTCTCTGGCAATACTCCTG 1125
Qy 1106 GCATACTTTGGCCATGCCACCTGTTGGCTTAACTGGCACCCTGCAGCCGATGGAGGGG 1165
Db 1126 TCTTTATTTATAGCAATGTCATCTCTTTGGCTCAACTGGCAGCTTACAGCAGACTGAANAAT 1185
Qy 1166 CAGATGTATGAGATCACGGAGGACACAGCCAGCAGTTGGCTGTGCGCAACCGACGTCTCC 1225
Db 1186 GACACATTTGAGA-----ATGGAAAGTGAATTTCTGATACCACTGCAACAAACACTGTG 1239
Qy 1226 CTATACCCCTCAGGGGCACTGGCTTAGAGACCCTGACAGGAAGGCAAGGNAACCACA 1285
Db 1240 TCATTACCTCTGGAGACA----- 1258
Qy 1286 GAAGGAAGCCAGTAGTTCTTCTCCAGAGGACAGTTTTCATAGATTCTGGAGAAATTGAT 1345
Db 1259 -ATGGAAATTAGGTGGATTTACCGAAGAAATTAACACCATAGATTCGGAGAACTTGAT 1317
Qy 1346 GTGGGAAGGCGAGCTCCAGAGATTCTCTCGCACTTTCTGGAGATCTCAAGTGTTC 1405
Db 1318 ATGGCCGAAGAGCAATTCAGAGATTCTCCCGGATCTTCTGGAGATCACAGCTCTTC 1377
Qy 1406 ATAGACCATCTGTGCATCTGAATTCATGTGTCTCTGGAAAGGAGCCCTGGTTGGC 1465
Db 1378 ATTGATCAGCCACAGTTTCTTAAATTCATATCTCTTCAAGAGGATGCAATTGATTGGA 1437
Qy 1466 ATTTATGCGAANAAGGCTCCCTCTCTCACATA-----CACAGTTTGACTTT 1513
Db 1438 GTATATGCCCGAAGAGTTACCGCTTCCCATACTCAGTCTCCGCCAGTATGACTTC 1497
Qy 1514 GTGGAGCTGTGGATGGCAGAGGCTCTTAACCCAGAGGCGCGAGGCTTAGAGGGGACC 1573
Db 1498 GTGGAGCTCTGGATGGCAGCAGGCTGATTGCCAGAGAGCAGCGAGGCTGCTTGAGACG 1557
Qy 1574 CGCGCCAGTCTCGGGGAACTGTGCCCCCTCCAGCCATGAGCAGGCTTCCATCCAGTAT 1633
Db 1558 GAGAGAGCGGGCGCAGCGAGATTCCTGACGCTTCATGAGGCGGCTTTATCCAGTAC 1617
Qy 1634 TTGGATTCAAGGAATCTGCGACTTGGCTTTTACAAATGACGGAAGGAGTCAGAAAGTGGTT 1693
Db 1618 TTGGATTCTGGAACTGCGAATCTGCTTTTATATGATGGGAAAATGCGAGCAGGTG 1677
Qy 1694 TCTTTTCTCACCACTGCCATTTAGTGTGGTGAATACTGCCCCAGCAACTGTCTATGGCAAT 1753
Db 1678 TCTTTTAATACCATTTATAGATCTGTGTGGAAATGTCCCGGAAATGGCATGGAAAT 1737
Qy 1754 GGTGACTGATCTCTGGGACCTGCCACTGCTCTCTGGGTTTCTTGGGCCCGACTGTGGC 1813
Db 1738 GGAGAAATCGTTTCTGGAACTTGGCAATGTTTTCAGGATTTCTGGGTCCGGATTGTCA 1797
Qy 1814 AGAGCCTCTCTGCCCGTCTCTGTAGCGGAATGSCCAATACATGAAGAGGAGATGCTTG 1873
Db 1798 AGAGCGGCTGTCCAGTGTATGTAGTGGCAACGGGCGAGTACTCCAAGGGCGCTGCCTG 1857
Qy 1874 TGCCACAGTGTGGAAGGCGCTGAGTGCAGTGTGCCCAACCAACAGTGTATCGATGTG 1933
Db 1858 TGTTTTCAGCGGCTGGAAGGGCACCGAGTGTGTATGTGCGGACTTACCCAGTGTATTGCCA 1917

Qy 1934 GCCTGCAGCAACCATGGCACCTGTCATCACGGGCACCTGTCATCTGCAACCTCGCTACAAG 1993
Db 1918 CAGTGTGGGGTCTGGGATTTGTATCATGGGCTCTGTGCTTGCACTCAGGATACAA 1977
Qy 1994 GCGAGAGCTGTGAGGAAGTGTGACTGTGATGGAACCCACATGTTTCAGGCCGGGGTGTCTGC 2053
Db 1978 GGAGAAAGTTGTGAAGAGCTGACTGTATAGACCCCTGGGTGTTCTTAATCATGGTGTGTG 2037
Qy 2054 GTGAGAGGCGAATGCCATTGCTTTGTGGATGGGAGGCACCAACTGCAGACCCCCCAGG 2113
Db 2038 ATCCACGGGGAATGTCACTGCACTCCAGATGGGAGGTAGCAATTTGTGAATACTGAAG 2097
Qy 2114 GCCACATGTTAGAACAGTGTTCAGGCCACGGAACTTCTCCCGGACACCCGGCTTTGC 2173
Db 2098 ACCATGTGTCAGACCAAGTGTCTCCGCCACAGAACTATCTTCAAGAAAGTGGCTCTCTGC 2157
Qy 2174 AGCTGTGACCCCAAGCTGTGGAACGACTGTCTATCGAGATCTGTGCTGCGCACTGT 2233
Db 2158 ACCTGTGACCTTAACCTGGACTGGCCAGACTGTCTAAACGAAATATGTTTCTGTGGACTGT 2217
Qy 2234 GGTGGCCATGGCGTGTGCGTGTGAGGGGCACCTGCGCTGCGAGGATGGCTGGATGGGGCA 2293
Db 2218 GGCTCACCGGGCTTTGCAATGGGGGACGTGTCTGTGGAAGAGCTGGACGGGCCCA 2277
Qy 2294 GCCTGCGAACAGCGGGCTGCCACCCGCTGTGCCGAGATGGGACCTTGCCTCGCAGCGC 2353
Db 2278 GCCTGTAAATCAGAGAGCTGCCACCCCTGTGTGCCGAGCACGGGACCTGCAAGGATGGC 2337
Qy 2354 AGTGCAGTGCAGCCCTGGCTGGAAATGGGAACACTGCACCACTGCTCACTACTCTGGAT 2413
Db 2338 AAGTGTGAATGCAAGCCAGGGCTGGAAATGGAGAGCACTGCACTATCGCTCACTATTTGGAT 2397
Qy 2414 AGGGTAGT-----TAAAGAGGGTTGCCCTGGGTGTGCAATGGCAAC 2455
Db 2398 AAGATAGTTAAAGACAAGTAGATATTAAGAGGGTTGTCTGCTGTGCAACAGCAAT 2457
Qy 2456 GGAGATGTACTTGTAGACCTGGAATGTGTGGCACTGGCTGTGCCAGTGTGGCTGGAGGA 2515
Db 2458 GGAAGATGTACTCTGGACCAAAATGGCGGACATTTGTGTGCCAGCCCTGGATGGAGGA 2517
Qy 2516 GCTGGCTGTGACACTTTCATGGAGACTGCTGCGGTGACAGCAAGAAAGCAATGATGGAGAT 2575
Db 2518 GCAGGCTGTGACGTAGCCATGGAGACTTTTTCACAGATAGCAAGCAATGAAGGGAT 2577
Qy 2576 GGCTGTGTGACTGTGACCTGACCTGCTGCTCCAGCCCTGTGCCCATATCAACCCG 2635
Db 2578 GGAATCATTTGACTGTGATGGATCCGATTTGCTGCTACAGAGTTCTCTGCCAGAAATCAGCCC 2637
Qy 2636 CTGTGCTTGGCTCCCTTAAACCTCTGGACATCATCCAGGAGACACAGTCCCTGTGTCA 2695
Db 2638 TATTGTGGGGACTGCGCGATCCTCAGGACATCATTAGCCAAAGCCTTCAATCGCCTTCT 2697
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Db 2698 CAGCAAGCTCCAAATCCCTTTTATGATCGAATCAGTTTCTTATAGATCTGATAGCACC 2757
Qy 2756 CACATAATCCCGGGAGAAACCCCTTTGATGGGGGATGCTGTGTATTTCGTGGGCAA 2815
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QY 2996 CTGCCATGGGATCGCTTTCTTTGTGTCATGGAAACCATCATCATGAGACATGAGAGGAGATGAG 3055
DB 2998 ATTCCATGGAAATGCTTTTATGTGATGGATACCTTAGTTCATGGAGAAAGAGAGATGAC 3057
QY 3056 ATTCCAGCTGTGACCTGAGCAAAATTTTGGCGGCCCCAAACCCAGTGTCTCTCCATCCCCA 3115
DB 3058 ATTCCAGCTGTGATCTGAGTGGATTCGTGAGGCCAAATCCCATCATTTGTGTATCATCACCT 3117
QY 3116 CTGACGCTCTCGCAGCTCTCTGTGAGAGAAAGGCCCATTTGTGCGGGAATTCAGGCT 3175
DB 3118 TTATCCACCTTTTTCAGATCTTCTCTGAGAGACAGTCCCATCATTTCCCGAAGACAGGTA 3177
QY 3176 TTGACGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGG 3235
DB 3178 CTCCACGAGAACTACAAATCCAGGAACAGATTTGAAACTCTCTACTTTGAGTTCCAGA 3237
QY 3236 ACCCTTGGGTACAAATCTGTCTGAGGATCAGGCTCACCCACCCGACCATCTCCCTTCAAC 3295
DB 3238 GCTGACAGGATATAAGTCAGTTCTCAAGATCACCATGACCCAGTCTATTATTCCATTAAAT 3297
QY 3296 CTATGAAGGTGACCTCATGTGAGGTTGAGGCGGCGCTCTTTCAGGAAGTGTTCGCT 3355
DB 3298 TTAATGAAGGTTTCATCTTATGAGTGTGTAGTAGGAAGACTCTTCCAAAGTGTTCCT 3357
QY 3356 GCAGCCCGACACCTGTCTTATTTATTTCAATTTGGGACAAAGACAGACGCTCTACACCAAGAAG 3415
DB 3358 GCCTGACCAAACTTGGGCTATCTTTTCATATGGGATAAACAGATGCATATAATCAGAAA 3417
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QY 3476 CTAAATCTGTGGGAAAAGAAACAAACAGTCTGACGGCTATGAATTTGACGGTCCAG 3535
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DB 3538 ATGGTGTGGCTGGACATTTAGATAAATCATCAGTCTGATGATGATACAGAACGCTATCTGTAC 3597
QY 3596 AAAGGGAATGGGAGAAACCAATTTGTGTGTCAGACGCTCTCTGTATTTGGAGCATCATG 3655
DB 3598 AAGGGAACCGGGAAACCAATTTCTCCAGCAGCCTCCAGTCTGAGTAGCATCATG 3657
QY 3656 GGCATTTGGGCGCGGAGAACATCTCTGCGCCAGCTGCAACGCTTGTGTCAGCGCAAC 3715
DB 3658 GGCATTTGGGCGAAGGCGCAGCATTTCTGCGCCAGTTGCAATTTGGATGATGTTAAAC 3717
QY 3716 AAGCTCTGCGCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGAT 3775
DB 3718 AAGTTACTGCGCCAGTGGCGCTAGCTTTGTGGATCGATGGCAGTCTGTACGTAGGCGAT 3777
QY 3776 TTCAACTACATTTAGAAGGATCTTCCCCTCTGGAAATGTCAACCAATCTCTAGAGCTGAGG 3835
DB 3778 TTCAACTACTGTGGCGGATATTTCCCCTCTTGGAAATGTAAACAGTGTCTTAGAACTAAGA 3837
QY 3836 AATAAGATTTACAGATAGTACAGTCCAGCAGACAAATACTACCTGGGCCACAGACCCC 3895
DB 3838 AATAAGATTTTAGACATAGCAGCAACCCAGCTCATAGATACTACCTTGGCAACGGATCCA 3897
QY 3896 ATGAGTGGGCGCGTCTTCTCTCTGACAGCAACAGCGCGGCTCTTTAAATTCAGTCC 3955
DB 3898 GTACGGGAGATCTGTACGTTTCTGACAAACACCCCGAGAAATTTATCCCCCAAGTCA 3957
QY 3956 ACTGTGTGTGAAGGACCTTTGTCAAGAACTCTGAGGTGGTTGGGGGACAGGTGACCAG 4015
DB 3958 CTTACGGGGCAAAAGACTTGACTTAAATAATGCAGAACTGTCTGACGGGACAGGGAGCAA 4017
QY 4016 TGCCTCCCTTTTGTATGACATCTGCTGCGGGATGTGGGGAAGGCCACAGAACCCACTC 4075
DB 4018 TGCCTTCCGTTTTCACGAGGCGAGATGTGGGGATGGAGGGAGGCGGTGGGAAGCCACACTC 4077
QY 4076 ACCAATCCAGGGGTATTACAGTGGACAAAGTTTGGGCTGATCTACTTTCGTGGATGGCAAC 4135

DB 4078 ATGAGTCCCAAGGAATGGCAGTTTGATAGAAATGGATTAATCTACTTTTGTGATGAACC 4137
QY 4136 ATGATCAGACGCGCATCGATCAGAAATGGGATCATCTCCACCTCTCGCTCTGAATGATCTC 4195
DB 4138 ATGATTTAGAAAGTTTGACCAAAATGGATCATATCACTCTCTGGGCTCTAACGATTTG 4197
QY 4196 ACATCAGCCCGGCCACTCAGCTGTGATTTCTGTGATGGATATTTCCAGGTAAGATGGAG 4255
DB 4198 ACTTCAGCCAGACCTTTAACTTTGTGACACAGCATGACATCAGCCAGGTAGCTCTGGAA 4257
QY 4256 TGGCCACAGACTTAGCCCATCAACCAATGGACAACTCACTTTATGTCTCGACACAAAT 4315
DB 4258 TGGCCCACTGACTAGCCATTAAACCTATGGATAACTCCATTTATGTCTCTGGATAATAAT 4317
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QY 4616 GATGTTTATGCCAAGATGCAAAAGTTAAATAACCATCTTCTTGGCTGTGTGTGCTGAT 4675
DB 4615 GATGGCTACGCCAAGGATGCCAACTCAGTGGCCCCATCCTCCTGCTGCTCTCCAGAT 4674
QY 4676 GGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAG 4735
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DB 4735 CTTTACTTTAACTCTATGAACTTCTATGAGTTGCGTCTCCAACTGATCAAGAACTCTAC 4794
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Qy 6053 GGCCGCGAGGGTGATATACAAAGTATGGCAAACTGTCAAAAGCTGGCAGAGCGCTCTATGAC 6112
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Qy 6113 ACCACAAGGTCAAGTTTCACTTATGACGAGCGGCGGCGATGCTGAGACCATCAACCTTA 6172
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Db 6415 TATTATGATTTAAACAGATCATTTCTACAGCTGTAAATGACCTATACGAGGACATTTGAT 6474
Qy 6473 GCATATGGCAGGATGAAGGAAGTGCAGTATGAGATCTTCGGCTCGCTCATGTACTGGATG 6532
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Qy 6833 GATATCTTTGAGTACAACTCAGCTGGCTGCTCATCAAGGCTCTACAAACCGGCTGGCAGC 6892
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Db 7315 CGGTGGCAACACCTGACATAGAAATCTGGA---AAGAAATTTGGGAAGGACCCAGCTCCT 7371

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 18:57:50 ; Search time 40060 Seconds
(without alignments)
11853.974 Million cell updates/sec

Title: US-10-029-020-13

Perfect score: 8354

Sequence: 1 gttgtggatgtgaggagc.....ccggaggtgacagagggac 8354

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 8354 | 100.0 | 8354 | 6 | AX556500 Sequence |
| 2 | 8225 | 98.5 | 8645 | 6 | AX600210 Sequence |
| 3 | 7779.2 | 93.1 | 8438 | 6 | AX675551 Sequence |
| 4 | 6975.4 | 83.5 | 8585 | 9 | AB025413 Mus muscu |
| 5 | 6701.6 | 80.2 | 7514 | 6 | CQ722991 Sequence |
| 6 | 6601.2 | 79.0 | 9722 | 9 | AF059485 Mus muscu |
| 7 | 6048.2 | 72.4 | 10826 | 8 | AB037723 Homo sapi |
| 8 | 4422.8 | 52.9 | 9264 | 5 | AB026980 |
| 9 | 4197.2 | 50.2 | 8993 | 8 | HSM806812 |
| 10 | 3544.6 | 42.4 | 8964 | 6 | AX952856 Sequence |
| 11 | 3544.6 | 42.4 | 8964 | 9 | AB025412 Mus muscu |
| 12 | 3502.2 | 41.9 | 8645 | 6 | AX662355 Sequence |
| 13 | 3473.8 | 41.6 | 8675 | 6 | AX662353 Sequence |
| 14 | 3422 | 41.0 | 8473 | 6 | AX662357 Sequence |
| 15 | 3398.8 | 40.7 | 8487 | 6 | AX662359 Sequence |
| 16 | 3397.8 | 40.7 | 8689 | 6 | AX250067 Sequence |
| 17 | 3397.8 | 40.7 | 8689 | 9 | AF086607 Rattus no |
| 18 | 3385 | 40.5 | 9826 | 6 | AX250008 Sequence |

| | | | | | |
|----|--------|------|------|---|--------------------|
| 19 | 3384.8 | 40.5 | 8797 | 6 | CQ777485 Sequence |
| 20 | 3384.8 | 40.5 | 8797 | 6 | AX250063 Sequence |
| 21 | 3384.8 | 40.5 | 8797 | 6 | AX250066 Sequence |
| 22 | 3384.8 | 40.5 | 8797 | 9 | AB025411 Mus muscu |
| 23 | 3352.8 | 40.1 | 7698 | 8 | AB040888 Homo sapi |
| 24 | 3351.4 | 40.1 | 9729 | 6 | AX250013 Sequence |
| 25 | 3330.4 | 39.9 | 8373 | 9 | AB025410 Mus muscu |
| 26 | 3320 | 39.7 | 8118 | 5 | GGA238613 |
| 27 | 3280 | 39.3 | 7816 | 9 | AF195418 Mus muscu |
| 28 | 3278.8 | 39.2 | 7706 | 6 | CQ714850 Sequence |
| 29 | 3258 | 39.0 | 8297 | 6 | CQ981507 Sequence |
| 30 | 3258 | 39.0 | 8297 | 8 | AF100772 Homo sapi |
| 31 | 3219 | 38.5 | 3486 | 8 | HSM806114 |
| 32 | 3165.8 | 37.9 | 8816 | 5 | AB026979 |
| 33 | 3158.4 | 37.8 | 8575 | 6 | AX921803 Sequence |
| 34 | 3137.4 | 37.6 | 7781 | 8 | AB032953 Homo sapi |
| 35 | 3070.8 | 36.8 | 8409 | 5 | GGA279031 |
| 36 | 3070.8 | 36.8 | 8409 | 6 | AX250068 Sequence |
| 37 | 3055.6 | 36.6 | 3320 | 6 | CQ850021 |
| 38 | 3055.6 | 36.6 | 3320 | 8 | AK127101 Homo sapi |
| 39 | 3051.8 | 36.5 | 5583 | 9 | AK122490 Mus muscu |
| 40 | 2991.2 | 35.8 | 7400 | 6 | CQ727408 Sequence |
| 41 | 2925.2 | 35.0 | 7713 | 8 | HSM808325 |
| 42 | 2794.6 | 33.5 | 3048 | 6 | CQ850546 Sequence |
| 43 | 2794.6 | 33.5 | 3048 | 8 | AK127705 Homo sapi |
| 44 | 2737.8 | 32.8 | 6751 | 6 | CQ716754 Sequence |
| 45 | 2622.2 | 31.4 | 5804 | 9 | AK122513 Mus muscu |

ALIGNMENTS

RESULT 1
AX556500
LOCUS AX556500 8354 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 13 from Patent WO02057453.
ACCESSION AX556500
VERSION AX556500.1 GI:25899736

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Location/Qualifiers

1. 8354

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match

Best Local Similarity

Matches 8354;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1 GTTGTGGATGTGGAGAGCGCGGGCGGAGCGCGATGGACGTGAAGAGAGGAGCCTTA 60

Db

1 GTTGTGGATGTGGAGAGCGCGGGCGGAGCGCGATGGACGTGAAGAGAGGAGCCTTA 60

Qy

61 CGGCTCGCTGACCCCGCGCGCGACCGCGCGCGCTACACCGAGTCTGTCGCGGACAG 120

Db

61 CGGCTCGCTGACCCCGCGCGCGACCGCGCGCGCTACACCGAGTCTGTCGCGGACAG 120

Qy

121 CGAGGAGGGGCAAGCCCGCAGAAATCGTACAGCTCCAGGAGACCCCTGAAGGCCTACGA 180

| | | | |
|----|------|---|------|
| Db | 121 | CGAGGAGGGCAAAAGCCCCGAGAAATCTGTACAGCTCCAGGAGACCCCTGAAGGCCTACGA | 180 |
| Qy | 181 | CCAGGACGCCCGCTAGCCTTATGGCAGCCGCGTCAAGGACATTGTGCGCGAGAGSCGA | 240 |
| Db | 181 | CGAGGACGCCCGCTAGCCTATGGCAGCCGCGTCAAGGACATTGTGCCGAGAGGCCGA | 240 |
| Qy | 241 | GGAAATCTGCGGCACAGGTGCCAACTTCAACCTTGCGGGAGCTGGGGCTGGAAGAAGTAAC | 300 |
| Db | 241 | GGAAATCTGCGGCACAGGTGCCAACTTCAACCTTGCGGGAGCTGGGGCTGGAAGAAGTAAC | 300 |
| Qy | 301 | GCCCCCTCACGGGACCTGTACCGGACAGACATTGGCCTGCCCAATGGCGTACTCCAT | 360 |
| Db | 301 | GCCCCCTCACGGGACCTGTACCGGACAGACATTGGCCTGCCCAATGGCGTACTCCAT | 360 |
| Qy | 361 | GGGGCTGGCTGTGATGCCGACATGGAGGCTGACAGGTGCTGTCCCTCTGAGCACCCCGT | 420 |
| Db | 361 | GGGGCTGGCTGTGATGCCGACATGGAGGCTGACAGGTGCTGTCCCTCTGAGCACCCCGT | 420 |
| Qy | 421 | CGCTGTGTGGGCGGGAGCACACGGTTCAGGCGCAGCTCCTGTCTCTCAGCGCGGCCAA | 480 |
| Db | 421 | CGCTGTGTGGGCGGGAGCACACGGTTCAGGCGCAGCTCCTGTCTCTCAGCGCGGCCAA | 480 |
| Qy | 481 | TTCCAAATCTCACACTCACCGACACCGGACATGAATAACTGAGACTGATCATCCGGGCGG | 540 |
| Db | 481 | TTCCAAATCTCACACTCACCGACACCGGACATGAATAACTGAGACTGATCATCCGGGCGG | 540 |
| Qy | 541 | CCTGACGAACACAGCGCGGCTCCGGAGCGCGCGCGCCGCTCTCGCACGCCCCACACCCC | 600 |
| Db | 541 | CCTGACGAACACAGCGCGGCTCCGGAGCGCGCGCGCCGCTCTCGCACGCCCCACACCCC | 600 |
| Qy | 601 | CAACCCAGACACAGCGGCTCCATTAATCCCTGAAACCGGGGCAACTTCACGCCGAGGAG | 660 |
| Db | 601 | CAACCCAGACACAGCGGCTCCATTAATCCCTGAAACCGGGGCAACTTCACGCCGAGGAG | 660 |
| Qy | 661 | CAACCCAGACCGCGGCCCGCAGGACACTCGCTCTCGGAGAGCCCTGCCCGCGCGCG | 720 |
| Db | 661 | CAACCCAGACCGCGGCCCGCAGGACACTCGCTCTCGGAGAGCCCTGCCCGCGCGCGC | 720 |
| Qy | 721 | CCAGGAGCTGCCACGCCACCGAGGAACTGCTGCTCAAACAGCAACATCCCCCTGGAGAC | 780 |
| Db | 721 | CCAGGAGCTGCCACGCCACCGAGGAACTGCTGCTCAAACAGCAACATCCCCCTGGAGAC | 780 |
| Qy | 781 | CAGGAACCTTAGGCAAGCAGCCATTCTTAGGGACATTTCAGGACAACTCATTAGATGGA | 840 |
| Db | 781 | CAGGAACCTTAGGCAAGCAGCCATTCTTAGGGACATTTCAGGACAACTCATTAGATGGA | 840 |
| Qy | 841 | CATTCTCGGCGCTCCGCGCATGATGGGCTTACAGTGACGGGCACTTCCTCTCTCAAGCC | 900 |
| Db | 841 | CATTCTCGGCGCTCCGCGCATGATGGGCTTACAGTGACGGGCACTTCCTCTCTCAAGCC | 900 |
| Qy | 901 | TGGAGGACACTCCCGCTCTTCTGACCAACATCACCAGGCTACCCACTGACGCTCCAGCAC | 960 |
| Db | 901 | TGGAGGACACTCCCGCTCTTCTGACCAACATCACCAGGCTACCCACTGACGCTCCAGCAC | 960 |
| Qy | 961 | AGTGTACTCTCTCGCGCCGACCCCTGCCCGCAGCACCTTCGCCCGCGCGGCTTTAA | 1020 |
| Db | 961 | AGTGTACTCTCTCGCGCCGACCCCTGCCCGCAGCACCTTCGCCCGCGCGGCTTTAA | 1020 |
| Qy | 1021 | CCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAGTGCGAGCCCTGAGCGGCATCTGTCAT | 1080 |
| Db | 1021 | CCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAGTGCGAGCCCTGAGCGGCATCTGTCAT | 1080 |
| Qy | 1081 | CTCAGCCACTCTGGTTCATCTCGCTGGGATCTTTGTGCGCATGACACCTGTTGGCCCTAAA | 1140 |
| Db | 1081 | CTCAGCCACTCTGGTTCATCTCGCTGGGATCTTTGTGCGCATGACACCTGTTGGCCCTAAA | 1140 |
| Qy | 1141 | CTGGCACTCGACGCCGATGGAGGGCGAGATGATAGATCACGGAGGACACAGCCAGCAG | 1200 |
| Db | 1141 | CTGGCACTCGACGCCGATGGAGGGCGAGATGATAGATCACGGAGGACACAGCCAGCAG | 1200 |
| Qy | 1201 | TTGGCTGTGCAACACCGAGCTCTCCCTATACCCCTCAGGGGGGACTGGCTTAGAGACCCC | 1260 |
| Db | 1201 | TTGGCTGTGCAACACCGAGCTCTCCCTATACCCCTCAGGGGGGACTGGCTTAGAGACCCC | 1260 |

[illegible]

Qy 2341 CTGCGCGAGCGCAAGTCGAGTCGACGCCCTGGCTGGAATGGCGAAACACTGCAACATCGC 2400
Db |||||
2341 CTGCGCGAGCGCAAGTCGAGTCGACGCCCTGGCTGGAATGGCGAAACACTGCAACATCGC 2400
Qy |||||
2401 TCACATATCTGGATAGGGTAGTTAAAGAGGGTTGGCCCTGGGTTGTGCMAATGGCAACGGCAG 2460
Db |||||
2401 TCACATATCTGGATAGGGTAGTTAAAGAGGGTTGGCCCTGGGTTGTGCMAATGGCAACGGCAG 2460
Qy |||||
2461 ATGTACCTTAGACCTGAATCGTGGCACTGCGTCTGCGACGTGCGACGTGGGCTGGAGAGGAGCTGG 2520
Db |||||
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2521 CTGTGACACTTCCATGGAGACTGCTGCGGTGACAGCAAAAGACAATGANTGGAGATGGCCCT 2580
Db |||||
2581 GGTGGACTGATGAGACCTGACTGCTGCTCCAGCCCTGTGCATATCAACCGCTGTG 2640
Qy |||||
2581 GGTGGACTGATGAGACCTGACTGCTGCTCCAGCCCTGTGCATATCAACCGCTGTG 2640
Db |||||
2641 CCTTGGCTCCCTAAACCTCTGGACATCATCCAGGAGACACAGTCCCTGTGTACAGCA 2700
Qy |||||
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Db |||||
2701 GAACCTACACTCCTTTCTATGACCGCATCAAGTTCTCGTGGGAGGACAGCAGCAGCAT 2760
Qy |||||
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2761 AATCCCGGGAGAAACCCCTTTGATGAGGGCATGCTTGTGTTATTCTGCTGGCCAAAGTGAT 2820
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Qy |||||
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Db |||||
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Qy |||||
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Db |||||
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Qy |||||
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Db |||||
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Qy |||||
4501 AAAGATCAACCGCATCAGGCGAGTCAACCTAGTGAGAGATCTCACTCGTTCTGGGCGC 4560
Db |||||

| | | | |
|----|------|---|------|
| Db | 4501 | AAAGATCAACCGCATCAGGCAGGTCACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGC | 4560 |
| Qy | 4561 | CCCCAGTGGCTGTGACTGTGTAATAAATGATGTCCAACTGTGATTTGTTTCTGGAGACGATGG | 4620 |
| Db | 4561 | CCCCAGTGGCTGTGACTGTGTAATAAATGATGTCCAACTGTGATTTGTTTCTGGAGACGATGG | 4620 |
| Qy | 4621 | TTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCTTGGCTGTGTGCTGATGGGA | 4680 |
| Db | 4621 | TTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCTTGGCTGTGTGCTGATGGGA | 4680 |
| Qy | 4681 | GCTCTACCTGGCCGACCTTGGGAAACATCCGAATTCGGTTTATCCGGAGAAACAAGCCCTTT | 4740 |
| Db | 4681 | GCTCTACCTGGCCGACCTTGGGAAACATCCGAATTCGGTTTATCCGGAGAAACAAGCCCTTT | 4740 |
| Qy | 4741 | CCTCAACACCCAGAAACATGTATGAGTCTCTTACCAATTTGACACGAGGCTCTATCTGTT | 4800 |
| Db | 4741 | CCTCAACACCCAGAAACATGTATGAGTCTCTTACCAATTTGACACGAGGCTCTATCTGTT | 4800 |
| Qy | 4801 | TGATACCAACCCGACAGCCTGTACACCAAGCCTGCCACAGGAGACTACCTGTACAA | 4860 |
| Db | 4801 | TGATACCAACCCGACAGCCTGTACACCAAGCCTGCCACAGGAGACTACCTGTACAA | 4860 |
| Qy | 4861 | CTTTCACCTACACTGGGGACGGCGACATCACACTCTATCAAGACAAATGCAACATGGT | 4920 |
| Db | 4861 | CTTTCACCTACACTGGGGACGGCGACATCACACTCTATCAAGACAAATGCAACATGGT | 4920 |
| Qy | 4921 | AAATGTCCGCCAGACTCTTACTGGGATGCCCTCTGGCTGTGTGTCCTCAGATGGCCAGGT | 4980 |
| Db | 4921 | AAATGTCCGCCAGACTCTTACTGGGATGCCCTCTGGCTGTGTGTCCTCAGATGGCCAGGT | 4980 |
| Qy | 4981 | GTACTGGGTGACCATGGGCACCAACAGTGCACCTCAAGAGTGTGACCAACAAGGACACGA | 5040 |
| Db | 4981 | GTACTGGGTGACCATGGGCACCAACAGTGCACCTCAAGAGTGTGACCAACAAGGACACGA | 5040 |
| Qy | 5041 | GTGGGCCATGATGACATACCATGGCAATTCGGCCCTTCTGGCAACCAAAAGCAATGAANA | 5100 |
| Db | 5041 | GTGGGCCATGATGACATACCATGGCAATTCGGCCCTTCTGGCAACCAAAAGCAATGAANA | 5100 |
| Qy | 5101 | CGATGGACAACTTTATGAGTACGACAGCTTTGGCCGCTGACAAATGTGACCTTCCC | 5160 |
| Db | 5101 | CGATGGACAACTTTATGAGTACGACAGCTTTGGCCGCTGACAAATGTGACCTTCCC | 5160 |
| Qy | 5161 | TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGTGCATGTCAGGTAGA | 5220 |
| Db | 5161 | TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGTGCATGTCAGGTAGA | 5220 |
| Qy | 5221 | GACCTCCAGCAAGGATGTCAACATAAACCAACCTGTGCTGCTGAGGCGCTTCTA | 5280 |
| Db | 5221 | GACCTCCAGCAAGGATGTCAACATAAACCAACCTGTGCTGCTGAGGCGCTTCTA | 5280 |
| Qy | 5281 | CACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGCCGATGGCTCTTGGG | 5340 |
| Db | 5281 | CACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGCCGATGGCTCTTGGG | 5340 |
| Qy | 5341 | GCTGCTGCTGGCCAAACCGCATGGAGTGGCGCTGCAGACTGAGCCCCCACTTCTGCTGG | 5400 |
| Db | 5341 | GCTGCTGCTGGCCAAACCGCATGGAGTGGCGCTGCAGACTGAGCCCCCACTTCTGCTGG | 5400 |
| Qy | 5401 | CACCGTCAACCCCAACCGTGGCAAGAGAAATGTACAGCTGCCCCATCGACAACGGCCCTCA | 5460 |
| Db | 5401 | CACCGTCAACCCCAACCGTGGCAAGAGAAATGTACAGCTGCCCCATCGACAACGGCCCTCA | 5460 |
| Qy | 5461 | CTGTGTGAGTGGCGCCAGCCAAAGACAGGCTCGGGCCAGGTCACTGTCTTTGGGG | 5520 |
| Db | 5461 | CTGTGTGAGTGGCGCCAGCCAAAGACAGGCTCGGGCCAGGTCACTGTCTTTGGGG | 5520 |
| Qy | 5521 | CCGGCTCGGGTGCAACACCGAAATCTCCTATCTCTGGAATTGATCGCGTAAACAGCAC | 5580 |
| Db | 5521 | CCGGCTCGGGTGCAACACCGAAATCTCCTATCTCTGGAATTGATCGCGTAAACAGCAC | 5580 |
| Qy | 5581 | AGAGAAGATCTATGATGACCAACCGAAATTCACCCCTTCGGATTCTGTACGACCGGCGGG | 5640 |
| Db | 5581 | AGAGAAGATCTATGATGACCAACCGAAATTCACCCCTTCGGATTCTGTACGACCGGCGGG | 5640 |

| | | | |
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| Qy | 5641 | GCGGCCAGCCTCTGGTCAACCCAGCAGCAGGCTGAATGGTGTCAACGTGACATACCTCCCC | 5700 |
| Db | 5641 | GCGGCCAGCCTCTGGTCAACCCAGCAGCAGGCTGAATGGTGTCAACGTGACATACCTCCCC | 5700 |
| Qy | 5701 | TGGGGTTTACATTTGCTGGCATCCAGAGGGGCATCTGTCTGAAAGAAATGGAATACGACCA | 5760 |
| Db | 5701 | TGGGGTTTACATTTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCA | 5760 |
| Qy | 5761 | GCGGGCCGATCACATCCAGGATCTTCGTGATGGGAACACATGGAGCTACACATACTT | 5820 |
| Db | 5761 | GCGGGCCGATCACATCCAGGATCTTCGTGATGGGAACACATGGAGCTACACATACTT | 5820 |
| Qy | 5821 | AGAGAAGTCCATGGTCTGCTACTACACAGCCAGAGCGAGTATATCTTTGAGTTCGACAA | 5880 |
| Db | 5821 | AGAGAAGTCCATGGTCTGCTACTACACAGCCAGAGCGAGTATATCTTTGAGTTCGACAA | 5880 |
| Qy | 5881 | GAATGACCGCTCTCTTTCTGTGACGATGCCCAAGCTGGCGGCGGACACCTAGAGACCAT | 5940 |
| Db | 5881 | GAATGACCGCTCTCTTTCTGTGACGATGCCCAAGCTGGCGGCGGACACCTAGAGACCAT | 5940 |
| Qy | 5941 | CCGCTCAGTGGCTACTACAGAAACATCTATCAGCCCTTGAGGGCAATGCCTCAGTCAT | 6000 |
| Db | 5941 | CCGCTCAGTGGCTACTACAGAAACATCTATCAGCCCTTGAGGGCAATGCCTCAGTCAT | 6000 |
| Qy | 6001 | ACAGGACTTCACTGAGGATGGGCACTCTTCTCAACCTTCTACCTGGGCACTGGCCGCGAG | 6060 |
| Db | 6001 | ACAGGACTTCACTGAGGATGGGCACTCTTCTCAACCTTCTACCTGGGCACTGGCCGCGAG | 6060 |
| Qy | 6061 | GGTGATATACAGTATGGCAAACTGTCAAAAGCTGGGAGAGCGCTCTATGACACCAACAA | 6120 |
| Db | 6061 | GGTGATATACAGTATGGCAAACTGTCAAAAGCTGGGAGAGCGCTCTATGACACCAACAA | 6120 |
| Qy | 6121 | GGTCAGTTTCACTTATGACAGAGCGGCACTGCTCAAGACCACTCAACCTTACAGAAATGA | 6180 |
| Db | 6121 | GGTCAGTTTCACTTATGACAGAGCGGCACTGCTCAAGACCACTCAACCTTACAGAAATGA | 6180 |
| Qy | 6181 | GGGCTTCACTGCAACCATCCGCTACCGTACAGTTGGGCCCCCTGATGACCGACAGATCTT | 6240 |
| Db | 6181 | GGGCTTCACTGCAACCATCCGCTACCGTACAGTTGGGCCCCCTGATGACCGACAGATCTT | 6240 |
| Qy | 6241 | CCGCTTCACTGAGGAAAGGCAATGGTCAACGCGCCGCTTTGACTACAACTATGACACAGCTT | 6300 |
| Db | 6241 | CCGCTTCACTGAGGAAAGGCAATGGTCAACGCGCCGCTTTGACTACAACTATGACACAGCTT | 6300 |
| Qy | 6301 | CCGGTGACACAGCATGAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCG | 6360 |
| Db | 6301 | CCGGTGACACAGCATGAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCG | 6360 |
| Qy | 6361 | CTATGATGATGTGTCAGGCAAGACAGAGCAGTTTGGGAAAGTTTGGTGTCTATTTACTATGA | 6420 |
| Db | 6361 | CTATGATGATGTGTCAGGCAAGACAGAGCAGTTTGGGAAAGTTTGGTGTCTATTTACTATGA | 6420 |
| Qy | 6421 | CATTAAACAGATCATCACAGCTGTGATGACCCACCAAGCAATTTTGTATGATATGG | 6480 |
| Db | 6421 | CATTAAACAGATCATCACAGCTGTGATGACCCACCAAGCAATTTTGTATGATATGG | 6480 |
| Qy | 6481 | CAGGATGAAGGAAGTGCAGTATGAGATCTCCGCTCGCTCATGTACTGATGATGACCGTCCA | 6540 |
| Db | 6481 | CAGGATGAAGGAAGTGCAGTATGAGATCTCCGCTCGCTCATGTACTGATGATGACCGTCCA | 6540 |
| Qy | 6541 | GTATGATAACTATGGGGCAGTGTGAAAGAGGAGCTGAAAGGTAGGACCTTACGCCAATAC | 6600 |
| Db | 6541 | GTATGATAACTATGGGGCAGTGTGAAAGAGGAGCTGAAAGGTAGGACCTTACGCCAATAC | 6600 |
| Qy | 6601 | CACCTGCTACTCTTATGATGATGATGCTGACGGCCAGCTGACAGACAGTCTCCATCAATGA | 6660 |
| Db | 6601 | CACCTGCTACTCTTATGATGATGATGCTGACGGCCAGCTGACAGACAGTCTCCATCAATGA | 6660 |
| Qy | 6661 | CAAGCCACTCTGGGCTACAGTACGACCTCAATGGGAACTCTTACTGAGGCGCTGG | 6720 |
| Db | 6661 | CAAGCCACTCTGGGCTACAGTACGACCTCAATGGGAACTCTTACTGAGGCGCTGG | 6720 |

||||| 83 GTTTGTGATNTGGAGAGCGGGCCCGAGGCCATGACGTGAGGAGAGGAAGCCTTA 142 Db
||||| 61 CCGCTCGTGACCCCGGCGCGGACGCGAGCGCGCTACACCACTCGTCCGCGGACAG 120 Qy
||||| 143 CCGCTCGTGACCCCGGCGCGGAGCGCGAGCGCGCTACACCACTCGTCCGCGGACAG 202 Db
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||||| 263 CCAGAGCCCGCTAGCTTAGCGAGCGCGGTCAAGGACATTTGCGCGCAGGAGGCCGA 322 Db
||||| 241 GGAATTTCCCGCACAGGTGGCACTTCACTCCCTGCGGAGCTGGGGCTGGAAGATTAAC 300 Qy
||||| 323 GGAATTTCCCGCACAGGTGGCACTTCACTCCCTGCGGAGCTGGGGCTGGAAGATTAAC 382 Db
||||| 301 GCCCCTCAGCGGACCCGTACCGGACAGACATTTGGCCCTGCCCAATGGGCTACTCCAT 360 Qy
||||| 383 GCCCCTCAGCGGACCCGTACCGGACAGACATTTGGCCCTGCCCACTGCGGCTACTCCAT 442 Db
||||| 361 GGGGCTGGCTCTGATGCGGACATGAGGCTGACACGGTGTGTCCTCCCTGAGCACCCCGT 420 Qy
||||| 443 GGGGCTGGCTCTGATGCGGACATGAGGCTGACACGGTGTGTCCTCCCTGAGCACCCCGT 502 Db
||||| 421 GCGTGTGGGCGGAGCACACGGTCAAGGGCGAGCTCTGCTGTCCTGTCAGCGCGGCCAA 480 Qy
||||| 503 GCGTGTGGGCGGAGCACACGGTCAAGGGCGAGCTCTGCTGTCCTGTCAGCGCGGCCAA 562 Db
||||| 481 TTCGAATCTCACACTCAGCGACACCGAGCATGAAGAAACATGAGACTGATCATCCGGGCGG 540 Qy
||||| 563 TTCGAATCTCACACTCAGCGACACCGAGCATGAAGAAACATGAGAC-----TCCGGGCGG 616 Db
||||| 541 CCTGCAGAAACACCGCGGCTCCGAGCGCGCGCGCGCTCTCGCAGCGCCACACCC 600 Qy
||||| 617 CTTGCAGAAACACCGCGGCTCCGAGCGCGCGCGCGCTCTCGCAGCGCCACACCC 676 Db
||||| 601 CAAACAGACACACCGCGGCTCCATTTAACTTCCCTGAACCGGGGCAACTTTCAACCGCAGGAG 660 Qy
||||| 677 CAAACAGACACACCGCGGCTCCATTTAACTTCCCTGAACCGGGGCAACTTTCAACCGCAGGAG 736 Db
||||| 661 CAAACAGCGCGGCGCCACGAGACCTCGCTCTCCGAGAGCGCCCTGCGCGGCGCGC 720 Qy
||||| 737 CAAACAGCGCGGCGCCACGAGACCTCGCTCTCCGAGAGCGCCCTGCGCGGCGCGC 796 Db
||||| 721 CCAGGAGCTGCCACCGCCAGGAGAACTGGCTGCTCAACAGCAACATCCCCCTGGAGAC 780 Qy
||||| 797 CCAGGAGCTGCCACCGCCAGGAGAACTGGCTGCTCAACAGCAACATCCCCCTGGAGAC 856 Db
||||| 781 CAGGAACTTAGGCAAGAGCCATTCCTAGGGAATTTGAGGAGCAATTTGAGATGGA 840 Qy
||||| 857 CAGAAACCTTAGGCAAGAGCCATTCCTAGGGAATTTGAGGAGCAACCTCAATTGAGATGGA 916 Db
||||| 841 CATTTCTCGCGCTCCCGCCATGATGGGCTTTACAGTGACGGGCACTTCTCTCAAGCC 900 Qy
||||| 917 CATTTCTCGCGCTCCCGCCATGATGGGCTTTACAGTGACGGGCACTTCTCTCAAGCC 976 Db
||||| 901 TGGAGGCACTTCCCGCTCTTCTGACCAACATCACCAGGGTACCACATGACGTCCAGCAC 960 Qy
||||| 977 TGGAGGCACTTCCCGCTCTTCTGACCAACATCACCAGGGTACCACATGACGTCCAGCAC 1036 Db
||||| 961 AGTGTACTCTTCGCGCCCGACCCCTGCCCGCAGACACTTTCGCGCGCGGCGCTTTAA 1020 Qy
||||| 1037 AGTGTACTCTTCGCGCCCGACCCCTGCCCGCAGACACTTTCGCGCGCGGCGCTTTAA 1096 Db
||||| 1021 CCTCAAGAGCCCTCAAGTACTGTAACTGGAAGTGGCAGCCCTGAGCGCCATCGTCA 1080 Qy
||||| 1097 CCTCAAGAGCCCTCAAGTACTGTAACTGGAAGTGGCAGCCCTGAGCGCCATCGTCA 1156 Db
||||| 1081 CTCAGCCACTCTGGTCATCTCTGGCATACTTTGTGGCCATGCACTGTTTGGCCTAAA 1140 Qy
|||||

1157 CTCAGCCACTCTGGTCATCTCTGTGGCATACTTTTGGGTAAGCACCT-----CTTCAA 1210 Db
1141 CTGGCACCTCAGCCGATGGAGGGGAGATGTATGATCAGCGAGGACACAGCCAGCAG 1200 Qy
1211 CTGGCACCTCAGCCGATGGAGGGGAGATGTATGATCAGCGAGGACACAGCCAGCAG 1270 Db
1201 TTGGCCTGTGCCAAACCGACGTCTCCCTATATACCCCTCAGGGGGCACTGGCTTAGAGACCC 1260 Qy
1271 TTGGCCTGTGCCAAACCGACGTCTCCCTATATACCCCTCAGGGGGCACTGGCTTAGAGACCC 1330 Db
1261 TGACAGAAAGGGCAAGAAACCAAGAAAGAACCCAGTAGTTTCTTTTCAGAGGACAG 1320 Qy
1331 TGACAGAAAGGGCAAGAAACCAAGAAAGAACCCAGTAGTTTCTTTTCAGAGGACAG 1390 Db
1321 TTTTCATAGATCTGGAGAAATGATGTGGGAAGCGAGCCTCCAGAAAGATTCTCTCTGG 1380 Qy
1391 TTTTCATAGATCTGGAGAAATGATGTGGGAAGCGAGCTTCCAGAAAGATTCTCTCTGG 1450 Db
1381 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATTCTGTGCATCTGAAATTCATATGTCTC 1440 Qy
1451 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATTCTGTGCATCTGAAATTCATATGTCTC 1510 Db
1441 TCTGGAAAGGCAAGCCCTCTGGTTGGCATTTATGGCAGAAAGGCCCTCCTCTCTCACATAC 1500 Qy
1511 TCTGGAAAGGCAAGCCCTCTGGTTGGCATTTATGGCAGAAAGGCCCTCCTCTCTCACATAC 1570 Db
1501 ACAGTTTGACTTTGTGGAGCTGTGGATGGCAGAGGCTCTTAACCCAGGAGGCGCGAG 1560 Qy
1571 ACAGTTTGACTTTGTGGAGCTGTGGATGGCAGAGGCTCTTAACCCAGGAGGCGCGAG 1630 Db
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1621 CTTCAATCAGATTTTGAATTCAGGAATCTGGCACTTGGCTTTTTCATATGACGGAAGGA 1680 Qy
1691 CTTCAATCAGATTTTGAATTCAGGAATCTGGCACTTGGCTTTTTCATATGACGGAAGGA 1750 Db
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1811 CTGCTATGGCAATGGTGA CTGCACTCTCTGGGACCTGCACTGTCTTCTGGGTTTCTCTGG 1870 Db
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1871 CCCCAGCTGTGGCAGAGCCTCTGCCCGTCTCTGTAGCGGAAATGCCCAATACATCAA 1930 Db
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1931 AGGCAGATGCTTTGTGCCACAGTGGCTGGAAGGGCTGAGTGCAGTGTGCCACCAACCA 1990 Db
1921 GTGTATCGATGTGCCCTGACGAAACCATGGCACTGCACTCATGCGGCACTTGCACTCTGCAA 1980 Qy
1991 GTGTATCGATGTGCCCTGACGAAACCATGGCACTGCACTCATGCGGCACTTGCACTCTGCAA 2050 Db
1981 CCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTGGACTGGACCCCACTATGTTTCAGG 2040 Qy
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2111 CCGGGGTGTCTGCTGAGAGGCAATGCCATTTGCTTTGTTGGGATGGGAGGCAACCACTG 2170 Db
2101 CGAGACCCCGCAGGCGCAATGCTTAGACCAAGTTTCAGGCAACCGGAACTTCTCTCCGGA 2160 Qy
2171 CGAGACCCCGCAGGCGCAATGCTTAGACCAAGTTTCAGGCAACCGGAACTTCTCTCCGGA 2230 Db
2161 CACCGGGTTTTCAGCTGTGACCAAGCTGGACACGACTGCTTCTATCGAGATCTG 2220 Qy
2231 CACCGGGTTTTCAGCTGTGACCAAGCTGGACACGACTGCTTCTATCGAGATCTG 2290 Db

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Db 4490 AGCCACCGCTTTGGCTGTTTTCACAAATGGGGTCTCTGTATATGCTGAGACTGATGAGAA 4549
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Db 4550 AAAGATCAACCGCATCAGCGAGGTCAACCACTAGTGGAGAGATCTCACTCGTGTGCTGGGC 4609
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Db 4610 CCCAGTGGCTGTGACTGTAAATAATGATGCCAACTGTGATGTTTCTGGAGACGATGG 4669
Qy 4621 TTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCTTGGCTGTGTGTGCTGATGGGA 4680
Db 4670 TTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCTTGGCTGTGTGTGATGGGA 4729
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Db 4730 GCTCTACGTGGCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAGCCTTT 4789
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Db 4910 CTTACCTTACACTGGGGAGGGGACATCACACTCATCACAGAACAAATGSCNACATGGT 4969
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Db 4970 AAATGTCCGCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCAGATGGCCAGGT 5029
Qy 4981 GTACTGGGTGACCAATGGGCAACCAAGTGCATCAAGAGTGTGACCAACAAGGACACGA 5040
Db 5030 GTACTGGGTGACCAATGGGCAACCAAGTGCATCAAGAGTGTGACCAACAAGGACACGA 5089
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Db 5090 GTTGGCCATGATGACATACCATGGCAATTCGGCCCTTCTGGCCACCAAAAGCAATGAAA 5149
Qy 5101 CGGATGGACAAATTTTATGATGACGACAGCTTTTGGCCGCTTGACAAATGTGACCTTCCC 5160
Db 5150 CGGATGGACAAATTTTATGATGACGACAGCTTTTGGCCGCTTGACAAATGTGACCTTCCC 5209
Qy 5161 TACTGGCCAGGTGAGCAGTTCGGAAGTGATACAGACAGTTCAGTGCATGTCAGGTAGA 5220
Db 5210 TACTGGCCAGGTGAGCAGTTCGGAAGTGATACAGACAGTTCAGTGCATGTCAGGTAGA 5269
Qy 5221 GACCTTCACGAGGATGATGATCACCATAACCAACCACTGTCTGCTCAGGGCCCTCTA 5280
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Db 6230 GGGCTTCACTGCAACCATCCGCTACCGTCAAGTTGGGCCCCCTGATTGACCCAGATCTT 6289
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Qy 6361 CTATGATGATGTGTGAGCAAGACAGAGCATTTGGGAAGTTTGGTGTCTATTACTATGA 6420
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Qy 6421 CATTAACCAAGATCATCACAGCTGTCTATGACCCACACCAAGCAATTTTGATGCAATATGG 6480
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Db 6530 CAGGATGAAGGAAGTGCAGATGAGATCTTCGCTCGCTCATGTACTGCATGACCGTCCA 6589
Qy 6541 GTATGATTAACATGGGGCGAGTAGTGAAGAGAGCTGAGGTAGGACCTACGCCAATAC 6600
Db 6590 GTATGATTAACATGGGGCGAGTAGTGAAGAGAGCTGAAAGTAGGACCTTACGCCAATAC 6649

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6325 GATCAACAGAGACCCCATGCTTCTATCGCTATGATGATGATGATGATGATGATGATGAT 6384
6352 GATCAACAGAGACCCCATGCTTCTATCGCTATGATGATGATGATGATGATGATGATGAT 6411

Db

| | | | | | |
|----------------------------|------|---|------|---|------|
| QY | 6385 | AGAGCAGTTTGGGAAGTTTGGTGCATTTACTATGACATTTAAACAGAGTATCATCCACAGC | 6444 | CTTTGGATTCCAGCTACACAAAGTGATCCCTGGTTATCCCAACACACATGATGTCAT | 7525 |
| DB | 6412 | AGAGCAGTTTGGGAAGTTTGGTGCATTTACTATGACATTTAAACAGAGTATCATCCACAGC | 6471 | CTTTGGATTCCAGCTACACAAAGTGATCCCTGGTTATCCCAACACACATGATGTCAT | 7551 |
| QY | 6445 | TGTCATGACCCACACCAAGCATTTTGAATGCATATGGCAGGATGAAGGAAGTGCAGTATGA | 6504 | GGAAACCCCTCTACAGCTCATCCACACACAGATGAAACCGCAGAGTGGCAACAACAGCA | 7583 |
| DB | 6472 | TGTCATGACCCACACCAAGCATTTTGAATGCATATGGCAGGATGAAGGAAGTGCAGTATGA | 6531 | GGAAACCCCTCTACAGCTCATCCACACACAGATGAAACCGCAGAGTGGCAACAACAGCA | 7611 |
| QY | 6505 | GATCTTCGCTCGCTCATGTACTTGGATGACCGTCCAGATGATATACATGGGGCGAGTAGT | 6564 | -----AGTCTATCTCTCGGGGTACAGTGTGAAGTACAGAAAGCA | 7620 |
| DB | 6532 | GATCTTCGCTCGCTCATGTACTTGGATGACCGTCCAGATGATATACATGGGGCGAGTAGT | 6591 | GCTAAGGCTTTGTGACCTTTAGAACCGTCTTATGGCTCCCAATCACCAG | 7671 |
| QY | 6565 | GAAGAAGGAGCTGAAGGTAGGACCTTACGCCAATACCCTCGCTACTCTCTATGAGTATGA | 6624 | GCTCAGGCTTTGTGACCTTTAGAACCGTCTTATGGCTCCCAATCACCAG | 7731 |
| DB | 6592 | GAAGAAGGAGCTGAAGGTAGGACCTTACGCCAATACCCTCGCTACTCTCTATGAGTATGA | 6651 | CTGCCACAGGCTCCAAAGACCAAGAGTTTTCATCCAGCGGCTCTATGGCTCCCAATCACCAG | 7740 |
| QY | 6625 | TGTCAGCGGCAGCTGACAGTGTCCATCAATGACCAAGCCACTCTCGCGCTACAGCTA | 6684 | CTGCCACAGGCTCCAAAGACCAAGAGTTTTCATCCAGCGGCTCTATGGCTCCCAATCACCAG | 7791 |
| DB | 6652 | TGTCAGCGGCAGCTGACAGTGTCCATCAATGACCAAGCCACTCTCGCGCTACAGCTA | 6711 | GGTCAAGTTTTCGCTTGAAGGATGGCCGAGTACCAAGACATCATAGTGTGGCCAAATGA | 7800 |
| QY | 6685 | CGACCTCAATGGGAACCTGCACCTTACTGAGCCCTGGGACAGTGCACGGCTCACACCACT | 6744 | GGTCAAGTTTTCGCTTGAAGGATGGCCGAGTACCAAGACATCATAGTGTGGCCAAATGA | 7851 |
| DB | 6712 | CGACCTCAATGGGAACCTGCACCTTACTGAGCCCTGGGACAGTGCACGGCTCACACCACT | 6771 | GGATGGGGAAGGGTTGCTGCCATCTTGAACCATGCCCATCTACCTAGAGAACCTGCACCT | 7860 |
| QY | 6745 | ACGGTATGACATCCGCGACCGCATCACTCGGCTGGGTGACGTGCAATACAAAGATGGATGA | 6804 | GGATGGGGAAGGGTTGCTGCCATCTTGAACCATGCCCATCTACCTAGAGAACCTGCACCT | 7911 |
| DB | 6772 | ACGGTATGACATCCGCGACCGCATCACTCGGCTGGGTGACGTGCAATACAAAGATGGATGA | 6831 | CGCATTTGATGGGTGGATACCCATTACTTTGTGAAACCAAGACCTTCAGAAAGGTGACCT | 7980 |
| QY | 6805 | GGATGGCTTCTGAGGCAGCGGGCGGTGATATCTTTGAGTACAACTCAGCTGGCGCTGCT | 6864 | GGCCATCTCTGGGCCCTCAGTGGGGGGCGGAAACCTTGGAGAAATGGGGTCAACGTCACCTGT | 7980 |
| DB | 6832 | GGATGGCTTCTGAGGCAGCGGGCGGTGATATCTTTGAGTACAACTCAGCTGGCGCTGCT | 6891 | GGCCATCTCTGGGCCCTCAGTGGGGGGCGGAAACCTTGGAGAAATGGGGTCAACGTCACCTGT | 8031 |
| QY | 6865 | CATCAAGGCTACAAACGGGCTGGAGCTGGAGTGTGAGTACCGCTACGATGGCGCTGGG | 6924 | GTCCAGATTCACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA | 8091 |
| DB | 6892 | CATCAAGGCTACAAACGGGCTGGAGCTGGAGTGTGAGTACCGCTACGATGGCGCTGGG | 6951 | GTACGGGGGACACTGTCTTTGAAACACACGCTACGGGACAAACGTTTGTAGGAGAGAGGCACG | 8151 |
| QY | 6925 | GGGCGGGTGTCCAGCAAGAGCAGCACAGCACCACTGACGAGTTCTTCTATGACAGACT | 6984 | GGTCTCTGAGCTGGCCCCCGCAGAGACCGCTGCGCCAAACGCTGGGCGCCCGCAGCAGAG | 8160 |
| DB | 6952 | GGGCGGGTGTCCAGCAAGAGCAGCACAGCACCACTGACGAGTTCTTCTATGACAGACT | 7011 | GGTCTCTGAGCTGGCCCCCGCAGAGACCGCTGCGCCAAACGCTGGGCGCCCGCAGCAGAG | 8211 |
| QY | 6985 | GACCAACCCCAACCAAGTCAACCACTGTACAAACCACTCCAGCTCTGAGATCACTCCCT | 7044 | ACTGCGGGGAAGGGAGGAGCGCTCGGGCTTGACAGAGGGGGAGAGCAGCAGAGTGTCT | 8220 |
| DB | 7012 | GACCAACCCCAACCAAGTCAACCACTGTACAAACCACTCCAGCTCTGAGATCACTCCCT | 7071 | ACTGCGGGGAAGGGAGGAGCGCTCGGGCTTGACAGAGGGGGAGAGCAGCAGAGTGTCT | 8271 |
| QY | 7045 | CTACTACGACTTGGCAAGGACACCTCTTTGGCATGGAGCTGAGCAGTGGTATGATTTTA | 7104 | GAGCACAGGGCGGGTGCAGGCTACGACGGCTTTTCTGTGATCTCTGTCTGGAGCAGTACCC | 8280 |
| DB | 7072 | CTACTACGACTTGGCAAGGACACCTCTTTGGCATGGAGCTGAGCAGTGGTATGATTTTA | 7131 | GAGCACAGGGCGGGTGCAGGCTACGACGGCTTTTCTGTGATCTCTGTCTGGAGCAGTACCC | 8331 |
| QY | 7105 | CATAGCTTGTGACAAACATCGGGACCCCTCTTGCTGTCTTTTGTGGAACAGGTTTATGAT | 7164 | AGAACTGTCTCAGACAGCGCCCAACCACTTCTATGAGACAGCAGCAGATGGGCCGAG | 8340 |
| DB | 7132 | CATAGCTTGTGACAAACATCGGGACCCCTCTTGCTGTCTTTTGTGGAACAGGTTTATGAT | 7191 | AGAACTGTCTCAGACAGCGCCCAACCACTTCTATGAGACAGCAGCAGATGGGCCGAG | 8391 |
| QY | 7165 | CAAGCAAACTCTGTACACAGCTATGGGAGATCTACATGGATACCAACCCCAACTTTCA | 7224 | GTGACAGAGAGGAC 8354 | |
| DB | 7192 | CAAGCAAACTCTGTACACAGCTATGGGAGATCTACATGGATACCAACCCCAACTTTCA | 7251 | GTGACAGAGAGGAC 8405 | |
| QY | 7225 | GATCATCATAGGCTACATGGTGGCTCTATGATCACTCAACAGCTTGTCCATGGG | 7284 | | |
| DB | 7252 | GATCATCATAGGCTACATGGTGGCTCTATGATCACTCAACAGCTTGTCCATGGG | 7311 | | |
| QY | 7285 | CCGCGGAGATTATGATGTCTGGCGGAGCGCTGGACTAGCCAGACCGAGCTCTGGAA | 7344 | | |
| DB | 7312 | CCGCGGAGATTATGATGTCTGGCGGAGCGCTGGACTAGCCAGACCGAGCTGTGGA | 7371 | | |
| QY | 7345 | GCACCTTAGTAGCAACAGCTCATGCTTTTAACTCTATATGTTTCAAAAAACAACCC | 7404 | | |
| DB | 7372 | GCACCTTAGTAGCAACAGCTCATGCTTTTAACTCTATATGTTTCAAAAAACAACCC | 7431 | | |
| QY | 7405 | CATCAGCAACTCCAGGACATCAAGTGTCTTATGACAGATGTTAAACGCTGCTCTCAC | 7464 | | |
| DB | 7432 | CATCAGCAACTCCAGGACATCAAGTGTCTTATGACAGATGTTAAACGCTGCTCTCAC | 7491 | | |
| RESULT 4 | | | | | |
| AB025413 | | | | | |
| LOCUS | | | | | |
| DEFINITION | | | | | |
| ACCESSION | | | | | |
| VERSION | | | | | |
| KEYWORDS | | | | | |
| SOURCE | | | | | |
| Mus musculus (house mouse) | | | | | |

| | | | | | | | |
|----|------|--|------|----|------|--|------|
| Qy | 3056 | ATTCCAGCTGTGACCTGAGCAATTTTGGCCGCCCCCAACCCAGTCGTCTCTCCATCCCA | 3115 | Qy | 4136 | ATGATCAGACGCATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAAATGATCTC | 4195 |
| Db | 3215 | ATCCCCAGCTGTGACCTGAGCAATTTTGGCCGCCCCCAACCCGTGGTCTCTCCATCCCA | 3274 | Db | 4295 | ATGATCAGACGTGTTGATCAAAATGGAATCATCTCCACTTTTGTGGGCTCCAATGACCTC | 4354 |
| Qy | 3116 | CTGACGCTCTTCGCCAGCTCTGTGCTGAGAAAGGCCCCCATTTGTGCCGGAATTCAGGCT | 3175 | Qy | 4196 | ACATCAGCCCCGGCACCTCAGCTGTGATTTCTGTGATGATATTTCCCAAGTAAGACTGGAG | 4255 |
| Db | 3275 | CTGACATCATTTCCGCCAGCTCTGTGCTGAGAAAGGCCCCCATTTGTGCCGGAATTCAGGCT | 3334 | Db | 4355 | ACCTCGGCCAGGCCCTCAGCTGTGATCTCGCTCATGGAGATTTCTCAGGTTCCGCTGGAG | 4414 |
| Qy | 3176 | TTGAGGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCGG | 3235 | Qy | 4256 | TGGCCACAGACACTTAGCCATCAACCCAAATGGCAACTCAGTTTATGTCTCGACAAACAAAT | 4315 |
| Db | 3335 | CTGCAAGAGGAAATCGTCACTCGCTGGCTGCAAGATGAGTTGAGTCACTCTGAGCAGCGC | 3394 | Db | 4415 | TGGCCACAGACACTTAGCCATCAACCCAAATGGAATTTCTCTATGTCTCGACACAAAT | 4474 |
| Qy | 3236 | ACCCCTGGCTCAAAATCTGTCTGAGGATGAGCTCACCCACCCGACCATCCCTTCAAC | 3295 | Qy | 4316 | GTGCTCTCGAAATCTCTGAAACCAACAGGTGGCAATTTGTGCGCGGAGGCCCATGAC | 4375 |
| Db | 3395 | ACTCTGGCTATAAGTCTGTCTGAGGATCAGTCTCACACACCCGACCATCCCTTCAAC | 3454 | Db | 4475 | GTGCTCTCGAAATCTCTGAAACCAACAGGTGGCAATTTGTGCGCGGAGGCCCATGAC | 4534 |
| Qy | 3296 | CTCATGAGGTGCACTCATGATGAGGTGGAGGCCGCTCTTCAGGAAGTGGTTGCT | 3355 | Qy | 4376 | TGCCAGTCCCTGGCATTTGACCACTTCTGCTAAGCAAGGTGGCCATCCAGCAACCCCTG | 4435 |
| Db | 3455 | CTCATGAAAGGTCCACCTCATGTTGGCAGTCAAGGTGGCTCTTCAGGAAGTGGTTGCT | 3514 | Db | 4535 | TGCCAGTCCCTGGCATTCGACCACTTCTGCTGAGCAAGGTAGCCATCCATGCCACCCCTG | 4594 |
| Qy | 3356 | GCAGCCCCAGACCTGTCTCTATTTTCAATTTGGGACAAGACAGAGCTCTACAAACGAGAAG | 3415 | Qy | 4436 | GAGTCAGCCACCGCTTTGGCTTTTACACAAATGGGGTCTCTGTATATTTGCTGAGACTGAT | 4495 |
| Db | 3515 | GCAGCTCTGACCTGTCTTACTTCTATCTGGGACAAGACAGATGTCTACAAACGAGAAG | 3574 | Db | 4595 | GAGTCAGCCACTGTCTCTGGCGCTTTCAACAATGGAGTCTTGTACATCGCTGAGCCGAC | 4654 |
| Qy | 3416 | GTGTTTGGCTTTCAAGAGCTTTGTTTCCGTGGGTATGATATGAAATCTCTGCCAGAT | 3475 | Qy | 4496 | GAGAAAAAGATCAACCCGATCAGGCAGTCAACCACTAGTGGAGAGATCTCACTCGTTGCT | 4555 |
| Db | 3575 | GTGTTTGGATTTCTCAGAAAGCCCTTTGTTTCCGTGGGTATGATATGAAATCTCTGCCAGAT | 3634 | Db | 4655 | GAGAAAAAGATCAATCGCATCAGGCAGTCACTACAAGTGGTGAATCTCACTGGTTGCT | 4714 |
| Qy | 3476 | CTAATCTGTGGAAAAAGAACACAGTGTGACAGGCTATGAAATTTGACGCGTCCAAG | 3535 | Qy | 4556 | GGGCCCCCGAGTGTGACTGTAAATATGATGCCAACTGTGATTTGTTTCTCGGAGAC | 4615 |
| Db | 3635 | CTGATCTCTGTGGGAGAAAGACAGCGGTGTGACAGGCTATGAAATTTGATGCTCCAG | 3694 | Db | 4715 | GGTCCCCCGAGTGTGACTGTAAATATGATGCCAACTGTGATTTGTTTCTCGGAGAT | 4774 |
| Qy | 3536 | CTTGAGGATGAGCCTAGACAAACATCATGCCCTCAACATTTCAAAGTGGTATCTGAC | 3595 | Qy | 4616 | GATGTTATGCAAGGATGCAAAAGTAAATACCCCATCTTCTTGGCTGTGTGTGCTGAT | 4675 |
| Db | 3695 | CTGGGGGCTGGAGTCTGATAAGCACCATGCCCTGAACATCCAGAGTGGCATCTGAC | 3754 | Db | 4775 | GATGTTATGCAAGGATGCAAAAGTAAATACCCCATCTTCTTGGCTGTGTGTGCTGAC | 4834 |
| Qy | 3596 | AAAGGGAATGGGAGAAACAGTTTGTGTCTGACGAGCTCTGTGATTTGGGAGCATATG | 3655 | Qy | 4676 | GGGAGGCTCTACGTGGCGGACCTTTGGGAAACATCCGAATTCGGTTATCCGGAAGAACAG | 4735 |
| Db | 3755 | AAAGGGAATGGGAGAAACAGTTTGTGTCTGACGAGCTCTGTGATTTGGGAGCATATG | 3814 | Db | 4835 | GGGAGGCTCTATGTGGCGGACCTTTGGGAAACATCCGAATTCGAATTTATCCGGAAGAACAG | 4894 |
| Qy | 3656 | GGCAATGGCGCGGAGAGCATCTCTGCCCCAGCTGCAACGGGCTTTGCTGACCGGCAAC | 3715 | Qy | 4736 | CCTTTCTCAACCCAGAACATGTATGAGCTGTCTTACCAATTTGACCAAGAGCTCTAT | 4795 |
| Db | 3815 | GGCAATGGCGCGGAGAGCATCTCTGCCCCAGCTGCAATGGTCTTGTGATGGCAAC | 3874 | Db | 4895 | CCTTTCTCAACCCAGAACATGTATGAGCTGTCTTACCAATTTGACCAAGAGCTCTAT | 4954 |
| Qy | 3716 | AAAGCTCTGGCCCCCGTGGCCCTCACTGTGGCTCTGACGGAGCTCTATGTGGGTGAT | 3775 | Qy | 4796 | CTGTTTGTATCCACCGCAAGCACCTGTATACCCAAAGCCTGCCACAGGAGACTACCTG | 4855 |
| Db | 3875 | AAAGCTCTGGCCCCCGTGGCCCTCACTGTGGCTCTGATGGGAGTCTCTACGTGGGAGAC | 3934 | Db | 4955 | CTCTTTGATACAGTGGCAAGCATCTGTACTCAGAGCCTACCCACAGGGGACTACCTG | 5014 |
| Qy | 3776 | TTCAACTATATTAGAAAGGATCTTCCCTCTGGAATGTGACCAACATCTTAGAGCTGAGG | 3835 | Qy | 4856 | TACAACTTCACTACATGGGGACGGGCAATCATCACTCATCACAGACAAATGGCAAC | 4915 |
| Db | 3935 | TTCAACTATATTAGAAAGGATCTTCCCTCTGGAATGTGACCAACATCTTAGAGATGAGA | 3994 | Db | 5015 | TACAACTTCACTTACACAGGGGACGGGCAATCATCACTCATCACAGACAAATGGCAAC | 5074 |
| Qy | 3836 | ATAAAGATTTTCAGACATAGTCACAGTCCAGCACACAAATCTACTGGCCACAGACCCC | 3895 | Qy | 4916 | ATGTTAAATGTCCGCGGAGACTCTACTGGGATGCCCTCTGGCTGGTCCGAGATGCG | 4975 |
| Db | 3995 | ATAAAGATTTTCAGACATAGTCACAGTCCAGCACACAAATCTACTGGCTACAGCC | 4054 | Db | 5075 | ATGTTAAATGTCCGCGGAGACTCTACTGGGATGCCCTCTGGCTGGTCCGAGATGCG | 5134 |
| Qy | 3896 | ATGAGTGGGGCGCTCTTCTTTCTGACAGCAACAGCCGGGGTCTTTAAATATCAAGTCC | 3955 | Qy | 4976 | CAGTGTACTGGGTGACCATGGCACCAACAGTGCATCAAGAGTGTGACCAACAAGGA | 5035 |
| Db | 4055 | ATGAGTGGGGCGCTCTTCTTTCTGACAGCAACAGCCGGGGTCTTTAAATATCAAGTCC | 4114 | Db | 5135 | CAGTGTACTGGGTGACCATGGCACCAACAGTGCATCAAGAGTGTGACCAACAAGGA | 5194 |
| Qy | 3956 | ACTGTGGTGGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGGGGACAGTGCACAG | 4015 | Qy | 5036 | CACGAGTTGGCCATGATGACATACATGGCAATTCGGGCTTCTGGCAACCAAAAGCAAT | 5095 |
| Db | 4115 | ACCACAGTGGTGAAGGACCTTGTGAAGAACTCCGAGTGGTGAAGGAGTGGTGAAGGAG | 4174 | Db | 5195 | CACGAGTTAGCCATGATGACCTTACCATGGCAACTCTGGGCTCTTGGCAACCAAAAGCAAT | 5254 |
| Qy | 4016 | TGCTCCCTTTGATGACACTCGCTGGGGGATGGTGGGAAGGCCACAGAGCCACACTC | 4075 | Qy | 5096 | GAAAACGATGGACAACTTTTATGATACGACAGCTTTGGCGCTTGACAAATGTGACC | 5155 |
| Db | 4175 | TGCTCCCTTTGATGATACCTCGCTGGGAGATGGTGGGAAGGCCACAGAGCCAGCTC | 4234 | Db | 5255 | GAAAACGATGGACAACTTTTATGATGATGACGTTTGGTGGCTTGACAAACGTGACC | 5314 |
| Qy | 4076 | ACCAATCCAGGGGATTTACAGTGGACAAATTTGGGCTGATCTATCTTCGTGATGGCACC | 4135 | Qy | 5156 | TTCCCTCTACTGGCCAGGTGAGAGTTTCCGAAGTGTATACAGACAGTTCAGTGTGATGCCAG | 5215 |
| Db | 4235 | ACTAACCCAGGGGAATTACAGTGGACAAATTTGGGCTCATTTATTTCTGTGACGGCACC | 4294 | Db | 5315 | TTTCCAACTGGCCAGGTGAGCAGTTTCCGAGCGATACAGACAGCTCAGTGCAGTGCAG | 5374 |
| | | | | Qy | 5216 | GTAGAGACTTCAGCAAGGATGATGTACCATTAACCAACCACTGTCTCTCCCTCAGCGCC | 5275 |

| | | | | | |
|----|------|--|------|--|--|
| Dd | 702 | -----GGAAGCC | 709 | | |
| Qy | 1297 | CAGTATGTTCTTCCAGAGACAGTTCATAGATTCTGGAGAAATTGATGTGGAGGCG | 1356 | | |
| Dd | 710 | CAGTATGTTCTTCCAGAGACAGTTCATAGATTCTGGAGAAATTGATGTGGAGGCG | 769 | | |
| Qy | 1357 | AGCCTCCAGAAAGATTCTCTCGGCATTCTCTGGAGATCTCAAGTGTTCATAGACCATCC | 1416 | | |
| Dd | 770 | AGCTTCCAGAAAGATTCTCTCGGCATTCTCTGGAGATCTCAAGTGTTCATAGACCATCC | 829 | | |
| Qy | 1417 | TGTGCATCTGAATTTCAATGTCTCTGGGAAAGGACGCCCTGGTGGCAATTTATGGCAG | 1476 | | |
| Dd | 830 | TGTGCATCTGAATTTCAATGTCTCTGGGAAAGGACGCCCTGGTGGCAATTTATGGCAG | 889 | | |
| Qy | 1477 | AAAGGCTCCCTCTTCAATACACAGTTTGATTTGTGGAGCTGCTGATGCGCAGGAG | 1536 | | |
| Dd | 890 | AAAGGCTCCCTCTTCAATACACAGTTTGATTTGTGGAGCTGCTGATGCGCAGGAG | 949 | | |
| Qy | 1537 | GCTCCTAAACAGAGGCGGAGCCTTAGAGGGGACCCCGCCAGTCTCGGGGAACTGT | 1596 | | |
| Dd | 950 | GCTCCTAAACAGAGGCGGAGCCTTAGAGGGGACCCCGCCAGTCTCGGGGAACTGT | 1009 | | |
| Qy | 1597 | GCCTCCCTCAGGCATGAGACAGCTTCATCCAGTATTTGGATTCAGGAATCTGGCACTT | 1656 | | |
| Dd | 1010 | GCCTCCCTCAGGCATGAGACAGCTTCATCCAGTATTTGGATTCAGGAATCTGGCACTT | 1069 | | |
| Qy | 1657 | GGCTTTTACAATGACGGAAGGAGTCAGAAAGTGGTTCCTTTCTCACCACTGCCATTGA | 1716 | | |
| Dd | 1070 | GGCTTTTACAATGACGGAAGGAGTCAGAAAGTGGTTCCTTTCTCACCACTGCCATTGA | 1129 | | |
| Qy | 1717 | GTGGTGGATTAACCTGCCCGCAGCACTGCTATGGCAATGGTGAATCTGGGACCTG | 1776 | | |
| Dd | 1130 | GTGGTGGATTAACCTGCCCGCAGCACTGCTATGGCAATGGTGAATCTGGGACCTG | 1189 | | |
| Qy | 1777 | CCACTGCTTCTGGGTTCTGGGCCCCGACTGTGGCAGAGCTCTCTGCCCCGTTGCTG | 1836 | | |
| Dd | 1190 | CCACTGCTTCTGGGTTCTGGGCCCCGACTGTGGCAGAGCTCTCTGCCCCGTTGCTG | 1249 | | |
| Qy | 1837 | TAGGGNAATGGCCNATACATGAAGCAGATGCTTGTGCCACAGTGGCTGGAAAGCGC | 1896 | | |
| Dd | 1250 | TAGGGNAATGGCCNATACATGAAGCAGATGCTTGTGCCACAGTGGCTGGAAAGCGC | 1309 | | |
| Qy | 1897 | TGAGTGGATGTGCCCAACCAACAGTGTATCGATGTGGCCTGCAGCAACCATGGCACCTG | 1956 | | |
| Dd | 1310 | TGAGTGGATGTGCCCAACCAACAGTGTATCGATGTGGCCTGCAGCAACCATGGCACCTG | 1369 | | |
| Qy | 1957 | CATCAGGGCACCTGCATCTGCAACCTGTGCTACAAGGGCAGAGCTGTGAGGAAGTGA | 2016 | | |
| Dd | 1370 | CATCAGGGCACCTGCATCTGCAACCTGTGCTACAAGGGCAGAGCTGTGAGGAAGTGA | 1424 | | |
| Qy | 2017 | CTGCATGGACCCNACATGTTACGCCCGGGTGTCTGCGTGAGAGGGCAATGCCATTTGCTT | 2076 | | |
| Dd | 1425 | ----- | 1424 | | |
| Qy | 2077 | TGTGGATGGGAGGCCAACCTGCAGACCCCGAGGCCACATGCTTAGACCAAGTGTTC | 2136 | | |
| Dd | 1425 | ----- | 1424 | | |
| Qy | 2137 | AGGCCAGGAACCTTCTCCCGGACACCGGGCTTTTGACGTGTGACCCAAAGCTGGATGG | 2196 | | |
| Dd | 1425 | ----- | 1424 | | |
| Qy | 2197 | ACAGGACTGTTTATCGAGATCTGTGCTGCGGACTGTGGTGGCCATGGCTGTGCGTAGG | 2256 | | |
| Dd | 1425 | -----GAGATCTGTGCTGCGGACTGTGGTGGCCATGGCTGTGCGTAGG | 1468 | | |
| Qy | 2257 | GGGCACCTGCGCTGCCAGAGATGCTGATGGGGGAGCCTGCGACAGCGGGCTGCCA | 2316 | | |
| Dd | 1469 | GGGCACCTGCGCTGCCAGAGATGCTGATGGGGGAGCCTGCGACAGCGGGCTGCCA | 1528 | | |
| Qy | 2317 | CCGCGCTGTGCCAGCATGGGACCTGCCCGCGAGCGGCAAGTGGCAGTGCAGCCCTGGCTG | 2376 | | |
| Dd | 1529 | CCGCGCTGTGCCAGCATGGGACCTGCCCGCGAGCGGCAAGTGGCAGTGCAGCCCTGGCTG | 1588 | | |
| Qy | 2377 | GAATGCCGAACACTGTCACCATCGCTCACTATCTGGATAGGGTAGTTAAAGAGGGTTGCC | 2436 | | |
| Dd | 1589 | GAATGCCGAACACTGTCACCATC-----GAGGTTGCC | 1621 | | |
| Qy | 2437 | TGGGTTGTGCAATGGCAACGGCAGATGTACCTTTAGACCTGGAATGGTTGGCACTGCGTCTG | 2496 | | |
| Dd | 1622 | TGGGTTGTGCAATGGCAACGGCAGATGTACCTTTAGACCTGGAATGGTTGGCACTGCGTCTG | 1681 | | |
| Qy | 2497 | CCAGCTGGGCTGGAGAGGAGCTGGCTGTGACACTTCATGAGACTGCCCTGCCGTGACAG | 2556 | | |
| Dd | 1682 | CCAGCTGGGCTGGAGAGGAGCTGGCTGTGACACTTCATGAGACTGCCCTGCCGTGACAG | 1741 | | |
| Qy | 2557 | CAAAGAACAATGATGGAGATGGCTGTGACTGCATGGAACCTGACTGCTGCCCTCCAGCC | 2616 | | |
| Dd | 1742 | CAAAGAACAATGATGGAGATGGCTGTGACTGCATGGAACCTGACTGCTGCCCTCCAGCC | 1801 | | |
| Qy | 2617 | CTGTGCCATATCAACCCGCTGTGCTTGGCTCCCTTAACCTCTGGAACATCATCCAGGA | 2676 | | |
| Dd | 1802 | CTGTGCCATATCAACCCGCTGTGCTTGGCTCCCTTAACCTCTGGAACATCATCCAGGA | 1861 | | |
| Qy | 2677 | GACACAGTCCCTGTCTCAGCAGAACCTTACACTCCTTCTATGACCGCATCAAGTTCCCT | 2736 | | |
| Dd | 1862 | GACACAGTCCCTGTCTCAGCAGAACCTTACACTCCTTCTATGACCGCATCAAGTTCCCT | 1921 | | |
| Qy | 2737 | CGTGGCAGGACAGCAGCACAATAATCCCGGGGAGAACCCCTTTGATGGAGGCGATGC | 2796 | | |
| Dd | 1922 | CGTGGCAGGACAGCAGCACAATAATCCCGGGGAGAACCCCTTTGATGGAGGCGATGC | 1981 | | |
| Qy | 2797 | TTGTGTTATTTCTGGGCCAAGTGATGACATCAGATGGAACCCCTGCTGGTGTGAACAT | 2856 | | |
| Dd | 1982 | TTGTGTTATTTCTGGGCCAAGTGATGACATCAGATGGAACCCCTGCTGGTGTGAACAT | 2041 | | |
| Qy | 2857 | CAGTTTTGTCAATAACCTCTCTTTGGATATCAATCAGCAGGCAAGATGGCAGCTTTGA | 2916 | | |
| Dd | 2042 | CAGTTTTGTCAATAACCTCTCTTTGGATATCAATCAGCAGGCAAGATGGCAGCTTTGA | 2101 | | |
| Qy | 2917 | CTTGGTGACAAATGGGGGACATCTCCATCATCTGCGGTTCCAGCGGACACCTTTTCATCAC | 2976 | | |
| Dd | 2102 | CTTGGTGACAAATGGGGGACATCTCCATCATCTGCGGTTCCAGCGGACACCTTTTCATCAC | 2161 | | |
| Qy | 2977 | ACAGGAGCACACCTGTGGCTGCCATGGGATCGCTTTTGTCAATGAAACCATCATCAT | 3036 | | |
| Dd | 2162 | ACAGGAGCACACCTGTGGCTGCCATGGGATCGCTTTTGTCAATGAAACCATCATCAT | 2221 | | |
| Qy | 3037 | GAGACATGAGGAATGAGATTTCCAGCTGTGACCTGAGCAATTTTCCCGCCCAACCC | 3096 | | |
| Dd | 2222 | GAGACATGAGGAATGAGATTTCCAGCTGTGACCTGAGCAATTTTCCCGCCCAACCC | 2281 | | |
| Qy | 3097 | AGTGTCTCTTCCATCCCACTGACCTCTTCCGACGCTCTCTGTCAGAGAAAGGCCCCAT | 3156 | | |
| Dd | 2282 | AGTGTCTCTTCCATCCCACTGACCTCTTCCGACGCTCTCTGTCAGAGAAAGGCCCCAT | 2341 | | |
| Qy | 3157 | TGTCCGGAATTCAGGCTTTGAGGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCT | 3216 | | |
| Dd | 2342 | TGTCCGGAATTCAGGCTTTGAGGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCT | 2401 | | |
| Qy | 3217 | GAGCTACTGAGCAGCGGACCCCTGGCTACAATCTGTCTCTGAGGATCAGCCTCACCA | 3276 | | |
| Dd | 2402 | GAGCTACTGAGCAGCGGACCCCTGGCTACAATCTGTCTCTGAGGATCAGCCTCACCA | 2461 | | |
| Qy | 3277 | CCGACCATCCCTTCAACCTCATGAGGTGACCTCATGCTGAGCGGTGAGGGCCGCT | 3336 | | |
| Dd | 2462 | CCGACCATCCCTTCAACCTCATGAGGTGACCTCATGCTGAGCGGTGAGGGCCGCT | 2521 | | |
| Qy | 3337 | CTTCAGGAAGTGGTTCGCTGACGCCAGACCTGTCTATTTATTTTTCATTTGGGACAAGAC | 3396 | | |
| Dd | 2522 | CTTCAGGAAGTGGTTCGCTGACGCCAGACCTGTCTATTTATTTTTCATTTGGGACAAGAC | 2581 | | |
| Qy | 3397 | AGAGCTCTACAACAGAGGTGTTGGGCTTTTTCAGAGCCCTTTTCTCGTGGGTTATGA | 3456 | | |
| Dd | 2582 | AGAGCTCTACAACAGAGGTGTTGGGCTTTTTCAGAGCCCTTTTCTCGTGGGTTATGA | 2641 | | |

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|----|------|---|------|----|------|--|------|
| Db | 4781 | TCGGATTCTGTACGACCAGCGGGCGGCCAGCCTCTGCTGCACCCAGCAGCAGGCTGAA | 4840 | QY | 6751 | TGACATCCCGCAGCCCGCATCACTCGGCTGGGTGACGTGCAATACAAAGATGGATGAGTGG | 6810 |
| QY | 5677 | TGGTGTCAACGTTGACATACCTCCCTGGGGTTACATGCTGGCATCCAGAGGGGCATCAT | 5736 | Db | 5921 | TGACATCCCGCAGCCCGCATCACTCGGCTGGGTGACGTGCAATACAAAGATGGATGAGTGG | 5980 |
| Db | 4841 | TGGTGTCAACGTTGACATACCTCCCTGGGGTTACATGCTGGCATCCAGAGGGGCATCAT | 4900 | QY | 6811 | CTTCTGAGGCGAGCGGGCGGTGATATCTTTGAGTACAACTAGCTGGCTGCTCATCAA | 6870 |
| QY | 5737 | GTCTGAAAGAAATGGAATACGACCAGGCGGGCCGCATCACATCCAGGATCTTCCTGATGG | 5796 | Db | 5981 | CTTCTGAGGCGAGCGGGCGGTGATATCTTTGAGTACAACTAGCTGGCTGCTCATCAA | 6040 |
| Db | 4901 | GTCTGAAAGAAATGGAATACGACCAGGCGGGCCGCATCACATCCAGGATCTTCCTGATGG | 4960 | QY | 6871 | GGCTACAAACCGGCTGGCAGCTGGAGTGTCAAGTACCCTACGATGGCTGGGGCGGGCG | 6930 |
| QY | 5797 | GAAGACATGAGGCTACACATCTATAGAGAAG-----TCATGGTGTCTACTACACAG | 5850 | Db | 6041 | GGCTACAAACCGGCTGGCAGCTGGAGTGTCAAGTACCCTACGATGGCTGGGGCGGGCG | 6100 |
| Db | 4961 | GAAGACATGAGGCTACACATCTATAGAGAAGGAGGTTTCCATGGTGTCTACTACACAG | 5020 | QY | 6931 | CGTGTCCAGCAAGAGCAGCCACAGCCACCACTGCAAGTCTTTCTATGCAAGACTGACCAA | 6990 |
| QY | 5851 | CCAGGCGCATATCTTTGAGTTCGACAAAGATGACCGCTCTCTTCTGTGACGATGCC | 5910 | Db | 6101 | CGTGTCCAGCAAGAGCAGCCACAGCCACCACTGCAAGTCTTTCTATGCAAGACTGACCAA | 6160 |
| Db | 5021 | CCAGGCGCATATCTTTGAGTTCGACAAAGATGACCGCTCTCTTCTGTGACGATGCC | 5080 | QY | 6991 | CGTGTCCAGCAAGAGCAGCCACAGCCACCACTGCAAGTCTTTCTATGCAAGACTGACCAA | 7050 |
| QY | 5911 | CAACGTTGGCGGCGAGACATCTAGAGACCATCCGCTCAGTGGGCTACTACAGAAACATCTA | 5970 | Db | 6161 | CGTGTCCAGCAAGAGCAGCCACAGCCACCACTGCAAGTCTTTCTATGCAAGACTGACCAA | 6220 |
| Db | 5081 | CAACGTTGGCGGCGAGACATCTAGAGACCATCCGCTCAGTGGGCTACTACAGAAACATCTA | 5140 | QY | 7051 | CGACTTGCAAGGACACCTCTTTGCCATGGAGCTGAGAGTGGTGTGATGATGATGATGATG | 7110 |
| QY | 5971 | TCAGCCCCCTGAGGGCAATGCTCAGTCAATACAGGACTTCACTGAGGATGGGCACTCTCT | 6030 | Db | 6221 | CGACTTGCAAGGACACCTCTTTGCCATGGAGCTGAGAGTGGTGTGATGATGATGATGATG | 6280 |
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| QY | 6031 | TCACACCTTCTACTGGGCACTGGCCCGCAGGTGATATACAAGTATGGCAAACTGTCAA | 6090 | Db | 6281 | TTGTGACAAACATCGGGACCCCTCTTCTGCTGTCTTTAGTGGAAACAGGTTTGTGATGATCAAGCA | 6340 |
| Db | 5201 | TCACACCTTCTACTGGGCACTGGCCCGCAGGTGATATACAAGTATGGCAAACTGTCAA | 5260 | QY | 7171 | AATCTCTGTACACAGCCTATGGGGAGATCTACATGATATCAACCCCACTTTTCAGATCAT | 7230 |
| QY | 6091 | GCTGGCAGAGAGCTCTATGACACCAACAGGTCAAGTTTCACTTATGACGAGACGGCAGG | 6150 | Db | 6341 | AATCTCTGTACACAGCCTATGGGGAGATCTACATGATATCAACCCCACTTTTCAGATCAT | 6400 |
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| QY | 6211 | GATTGGGCCCCGTTGACCGACAGATCTTCCGGCTTCACTGAGGAAGGCTGTCAACGC | 6270 | Db | 6461 | AGATTATGATGTCTGCGCGGACCTGGAGCTAGCCAGCAGCAGCTGTGGAGGACACCT | 6520 |
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| QY | 6271 | CCGTTTTGACTTACAACTATGACAAACAGCTTCCGGGTGACAGCATGAGCTGTGATCAA | 6330 | Db | 6521 | TAGTAGCAGCAACGTCATGCTTTTAACTCTATATATGTTTCAAAAACAAACCCCATCAG | 6580 |
| Db | 5441 | CCGTTTTGACTTACAACTATGACAAACAGCTTCCGGGTGACAGCATGAGCTGTGATCAA | 5500 | QY | 7411 | CAACTCCAGGACATCAAGTGTCTTATGACAGATGTTAAACAGCTGCTGCTCACTTTGG | 7470 |
| QY | 6331 | CGAGACCCCACTGCCCCATGATCTCTATGCTATGATGATGTGTGAGGCAAGACAGAGCA | 6390 | Db | 6581 | CAACTCCAGGACATCAAGTGTCTTATGACAGATGTTAAACAGCTGCTGCTCACTTTGG | 6640 |
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| QY | 6391 | GTTTGGGAAGTTTGGTGTCTATTTACTATGACATTTAAACAGATCATACCAAGCTGTCTAT | 6450 | Db | 6641 | ATTCCAGCTTACACAAAGTATCCCTGGTTATCCCAACCCAGACATGGATGCCATGGAACC | 6700 |
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RESULT 6
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LOCUS Mus musculus Doc4 (Doc4) mRNA, complete cds.
DEFINITION Mus musculus Doc4 (Doc4) mRNA, complete cds.
ACCESSION AF059485
VERSION AF059485.1 GI:3170614
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Wang,X.Z., Kuroda,M., Sok,J., Batchvarova,N., Kimmel,R., Chung,P.,
Zinsner,H. and Ron,D.
TITLE Identification of novel stress-induced genes downstream of chop
JOURNAL EMBO J. 17 (13), 3619-3630 (1998)
PUBMED 9649432
REFERENCE
AUTHORS Wang,X.-Z. and Ron,D.
TITLE Direct Submission
JOURNAL Submitted (14-APR-1998) Skirball Institute, New York University
Medical Center, 550 First Ave., New York, NY 10016, USA
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ORIGIN

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Best Local Similarity 86.7%; Pred. No. 0;
Matches 7426; Conservative 5; Mismatches 874; Indels 264; Gaps 4;
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Db |||||||

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| QY | 2126 | GACCAAGTGTTCAGGCCACGGAACTCTTCTCCGGACACACCGGCTTTGGAGCTGTGACCCA | 2185 |
| Db | 2890 | GACCAAGTGTTCAGGCCACGGAACTCTTCTCCGGACACACAGGACTTTGCAACTGTGAOCCA | 2949 |
| QY | 2186 | AGCTGGACTGACACAGCTGTCTATCAGATCTGTGCTGCGGACTGTGTGGCCATGGC | 2245 |
| Db | 2950 | AGCTGGACTGACACAGCTGTCTATCAGATCTGTGCTGCGGACTGTGTGGCCATGGC | 3009 |
| QY | 2246 | GTGTCCGTAGGGGGACCTGCGCTGCGAGGATGGCTGGATGGGGGCGACCTGCGACCAAG | 2305 |
| Db | 3010 | GTCTCGGTAGGAGGACCTGCGCTGTGAGATGGTTGGATGGGGGCGCATGCGACCA | 3069 |
| QY | 2306 | CGGGCTGCGCACCCCGCTGTGCGGAGCATGGGACCTGCGGAGCGGCAAGTGTGGAGTGC | 2365 |
| Db | 3070 | CGGGCTGCGCACCCCGCTGTGCGGAGCATGGGACCTGCGGAGCGGCAAGTGTGGAGTGC | 3129 |
| QY | 2366 | AGCCCTGGCTGGAATGGCGMACACTGCACCATCGCTCACTATCTGGATAGGATAGTTAA | 2425 |
| Db | 3130 | ACCCCGGCTGGAATGGAGAGCACTGCACATC----- | 3162 |
| QY | 2426 | GAGGGTTGCTTGGGTTGTGCAATGGCAAACGACAGATGTACTTAGACTGAATGGTTGG | 2485 |
| Db | 3163 | GAGGGCTGTCTGGCTTGTGCAATGGAAATGGACATGTACCTTGGACCTGAAATGGTGG | 3222 |
| QY | 2486 | CACTGCGTGTGCGAGCTGGGCTGGAGAGGAGTGGCTGTGACACTTCCATGGAGACTGCC | 2545 |
| Db | 3223 | CACTGTGTGTCAGCTGGGCTGGGAGGAGTGGCTGTGACACTTCCATGGAAACGGGC | 3282 |
| QY | 2546 | TGCGGTGACAGCAAAAGACAATCATGGAGATGGCTGTGGACTGCATGGAGACCTCACTGC | 2605 |
| Db | 3283 | TGTGAGACGGCAGGACAAACGACGGAGTGGCTTGTGGAGTGCATGGACCTGACTGC | 3342 |
| QY | 2606 | TGCCTCCAGCCCTGTGCGCATATCAACCGCTGTGCTTGGCTTCCCTTAAACCTCTGGAC | 2665 |
| Db | 3343 | TGCCTCCAGCCCTGTGCTCATGTCAACCGCTGTGCTTGGCTTCCCTTAAACCTCTGGAC | 3402 |
| QY | 2666 | ATCATCCAGGAGACACAGTCTCTGTGTCAAGCAGAACCTACACTCTTCTATCAGCCG | 2725 |
| Db | 3403 | ATCATCCAGGAGACACAGTCTCTGTATCCAGCAGAACCTGAATCTCTTCTACCATGCA | 3462 |
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| Db | 3523 | GGAGGSCATGCTGTGTATTCTGTGGCCAAAGTGTGATGACATCAGATGGGACCCCTTGGTT | 3582 |
| QY | 2846 | GGTGTGAACATCAGTTTCTCAATACCCCTCTCTTTGGATATACAAATCAGCAGGCAAGAT | 2905 |
| Db | 3583 | GGCGTGAACATCAGTTTCTCAATACCCCTCTCTTTGGATATACAAATCAGCAGGCAAGAT | 3642 |
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| QY | 2966 | CTTTTCATCACAGAGACACCCCTGTGGTGCCATGGGATGGCTTCTTTGTCAATGNA | 3025 |
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| QY | 3086 | CGCCCCAACCCAGTCTCTCTCCATCCCACTGACGCTCTCTTCCGACGCTCTGTGAGAG | 3145 |
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| QY | 3146 | AAAGGCCCAATTGTGCGGGAATTTCAAGCTTTGACAGGAGAAATCTCTATCTTGTGCTGC | 3205 |
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| QY | 3206 | AAATGAGGCTGAGCTACCTGAGCAGCCGACCCCTGGCTACAAATCTGCTCTGAGATC | 3265 |
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| QY | 3266 | AGCTCACCCACCCGACCATCCCTTCAACCTCATGAGAGTGCACCTCATGAGCGGTG | 3325 |
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| QY | 3326 | GAGGGCCGCTCTTCAAGAAAGTGTTCGCTGACGCCACACCTGTCTCTATTATTTTCAAT | 3385 |
| Db | 4063 | GAGGGCCGCTCTTCAAGAAAGTGTTCGCTGACGCCACACCTGTCTCTATTATTTTCAAT | 4122 |
| QY | 3386 | TGGGACAAGACAGACGCTTACAACAGAGGTGTGTTGGGCTTTTCAGAAAGCTTTGTTTC | 3445 |
| Db | 4123 | TGGGACAAGACAGATGTCTACAAACAGAGGTGTGTTGGACTCTCAGAAAGCTTTGTTTC | 4182 |
| QY | 3446 | GTGGGTTATGAATATGAAATCTTCCGCGAGATCTAATCTCTGTGGGAAAAAGAACACAGTG | 3505 |
| Db | 4183 | GTGGGTTATGAAATATGAAATCTTCCGCGAGATCTAATCTCTGTGGGAAAAAGAACACAGTG | 4242 |
| QY | 3506 | CTGCAGGCTATGAAATTTGACGCTTCCAAAGCTTGGAGGATGGAGCTTAGACAAACATCAT | 3565 |
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| Db | 4423 | CCAGCTGCAATGCTTGTGATGGCAACAAGCTCTTGGGCCCAAGTGGCCCTCACCTGT | 4482 |
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| QY | 3806 | GGAAATGTCAACCAATCTTAGAGCTGAGGAAATAAGATTTTCAGACATAGTCACAGTCCA | 3865 |
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| QY | 3926 | AACAGCGCGGGCTTTTAAATCAAGTCCATGTGTGGTGAAGGACCTTGTCAAGAAC | 3985 |
| Db | 4642 | AACAGCGCGGGCTTTCAAGGTCAAGTCCACCAAGTGGTGAAGGACCTTGTGAAGAAC | 4701 |
| QY | 3986 | TCTGAGGTGTTGCGGGACAGGTGACCAAGTCCCTCCCTTTTGTATGACATCTGCTGCGGG | 4045 |
| Db | 4702 | TCCGAGGTGTTGAGGAGGACTGGTGACCAAGTCCCTCCCTTTTGTATGACATCTGCTGCGGA | 4761 |
| QY | 4046 | GATGTGGGAAGGCCACAGAAAGCCACATCAACCAATCCAGGGGTATTACAGTGAACAG | 4105 |
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| QY | 4226 | GTCTGAGATATTTCCAGGTGAAGCTGGAGTGGCCCAACAGATTTAGCCATCAACCAATG | 4285 |
| Db | 4942 | GTCTGAGATATTTCTCAGGTTCCGCTGGAGTGGCCCAACAGATTTAGCCATCAACCAATG | 5001 |
| QY | 4286 | GACAACTCATTTTATGTCTCGAACAAATGTGGTCTCTGCAAAATCTCTGAAAAACCCAG | 4345 |

| | | | | | | | | | |
|----|------|--------------------------|---|------|----|------|-------------------------|---|------|
| Db | 5002 | GATAAATCTCTATGTCTCGACAA | CAATGTGGTCTCGAAATCTCCGAAACACACCAG | 5061 | Db | 6082 | GTGGCTTTCAGACTGAGCCACAC | CTGTGGTGGCAGTGTCAACCCCACTGTAGGCAAG | 6141 |
| Qy | 4346 | GTGGCAATGTGCGCGGAGCCCATG | CAGTCCAGGTCCTGGCATTGACCACTTCCCTG | 4405 | Qy | 5426 | AGGAATGTCACTGCTGCCATCGA | CAACGCCTCAACCTGGTGGAGTGGCGCAGCGCAA | 5485 |
| Db | 5062 | GTACGCATTTGCTGGGAGGCCAT | GCACTGGCAGGTCCCTGGCATTCGACCAATTCCTG | 5121 | Db | 6142 | AGGAATGTCACTGCTGCCATTC | GAATGCCTCAACCTGGTGGAGTGGCGCAGCGCAAG | 6201 |
| Qy | 4406 | CTAAGCAAGTGGCCATCTCAGCA | AACTCGGAGTCAGCCAGTTCAGGCTTTTTCACAC | 4465 | Qy | 5486 | GAGCAGGCTCGGGCCAGGTCTA | CTGTCTTTTGGGCGCGCTGCGGTGACAAACCGAAAT | 5545 |
| Db | 5122 | CTGACNAGTAGCCATCCATGCA | CCCTGGAGTCAGCCACTGCTCTGGCCGTTTTCACAC | 5181 | Db | 6202 | GAGCAGGCTCGTGGCCAGGTCA | CCGCTCTTTTGGACCCGCTTTGCGGGTTTCAACACCGAAAC | 6261 |
| Qy | 4466 | AATGGGTCTGTATATTTGCTGA | CTGATGAGAAAAGATCAACCGCATCAGGCAAGTTC | 4525 | Qy | 5546 | CTCTCTCTCTGCACTTTTGTAT | CGCGTAAACGACAGAGAAGATCTATGATGACCAACCGC | 5605 |
| Db | 5182 | AATGGAGTCTGTACATCGCTGA | CCGAGACCGACGAGAAAAAGATCAATCGCATCAGCCAGGTC | 5241 | Db | 6262 | CTCTCTCTCTTGGACTTTGAC | CGGTGCACAGCAGAGAAGATCTACGATGACCATCGC | 6321 |
| Qy | 4526 | ACCACTAGTGGAGATCTCACTC | GTGTGGGGCCCCAGTGGCTGTGACTGTAAAT | 4585 | Qy | 5606 | AAAGTTCAACCTTCGGATTTCT | GACACACGAGGCGCGCCAGCCCTCTGGTCAACCCAGC | 5665 |
| Db | 5242 | ACTACAAAGTGTGAGATCTCA | CTGGTGTGGTGGCCCCAGTGGCTGTGAAAT | 5301 | Db | 6322 | AAAGTTCAACCTTCGGATCTTA | TATGACAGGACGAGGAGCCAGCTTCTGGTCAACCTAGC | 6381 |
| Qy | 4586 | GATGCCAACTGTGATTTTCTG | GAGACGATGTTATGCCAAGGATGCAAAAGTTAAAT | 4645 | Qy | 5666 | AGCAGGCTGAATGGTGTCAAC | CGTGACATCTCCCTGGGGGTTTACATTTGCTGGCATCCAG | 5725 |
| Db | 5302 | GATGCCAACTGTGACTGCTCT | CTGGAGATGATGGTTACGCCAAGATGCAAGCTGAAT | 5361 | Db | 6382 | AGCAGGCTGAATGGTGTAAAT | GTGACTACTCCCTCGAGGTCAATTTGCTGGAAATCCAA | 6441 |
| Qy | 4646 | ACCCCACTCTTCTTGGCTGTG | CTGTGATGGGAGCTCTACGTGGCCGACCTTGGGAAC | 4705 | Qy | 5726 | AGGGGATCATGTCTGAAAGNA | TGGAATACGACCGCGGGCCGCATCAATCCAGATC | 5785 |
| Db | 5362 | ACCCCACTCGTCTTGGCTGT | GCTGACGGGAGCTCTATGTGGCCGACCTGGGAAC | 5421 | Db | 6442 | AGGGGATCATGTCTGAGAGNA | TGGAATATGATCAGGCGGGCGCATCAATCCCGATC | 6501 |
| Qy | 4706 | ATCCGAATTCGTTTATCCGA | AGAACAAAGCTTCTCAACCCAGCAATGATGAG | 4765 | Qy | 5786 | TTGCTGATGGGAAGACATGGA | GTACATCTTACAGAAAGTCCATGGTGTCTACTA | 5845 |
| Db | 5422 | ATCCGAATTCGATTTATCCG | AGAACAAAGCTTCTTCTGAACTCAAGACATGTACGAG | 5481 | Db | 6502 | TTTGAGACGGGNAATGTGGAG | CTACAGTACTTAGAGATCCATGGTGTCTCATCTC | 6561 |
| Qy | 4766 | CTGTCTTCAACCAATTTGAC | AGGAGCTCTATCTGTGTTGATACCAACCGCAAGCACTGTAC | 4825 | Qy | 5846 | CACAGCAGAGGCAATATCTTT | GAGTTTGCACAAAGATGACCGCTCTCTTCTGTGACG | 5905 |
| Db | 5482 | CTATCTCTCCCACTGACACCA | AGGAGCTGTACTCTTTGATACCACTGAGCAAGCATCTGTAC | 5541 | Db | 6562 | CACAGCAGAGGCAATATCTTT | CGAGTTTGCAAGAAATGACCGCTCTCTTCTGTGACC | 6621 |
| Qy | 4826 | ACCCAAAGCTGCCACAGGAGA | CTACCTGTGACAACTTCACTCACTGGGGACGGCAC | 4885 | Qy | 5906 | ATGCCCCAAGTGTGGCGGCA | CACTAGAGCAATCCGCTCAGTGGGCTACTACAGAAAC | 5965 |
| Db | 5542 | ACTCAGAGCTTACCCACAGG | AGGACTACTGTGACAACTTCACTTACACAGGGGACGGGAC | 5601 | Db | 6622 | ATGCCCCAAGTGTGGCGGCA | CGCTGAGACCATCCGCTCAGTGGGCTACTACAGAAAC | 6681 |
| Qy | 4886 | ATCACACTATCACAGACAAAT | TGGCAACATGTTAAATGTCCGCCAGAGCTCTACTGGG | 4945 | Qy | 5966 | ATCTATCAGCCCCCTCAGGG | CAATGCTCAGTACAGAGCTTCACTGAGGATGGGCAC | 6025 |
| Db | 5602 | ATCACATATCACCGAACAAAT | TGGCAACATGTTGAACTGCGCCAGAGCTCTTACCGGG | 5661 | Db | 6682 | ATCTACAGCCCCCGGAGGCA | ACGCTCAGTCTTTCAGGACTTCACTGAGGATGGACAC | 6741 |
| Qy | 4946 | ATGCCCCCTGCTGGTGGTCC | CAGATGGCCAGGTGACTGGGTGACCATGGGCAACCAAC | 5005 | Qy | 6026 | CTCCTTTCACACCTTCTACT | CTGGGCACTGGCCGAGGTTGATATCAAGTATGGAACATG | 6085 |
| Db | 5662 | ATGCCCCCTGCTGGTGGTCC | CAGATGGCCAGGTGACTGGGTGACCATGGGCAACCAAC | 5721 | Db | 6742 | CTGTTTACATACCTTCTACT | TTGGGCAACGCGCGCGGTGATTTTACAAGTATGCAAGTTG | 6801 |
| Qy | 5006 | AGTGCACTCAAGAGTGTGACA | CAAGGACACGAGTTGGCCATGATGACATACCATGGC | 5065 | Qy | 6086 | TCAAAGCTGCGAGAGCTCTGT | ATGACCAACAGGTGAGTTTCACTTATGACGAGACG | 6145 |
| Db | 5722 | AGCGCACTCAGAAAGTGTGA | CCACACAGGACACGAGCTAGCCATGATGACCTACCATGGC | 5781 | Db | 6802 | TCAAAGCTGCGAGAGCTCTGT | ATGACCAACAGGTGAGTTTCACTTACGAGGAGACC | 6861 |
| Qy | 5066 | AATTCGCGCTTCTGGCAACA | AAAGCAATGAAACCGGATGGACAAATTTTATGAGTAC | 5125 | Qy | 6146 | GCAGGCACTGTAAGAACCAT | CAACCTTACAGAAATGAGGGCTTCACTGACCACTCCGCTAC | 6205 |
| Db | 5782 | AACTCTGGCTCTTGGCAACA | AAAGCAATGAAACCGGATGGACAACTTTTATGAGTAT | 5841 | Db | 6862 | GCAGGCACTGTAAGAACCAT | CAACCTTACAGAAATGAGGGCTTCACTTACGATTCGCTAC | 6921 |
| Qy | 5126 | GACAGCTTTGGCGCTGACAA | ATGTCACCTTCCCTACTGCGCAGGTGAGCAGTTTCCGA | 5185 | Qy | 6206 | CGTCAGATTTGGGCGCTGAT | TGACCGACAGATCTTCCGCTTCACTGAGGAGGCAATGGTC | 6265 |
| Db | 5842 | GACAGTTTGGTGCCTTGACA | AAAGCAATGAAACCGGATGGACAACTTTTATGAGTAT | 5901 | Db | 6922 | CGTCAGATTTGGGCGCTGAT | TGACCGACAGATCTTCCGCTTCACTGAGGAGGCAATGGTC | 6981 |
| Qy | 5186 | AGTGATACAGACAGTTTCA | GTCATGTCAGGTAGAGACCTCCAGCAAGGATGATGTCAACC | 5245 | Qy | 6266 | AAGCCCGCTTTTGGCTTGA | CTAACAATGACCAACAGCTTCCGGGTGACGAGGCTGGT | 6325 |
| Db | 5902 | AGCGCACTCAGAAAGTGTGA | CCACACAGGACACGAGCTAGCCATGATGACCTACCATGGC | 5961 | Db | 6982 | AATGCCCGTTTGGTTTACAA | CTATGACCAACAGTTTCCGCTTCACTGAGGCTGGT | 7041 |
| Qy | 5246 | ATAACCAACAACTGTGTGCT | CAGGCGCTTTCACACATCTGCTGCAAGACCAAGTCCGG | 5305 | Qy | 6326 | ATCAACGAGACCCCACTTGC | CACTTGTATCTATGCTATGATGTGTGTCAGGCAAGACA | 6385 |
| Db | 5962 | ATAACCAACCACTGTCTGT | TTGCTGGGTGCTTCTACACCTCTTACACCTGTTTACAAAGACCAAGTCCGG | 6021 | Db | 7042 | ATCAATGAGACCCCACTTGC | CCCACTTACCTTACCGCTATGATGTGTGTCAGGAGACA | 7101 |
| Qy | 5306 | AACAGCTACTACATCGGGCG | AGTGGCTCTTGGCGGCTGCTGGCCACAGGCAATGGATGGAG | 5365 | Qy | 6386 | GAGCAGTTTGGGAAGTTTGG | TGTGTCATTTACTATGACATTAACCCAGATCATCAACACAGCT | 6445 |
| Db | 6022 | AACAGCTACTACATCGGGCG | AGTGGCTCTTGGCGGCTGCTGGCCACAGGCAATGGATGGAG | 6081 | Db | 7102 | GAGCAGTTTGGGAAGTTTGG | TGTGTCATTTACTACGACATCAACCCAGATCATTAACACAGCC | 7161 |
| Qy | 5366 | GTGGCGCTGACAGCTGAGCC | CCCCCACTTGTGGCTGGCACCCTCAACCCCAACCGTGGGCAAG | 5425 | Qy | 6446 | GTATGACCCACACCAAGCA | ATTTTGTATGTCATATGGCAGGATGAAGGAGTGCAGTATGAG | 6505 |
| Db | | | | | Db | 7162 | GTATGACCCCACTCAGAGCA | CTTTTGTGCTTATGGCAGGATGAAGGAGTACAGTATGAG | 7221 |

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 TITLE Direct Submission
 JOURNAL Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Kazusa-kamatari 2-6-7, Kisarazu, Chiba, 292-0818, Japan (E-mail:cdmainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:81-438-52-3913, Fax:81-438-52-3914)
 COMMENT On Aug 5, 2005 this sequence version replaced gi:20521827.
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| Db | 61 | AAGTCGAGTGCAGCCCTGGCTGGAAATGGCGAACA | CTGCACCATCGCTCACTATCTGGAT | 120 |
| QY | 2414 | AGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAAT | TGCAACGGCAGATGTACCTTTAGAC | 2473 |
| Db | 121 | AGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAAT | TGCAACGGCAGATGTACCTTTAGAC | 180 |
| QY | 2474 | CTGAATGGTTGGCACTGGCTCTGCAGAGCTGGGCTG | GGAGGAGCTGGCTGTGACACTTCC | 2533 |
| Db | 181 | CTGAATGGTTGGCACTGGCTCTGCAGAGCTGGGCTG | GGAGGAGCTGGCTGTGACACTTCC | 240 |
| QY | 2534 | ATGGAGACTGCTCGCTGGTGAACAGAAAAGACAAT | TGATGGAGATGGCTGTGACATGTCATG | 2593 |
| Db | 241 | ATGGAGACTGCTCGCTGGTGAACAGAAAAGACAAT | TGATGGAGATGGCTGTGACATGTCATG | 300 |
| QY | 2594 | GACCCCTGACTGCTGCTCCAGCCCTGTCACATATCA | CCCCCTGTGCCCTTCCCTCCCT | 2653 |
| Db | 301 | GACCCCTGACTGCTGCTCCAGCCCTGTCACATATCA | CCCCCTGTGCCCTTCCCTCCCT | 360 |
| QY | 2654 | AACCCCTCTGGACATCATCCAGGAGACACAGGTCC | CTGTGTCTACAGCAGAACCTACACTCC | 2713 |
| Db | 361 | AACCCCTCTGGACATCATCCAGGAGACACAGGTCC | CTGTGTCTACAGCAGAACCTACACTCC | 420 |
| QY | 2714 | TTCTATGACCGCATCAAGTTCTCTGTCGGCAGGGA | CAGCAGCATATATCCCGGGAG | 2773 |
| Db | 421 | TTCTATGACCGCATCAAGTTCTCTGTCGGCAGGGA | CAGCAGCATATATCCCGGGAG | 480 |
| QY | 2774 | AACCCCTTTGATGGAGGCGATCTTGTGTATTCTGT | TATTCGTGGCAAGTATGATCATCATGATGA | 2833 |
| Db | 481 | AACCCCTTTGATGGAGGCGATCTTGTGTATTCTGT | TATTCGTGGCAAGTATGATCATCATGATGA | 540 |
| QY | 2834 | ACCCCTCTGTTGGTGTGAACATCAGTTTGTCAATA | ACCCCTCTCTTTTGGATATACAATC | 2893 |
| Db | 541 | ACCCCTCTGTTGGTGTGAACATCAGTTTGTCAATA | ACCCCTCTCTTTTGGATATACAATC | 600 |
| QY | 2894 | AGCAGCAAGATGGCAGCTTTGATGTTGTTGTTGTT | GTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 2953 |
| Db | 601 | AGCAGCAAGATGGCAGCTTTGATGTTGTTGTTGTT | GTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 660 |
| QY | 2954 | TTTCGAGCGGCACTTTTCATCAGCAGGACACAC | CCCTGTGCTGCTGCTGCTGCTGCTGCTGCTG | 3013 |
| Db | 661 | TTTCGAGCGGCACTTTTCATCAGCAGGACACAC | CCCTGTGCTGCTGCTGCTGCTGCTGCTGCTG | 720 |
| QY | 3014 | TTTGTGATCGAAACCATCATCATGATGAGACAT | TGAGAGATGAGATTCCTGCTGCTGCTGCTG | 3073 |
| Db | 721 | TTTGTGATCGAAACCATCATCATGATGAGACAT | TGAGAGATGAGATTCCTGCTGCTGCTGCTG | 780 |
| QY | 3074 | AGCAATTTTTCGCGCGCCCAACCCAGTCTCTCT | CCATCCCACTGACGTCTTTCGCGCAGC | 3133 |
| Db | 781 | AGCAATTTTTCGCGCGCCCAACCCAGTCTCTCT | CCATCCCACTGACGTCTTTCGCGCAGC | 840 |
| QY | 3134 | TCCTGTGAGAGAAAGGCGCCCATTTGTCGCGGAA | ATTCAGGCTTTGAGGAGGAGGAAATCTCT | 3193 |
| Db | 841 | TCCTGTGAGAGAAAGGCGCCCATTTGTCGCGGAA | ATTCAGGCTTTGAGGAGGAGGAAATCTCT | 900 |
| QY | 3194 | ATCTCTGCTGCAAGATGAGGCTGAGCTACCTGAG | CAGCGCGGACCCCTGGCTACAAATCT | 3253 |
| Db | 901 | ATCTCTGCTGCAAGATGAGGCTGAGCTACCTGAG | CAGCGCGGACCCCTGGCTACAAATCT | 960 |
| QY | 3254 | GTCTGAGGATCAGCCCTACCCACCCGACCATCC | CTTCAACCTCATGAAGTGTGACCTC | 3313 |
| Db | 961 | GTCTGAGGATCAGCCCTACCCACCCGACCATCC | CTTCAACCTCATGAAGTGTGACCTC | 1020 |
| QY | 3314 | ATGCTAGCGGTGAGGCGCGCTCTTTCAGGAAGT | TGTTGCTGTCAGCCCCCAGACCTGTCC | 3373 |
| Db | 1021 | ATGCTAGCGGTGAGGCGCGCTCTTTCAGGAAGT | TGTTGCTGTCAGCCCCCAGACCTGTCC | 1080 |
| QY | 3374 | TATTATTTTTCATTTGGGACAGACAGACGCTCA | CAACCGAGAGGTGTTTGGGCTTTTCAGAA | 3433 |
| Db | 1081 | TATTATTTTTCATTTGGGACAGACAGACGCTCA | CAACCGAGAGGTGTTTGGGCTTTTCAGAA | 1140 |
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 1 GCCTGCGACCGCGGGCTGCCACCCCGCTGTGTCGAGCATGGGACCTGCCGCGACGGC 60

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| QY | 5654 | TGGTCACCACGAGCAGGCTGAATGGTGTCAACGTCGACATACCTCCCTGGGGGTTTACATT | 5713 | 6734 | CTCACACCACTACGGTATGACATCCGCGACCCGACATCACTCGGCTGGGTGACGTCGAATAC | 6793 |
| Db | 3361 | TGGTCACCACGAGCAGGCTGAATGGTGTCAACGTCGACATACCTCCCTGGGGGTTTACATT | 3420 | 4441 | CTCACACCACTACGGTATGACATCCGCGACCCGACATCACTCGGCTGGGTGACGTCGAATAC | 4500 |
| QY | 5714 | GCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATAACGACAGGGCGGCCGCATC | 5773 | 6794 | AAAGTGGATGAGGATGGCTTCTGAGGAGCGGGGGGTGATATCTTTGAGTACAACACTCA | 6853 |
| Db | 3421 | GCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATAACGACAGGGCGGCCGCATC | 3480 | 4501 | AAAGTGGATGAGGATGGCTTCTGAGGAGCGGGGGGTGATATCTTTGAGTACAACACTCA | 4560 |
| QY | 5774 | ACATCCAGGATCTTCGCTGATGGGAAGACATGAGCTACACATATCTTAGAAGATCCATG | 5833 | 6854 | GCTGGCTCTCTCATCAAGGCCCTACAAACCGGGCTGGCAGCTGGAGTGTCAAGTACCGCTAC | 6913 |
| Db | 3481 | ACATCCAGGATCTTCGCTGATGGGAAGACATGAGCTACACATATCTTAGAAGATCCATG | 3540 | 4561 | GCTGGCTCTCTCATCAAGGCCCTACAAACCGGGCTGGCAGCTGGAGTGTCAAGTACCGCTAC | 4620 |
| QY | 5834 | GTGCTGCTACTACACAGCCAGAGCGAGTATATCTTTGAGTTCGACAAAGATGACCGCTC | 5893 | 6914 | GATGGCTGGGGCGGCGCTGTCTCAGCAAGAGAGCCACAGCCACCACTCTGCAGTTCTTC | 6973 |
| Db | 3541 | GTGCTGCTACTACACAGCCAGAGCGAGTATATCTTTGAGTTCGACAAAGATGACCGCTC | 3600 | 4621 | GATGGCTGGGGCGGCGCTGTCTCAGCAAGAGAGCAGCACAGCCACCACTCTGCAGTTCTTC | 4680 |
| QY | 5894 | TCCTTGTGACGATGCCCAACGTTGGCGGCGCAGACACTAGAGACCATTCGCTCAGTGGGC | 5953 | 6974 | TATGCAGACCTGACCAACCCGACCCGACCCCTGACCACTCTGACCAACCACTCCAGCTCTGAG | 7033 |
| Db | 3601 | TCCTTGTGACGATGCCCAACGTTGGCGGCGCAGACACTAGAGACCATTCGCTCAGTGGGC | 3660 | 4681 | TATGCAGACCTGACCAACCCGACCCGACCCCTGACCACTCTGACCAACCACTCCAGCTCTGAG | 4740 |
| QY | 5954 | TACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTCAGTCATACAGGACTTCACT | 6013 | 7034 | ATCACCTCCCTCTACTACTACGACTTGCAGGACACCTCTTTGCCATGGAGCTGAGCAGTGGT | 7093 |
| Db | 3661 | TACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTCAGTCATACAGGACTTCACT | 3720 | 4741 | ATCACCTCCCTCTACTACTACGACTTGCAGGACACCTCTTTGCCATGGAGCTGAGCAGTGGT | 4800 |
| QY | 6014 | GAGGATGGGCACCTCCTTTCACACCTTCTACCTGGGCACCTGGCGCAGGGTGTATACAAG | 6073 | 7094 | GATGAGTTTTTACATAGCTTTGTGACAAACATCGGAGACCCCTCTTGTCTGTCTTTAGTGAACA | 7153 |
| Db | 3721 | GAGGATGGGCACCTCCTTTCACACCTTCTACCTGGGCACCTGGCGCAGGGTGTATACAAG | 3780 | 4801 | GATGAGTTTTTACATAGCTTTGTGACAAACATCGGAGACCCCTCTTGTCTGTCTTTAGTGAACA | 4860 |
| QY | 6074 | TATGGCAAACTGTCAAAAGCTGGCAGAGACGCTCTATGACACCAACCAAGGTTCAGTTCAAC | 6133 | 7154 | GGTTTGATGATCAGCAAAATCTGTACACAGCTATGGGGAGATCTACATGGATACCAAC | 7213 |
| Db | 3781 | TATGGCAAACTGTCAAAAGCTGGCAGAGACGCTCTATGACACCAACCAAGGTTCAGTTCAAC | 3840 | 4861 | GGTTTGATGATCAGCAAAATCTGTGTATACAGCCCTATGGGGAGATCTACATGGATACCAAC | 4920 |
| QY | 6134 | TATGACAGACGGCAGCATCTGTGAAGACCATCAACCTACAGATGAGGGCTTCACTGAC | 6193 | 7214 | CCCAACTTTTTCAGATCATATAGGCTACCATGGTGGCTCTATGATCCACTCACCAAGCTT | 7273 |
| Db | 3841 | TATGACAGACGGCAGCATCTGTGAAGACCATCAACCTACAGATGAGGGCTTCACTGAC | 3900 | 4921 | CCCAACTTTTTCAGATCATATAGGCTACCATGGTGGCTCTATGATCCACTCACCAAGCTT | 4980 |
| QY | 6194 | ACCATCCGCTACCGTACAGTTGGGCCCTCTGATTGACCGACAGATCTTTCGCTTCACTGAG | 6253 | 7274 | GTCCACATGGGCGGCGAGATTATGATGTGCTGGCGGACCGCTGGAGCTAGCCACAGCCAC | 7333 |
| Db | 3901 | ACCATCCGCTACCGTACAGTTGGGCCCTCTGATTGACCGACAGATCTTTCGCTTCACTGAG | 3960 | 4981 | GTCCACATGGGCGGCGAGATTATGATGTGCTGGCGGACCGCTGGAGCTAGCCACAGCCAC | 5040 |
| QY | 6254 | GAAGGCATGTCTCAACGCCGCTTTTGACTACAACCTATGACAAACAGCTTTCGGGTGACGAGC | 6313 | 7334 | GAGCTGTGAAGCACCTTAGTAGCAGCAACGTCATGCTTCTATCTATATGTTCAAA | 7393 |
| Db | 3961 | GAAGGCATGTCTCAACGCCGCTTTTGACTACAACCTATGACAAACAGCTTTCGGGTGACGAGC | 4020 | 5041 | GAGCTGTGAAGCACCTTAGTAGCAGCAACGTCATGCTTCTATCTATATGTTCAAA | 5100 |
| QY | 6314 | ATGACGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCGCTATGATGTG | 6373 | 7394 | AACAACACCCCATCAGCAACTCCAGGACATCAAGTGTCTTATGACAGATGTTAAACAGC | 7453 |
| Db | 4021 | ATGACGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCGCTATGATGTG | 4080 | 5101 | AACAACACCCCATCAGCAACTCCAGGACATCAAGTGTCTTATGACAGATGTTAAACAGC | 5160 |
| QY | 6374 | TCAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATTAACAGATC | 6433 | 7454 | TGGCTGCTCACCTTTTGGATTCCAGCTTACCAACGTCATCCCTGGTTATCCAAACCCAGAC | 7513 |
| Db | 4081 | TCAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATTAACAGATC | 4140 | 5161 | TGGCTGCTCACCTTTTGGATTCCAGCTTACCAACGTCATCCCTGGTTATCCAAACCCAGAC | 5220 |
| QY | 6434 | ATCACCAAGCTGTCTATGACCCACCAACGATTTTGTGATGATGATGATGATGATGATG | 6493 | 7514 | ATGGATGCCATGGAACCTCTTACGAGCTCATCCACACAGATGAACCGCAGGAGTGG | 7573 |
| Db | 4141 | ATCACCAAGCTGTCTATGACCCACCAACGATTTTGTGATGATGATGATGATGATGATG | 4200 | 5221 | ATGGATGCCATGGAACCTCTTACGAGCTCATCCACACAGATGAACCGCAGGAGTGG | 5280 |
| QY | 6494 | GTGACGATGAGATCTTTCGCTCGCTCATGTATCTGATGATGATGATGATGATGATG | 6553 | 7574 | GACACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTACAGAGCAGCTCAAGGCCCTT | 7633 |
| Db | 4201 | GTGACGATGAGATCTTTCGCTCGCTCATGTATCTGATGATGATGATGATGATGATG | 4260 | 5281 | GACACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTACAGAGCAGCTCAAGGCCCTT | 5340 |
| QY | 6554 | GGGCGAGTGTGAAGAGGAGCTGAAGGTAGGACCTTACGCCAATACCACTCCGCTACTCC | 6613 | 7634 | GTCACTTTAGAACCGTTTGGATTCGACCTTATGGCTCCACAAATCACAGCTCCAGCAGGCT | 7693 |
| Db | 4261 | GGGCGAGTGTGAAGAGGAGCTGAAGGTAGGACCTTACGCCAATACCACTCCGCTACTCC | 4320 | 5341 | GTCACTTTAGAACCGTTTGGATTCGACCTTATGGCTCCACAAATCACAGCTCCAGCAGGCT | 5400 |
| QY | 6614 | TATGATGATGATGTGACGGCCAGCTGCAGACAGTCTCCATCAATGACAAAGCCACTCTGG | 6673 | 7694 | CCAAAGACCAAGAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGGGGTCAAGTTTGGC | 7753 |
| Db | 4321 | TATGATGATGATGTGACGGCCAGCTGCAGACAGTCTCCATCAATGACAAAGCCACTCTGG | 4380 | 5401 | CCAAAGACCAAGAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGGGGTCAAGTTTGGC | 5460 |
| QY | 6674 | CGCTACAGCTACGACCTCAATGGGAACTTGACCTTACTGAGCCCTGGGAAACAGTGACCGG | 6733 | 7754 | TTGAAGGATGGCGAGTGACCAAGAGTGTGGCCAAATGAGGATGGCGGAGG | 7813 |
| Db | 4381 | CGCTACAGCTACGACCTCAATGGGAACTTGACCTTACTGAGCCCTGGGAAACAGTGACCGG | 4440 | 5461 | TTGAAGGATGGCGAGTGACCAAGAGTGTGGCCAAATGAGGATGGCGGAGG | 5520 |
| | | | | 7814 | GTTGCTGCCATCTTTGAACCATGCCCCACTACCTAGAGAACCTGCACTTCACTTGTGAGG | 7873 |

| | | | |
|----|------|---|------|
| Db | 5521 | GTTCGTCGCATCTTGAAACCATGCCCACTACCTAGAGAACCTGCACCTTACCACTTGAATGGG | 5580 |
| Qy | 7874 | GTGGATACCCATTACTTTGTGAAACACAGACCTTCAGAAGGTGACCTGGCCATCTCTGGGC | 7933 |
| Db | 5581 | GTGGATACCCATTACTTTGTGAAACACAGACCTTCAGAAGGTGACCTGGCCATCTCTGGGC | 5640 |
| Qy | 7934 | CTCAGTGGGGGGCGGCGAACCCCTGGAGAAATGGGGTCAACGTCACCTGTGTCACAGATCAAC | 7993 |
| Db | 5641 | CTCAGTGGGGGGCGGCGAACCCCTGGAGAAATGGGGTCAACGTCACCTGTGTCACAGATCAAC | 5700 |
| Qy | 7994 | ACAGTACTTAATGSCAGGACTAGACGCTACACAGACATCCAGTCCAGTACCGGGCACTG | 8053 |
| Db | 5701 | ACAGTACTTAATGSCAGGACTAGACGCTACACAGACATCCAGTCCAGTACCGGGCACTG | 5760 |
| Qy | 8054 | TGCTTGAACACACGCTACGGGCAACCGTTGGATGAGAGAGAGCGACGGGTCTCTGGAGCTG | 8113 |
| Db | 5761 | TGCTTGAACACACGCTACGGGCAACCGTTGGATGAGAGAGAGCGACGGGTCTCTGGAGCTG | 5820 |
| Qy | 8114 | GCCCGGCAGAGAGCCGTGCGCCAAAGCGTGGGCCCGCGAGCAGCAGAGACTGCGGGGAAGG | 8173 |
| Db | 5821 | GCCCGGCAGAGAGCCGTGCGCCAAAGCGTGGGCCCGCGAGCAGCAGAGACTGCGGGGAAGG | 5880 |
| Qy | 8174 | GAGGAAGCCTGCGGGCTCGACAGAGGGGGAGAAGCAGCAGCTGTGTGAGCACAGGGCGG | 8233 |
| Db | 5881 | GAGGAAGCCTGCGGGCTCGACAGAGGGGGAGAAGCAGCAGCTGTGTGAGCACAGGGCGG | 5940 |
| Qy | 8234 | GTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAACTGTGCAGAC | 8293 |
| Db | 5941 | GTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAACTGTGCAGAC | 6000 |
| Qy | 8294 | AGCGCCAAACAATCCACTTCATGAGACAGAGCGAGATGGGCCCGGAGGTACACAGAGGA | 8353 |
| Db | 6001 | AGCGCCAAACAATCCACTTCATGAGACAGAGCGAGATGGGCCCGGAGGTACACAGAGGA | 6060 |
| Qy | 8354 | C 8354 | |
| Db | 6061 | C 6061 | |

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RESULT 8
AB026980 linear VRT 05-NOV-1999
LOCUS          9264 bp mRNA
DEFINITION    Danio rerio mRNA for ten-m4, complete cds.
ACCESSION     AB026980
VERSION        AB026980.1 GI:5307784
KEYWORDS       ten-m4.
SOURCE         Danio rerio (zebrafish)
ORGANISM       Danio rerio
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                Cypriniformes; Cyprinidae; Danio.
REFERENCE      1 (sites)
                Mieda, M., Kikuchi, Y., Hirate, Y., Aoki, M. and Okamoto, H.
                Compartmentalized expression of zebrafish ten-m3 and ten-m4,
                homologues of the Drosophila ten(m)/odd Oz gene, in the central
                nervous system
                Mech. Dev. 87 (1-2), 223-227 (1999)
                10495292
                2 (bases 1 to 9264)
                Mieda, M.
                Direct Submission
                Submitted (06-MAY-1999) Michihiro Mieda, Brain Science Institute,
                RIKEN, Lab. for Developmental Gene Regulation; 2-1 Hiroosawa,
                Wako-shi, Saitama 351-0198, Japan (E-mail:mieda@brain.riken.go.jp,
                Tel:81-48-467-9713, Fax:81-48-467-9714)
                Sequence updated (29-Jun-1999).
                Location/Qualifiers
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                        /dev_stage="embryo"
COMMENT
FEATURES
    source

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156 TCGAGTGAAGCCCTCAAAGCTTCGACCGAGACTCCAGACTGCTTATGGCAGCGGTC 502 Db
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503 AAAGACCTGGTGACCATGAGGCGGACGAGTTTCAGCAGACAAGGGCGGACTTTTCTCTC 562 Db
275 CGGAGCTGGGCTGGAGAGAGTAAAGCGCCCTTCACGGGACCTGTACCGGACAGACATT 334 QY
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335 GGCCTGCCCAATGCGGCTACTCCATGCGGGGCTGGCTCTGATGCCACATGAGGCTGAC 394 QY
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535 -----534 QY
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RESULT 9
HSM806812
LOCUS Homo sapiens mRNA; cDNA DKEFZp686K1107 (from clone DKEFZp686K1107).
DEFINITION
ACCESSION BX640737
VERSION BX640737.1 GI:34364828
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 8993)
AUTHORS Pouatka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,
Wewes, H.W., Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
Wiemann, S.
CONSTRM The German Human cDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764

Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp686K11107) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.

source

source

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RESULT 10
AX952856
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DEFINITION Sequence 132 from Patent WO03093305.
ACCESSION AX952856
VERSION AX952856.1 GI:40783120
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1

AUTHORS Lovejoy, D., Chewpoy, R.B., Barsyte, D. and Rotzinger, S.
TITLE Teneurin c-terminal associated peptides (tcap) and methods and uses thereof
JOURNAL Patent: WO 03093305-A 132 13-NOV-2003;
Lovejoy, David (CA); Chewpoy, R. Bradley (CA); Barsyte, Dalia (CA); Rotzinger, Susan (CA)
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| Qy | 1466 | ATTATTGGAGAAAGCCCTCCCTCTTCATACATACACAGTTTGTGAGTGTGGAGCTGTG | 1525 | Qy | 2546 | TGCGGTGCACAGCAAGAACAAACGAAGGAGACGGACTCATTTGACTGCATGGATCTGC | 2605 |
| Dd | 1337 | GTGTACGGCCGGAAGGCTTACCGCTTCCATCTCTCAGTACGACTTTGTGGAATCTAG | 1396 | Dd | 2417 | TGTACAGACAGCAAGAACAAACGAAGGAGACGGACTCATTTGACTGCATGGATCTGC | 2476 |
| Qy | 1526 | GATGGCAGAGGCTCTTAACCCAGGAGGCGGAGCTAGAGGGACCCCGGCCAGTCT | 1585 | Qy | 2606 | TGCTTCAGGCCCTGTGTGCCATATCAACCGCTGTGCTTGGCTCCCTTAAACCTCTGGAC | 2665 |
| Dd | 1397 | GATGTTAGCAGTTTAAATTCGAGAGAGCAGCGGAACTGTGTGAGTCCGAAAGAGCCGG | 1456 | Dd | 2477 | TGCTTCAGAGCTCTCTGCCAAACACGCCCTACTGTCTGGCTGCTGATCTCTCAGAT | 2536 |
| Qy | 1586 | CGGGAACTGTGCCCTCCAGCCATGACAGAGGCTTCATCCAGTATTTGGATTCAGGA | 1645 | Qy | 2666 | ATCATCCAGGAGACACAGGTCCCTGTGTACAGAGAACCTACACTCTTCTTATGACCGC | 2725 |
| Dd | 1457 | CGGCAGGCGAGATCTGTACGCTGCAAGAGCTGGCTTCACTCAGTACTTGGATCTGGA | 1516 | Dd | 2537 | ATCATTAGCCAAAGCCTTCAGACACCATCTCAGCAAGCTGCAAGTCTTCTTATGACCGA | 2596 |
| Qy | 1646 | ATCTGGCATTTGGCTTTTAAATGACGGAAAGGAGTCAAGTGGTTCCTTCTCACC | 1705 | Qy | 2726 | ATCAAGTTCTCTGGGAGGAGCAGCAGCAGATATCCCGGGAGAACCCCTTTGAT | 2785 |
| Dd | 1517 | ATCTGGCATCTGGCTTTTAAACGACGGGAAACCCAGAGCAGTCTCTTTAAACAG | 1576 | Dd | 2597 | ATCAGTTTCTGATGGATCGGATAGCACCCACGCTGCTCTGGAGAAAGTCCGTTCAAT | 2656 |
| Qy | 1706 | ACTGCAATTTAGTCCGTGGATAAATGCGCCAGCAACTGCTATGCGAATGTTGACTGCATC | 1765 | Qy | 2786 | GGAGGCACTGTGTGTTTATTCTGGCCAAAGTGAATGACATCAGATGGAAACCCCTGTGT | 2845 |
| Dd | 1577 | ATCGTTATAGAGTCTGTGTGGAAATGCCCGGAAATGGCCATGGAATGAGAGTGTGT | 1636 | Dd | 2657 | AAGAGTCTTGTGCTCGTCAATCAGAGCCCAAGTACTAACAGCTGATGGAACCCCACTTAT | 2716 |
| Qy | 1766 | TCTGGACCTGCCAGTCTCTCTGGGTTTCTGGGCGCCGACTGTGGCAGAGCCTCTGTC | 1825 | Qy | 2846 | GGTGTGAACATCAGTTTTGTCAATAACCCCTCTCTTTGGATATACAAATCAGCAGGCAAGAT | 2905 |
| Dd | 1637 | TCTGAACTTGGCATTTGTTTCCCGGGTTCTAGTCCGATTTGTTCAAGAGCAGCCTGT | 1696 | Dd | 2717 | GGCGCTCAACGTCTGTTTTTACACTACTCGGAATATGGATATACCAATTTACCGCCAGAT | 2776 |
| Qy | 1826 | CCCGTGTCTGTAGCGGAAATGGCAATACATGAAGGAGCAGTCTTGTGCCAGTGGC | 1885 | Qy | 2906 | GGCAGTTTGAATCTGGTGAGCAAAATGCGGCACTCTCCATCATCTCTCGGTTCCAGCGGCA | 2965 |
| Dd | 1697 | CCGGTGTCTGTAGTGGCAACGGCAATACTCCAGGGCCGCTGCTGTGCTTCAAGTGC | 1756 | Dd | 2777 | GGAAATTTGACTGTGGTGGCAAAATGTTGGCGCTTCTCTGACTTTGGTATTGAGCGGTTCC | 2836 |
| Qy | 1886 | TGGAAGGCGCTGAGTGGAGTGGCCCAACCAACAGTGTATCGATGTGGCTGCGAGCAAC | 1945 | Qy | 2966 | CTTTTCATCACAGGAGCACACCTGTGGCTGCCATGGGATCGCTCTTCTTCATGGA | 3025 |
| Dd | 1757 | TGGNAGGCGACCGAGTGTGACGTGCCGACGACCCAGTGTGATGACCCGAGTGGCGGGT | 1816 | Dd | 2837 | CAATCTCTCAGTACAGTACACACTGTGTGGAATTCCTCGGAATGTCTTTTATGTGATGAT | 2896 |
| Qy | | | | Qy | 3026 | ACCATCATCATGAGCATGAGGAGATGAGATTTCCAGCTGTGACCTGAGCAATTTTGGC | 3085 |

| | | | | | | | |
|----|------|---|------|----|------|--|------|
| QY | 5243 | ACGTAACCAACCAACCTGTCTGCTCAGGCGCTTCTACACACTGCTGCAAGCAACGATC | 5302 | QY | 6323 | GTGATCAAGGAGACCCACTGCCATTGATCTCTATCGCTATGATGATGTGTGTCAGGCAAG | 6382 |
| Db | 5114 | AGCATCACTTGGAACTTGTCTCCTCATCGATTCTTCTACACCATGGTCCAGAACGATTA | 5173 | Db | 6194 | GTTCATCAATGAACACCACTGCCATTGATCTATACCAAGTTTGTATGACATCTCTGCGAAA | 6253 |
| QY | 5303 | CGGAACAGCTACTACATCGGGGCGATGGCTCTCTTGGCGGTGCTGTGCGCAACGGCATG | 5362 | QY | 6383 | ACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTCTATGACATTTAACAGATCATCACCA | 6442 |
| Db | 5174 | AGAAACAGTTACAGATTGGTATGATGGTCTCCCTTAGAATCTTCTATGCGCAGTGTCTG | 5233 | Db | 6254 | GTGAGCAGTTTGGAAAAATTCGAGTGATATACGACATCAACCAAAATCATTTCCACG | 6313 |
| QY | 5363 | GAGTGGCGCTGACAGATGAGCCCCACTTGTGCTGCGACCGTCAACCCACCGTGGGC | 5422 | QY | 6443 | GCTGTATGACCCACACCAAGCAATTTTGTATGTCATATGGCAGGATGAAGAACTGCAGTAT | 6502 |
| Db | 5234 | GACTCTCACTACAGACAGACCCACGTTCTGCTGCGACGGCGAATCCCAAGTAGCC | 5293 | Db | 6314 | GCGTGTATGACTTATACAAAGCAGCTTTGATGCTCATGGCGCATCAAGAGATCCAATAT | 6373 |
| QY | 5423 | AAGAGGATGTACAGTCCCATCGACAAACGGCTCAACCTGTGGAGTGGCGCCAGCGC | 5482 | QY | 6503 | GAGATCTTCGCTCGCTCATGTACTGATGACCGCTGAGTATGATAAATGATGGGCGAGTA | 6562 |
| Db | 5294 | AAAGAAACATGACTCTTCCCGGTGAGAACGGCGAGAACTCTGGTGGAGTGAGATTCCGA | 5353 | Db | 6374 | GAGATATTTAGGTCAGTCACTCATGTACTGGAATTAACAATTCATATGATAATATGGCGGGTA | 6433 |
| QY | 5483 | AAAGAGCAGGCTCGGGGCGAGGTCACTGTCTTTGGGCGCGCTGCGGCTCAATGGCGC | 5542 | QY | 6563 | GTGAAGAAAGGAGGTGAAGGTAGGACCTACGGCCATACCACTCGCTACTCTCTATGAGTAT | 6622 |
| Db | 5354 | AAAGAAACAGCCAGGCGAAAGTCAACGTATTCGGCGGAACTCAGGGTCAATGGCGC | 5413 | Db | 6434 | ACCAAGAGAGAGATTAAAAATTTGGGCTTTTGGCCACACTACCAATACCGGTACGAGTAC | 6493 |
| QY | 5543 | ATCTCTCTATCTCTGACTTTTGATCGCTAAACGSCACACGACAGAGAAATCTATGATGACC | 5602 | QY | 6623 | GATGCTGACGGCGAGCTGCAGACAGTCTCCATCAATGACAAGCCACTCTGGGCGCTACAGC | 6682 |
| Db | 5414 | AACTTACTCTCAGTGGACTTTGATCGGACCAACCAAGACGGAAGATCTATGATGACCAC | 5473 | Db | 6494 | GAGTGTATGAGCAGCTCCAAACAGTTTACCTAAACGAAAAAGATCATGTGGCGGTACAAC | 6553 |
| QY | 5603 | CGCAAGTTCACCTTTCGGATTCTGTACGACGAGCGGGGGCGCCAGCCTCTGTGTACCC | 5662 | QY | 6683 | TACGACCTCAATGGGAACCTGCACTTACTGAGCCCTGGGAACAGTGCACGGCTCACACCA | 6742 |
| Db | 5474 | CGGAATTTCTCTGAGGATCGCTTACGACAGCTCGGGCGACCCGACTCTCTGGGTGCGC | 5533 | Db | 6554 | TACGACCTAAATGGAAACCTTCCACTTGTCTCAACCCAGCAGCAGCGCCGCTGACCCCT | 6613 |
| QY | 5663 | AGCAGAGGCTGAATGGTGTCAACGTGACATCTCCCTGGGGTTACATTTGCTGGCATC | 5722 | QY | 6743 | CTAGGTTATGACATCGCGACCGCATCTCGGCTGGGTGAGCTGCAATACAAAGATGGAT | 6802 |
| Db | 5534 | AGTAGCAACTAATGCGAGTGAACGTCACTTACTCATCCCGGTCAATTTGCCAGCATC | 5593 | Db | 6614 | CTGCGCTATGACCTGCGCGACAAATCAACCCGCTGGCGATGTTTCACTACCGGTGGAT | 6673 |
| QY | 5723 | CAGAGGGGATCATGTCTGAAAGAAATGGAAATACGACGAGGGGGCGGCAATCAATCCAGG | 5782 | QY | 6803 | GAGGATGGCTTCTGAGGCGACGGGGGTGATATCTTTTGTAGTACAACTCAGTGGGCTG | 6862 |
| Db | 5594 | CAGAGAGGACCAACGAGCGAAAGGTGGACTATGACAGCCAGGGGAGGATCGTATCTCGG | 5653 | Db | 6674 | GAAGTGTTCCTGCTCAGAGGGGCACCTGAAATTTTGAATACAGCTCAAAAGGGCTT | 6733 |
| QY | 5783 | ATCTTCGTGATGGGAAGACATGAGCTACATCTTATAGAAATCCATGGTGTCTGCTA | 5842 | QY | 6863 | CTCATAGGCGCTTACAACCGGCTGGCAGCTGGAGTCTCAGGTACCGCTACGATGGCGCTG | 6922 |
| Db | 5654 | GTCTTTGCGGATGGGAAACATGGAGTTACAGTACTTGGAAAGTCCATGGTCTTCTG | 5713 | Db | 6734 | CTGATCAGTCTACAGTAAAGGCGAGTGGCTGGACAGTATCTATCGGTACGAGCGCTG | 6793 |
| QY | 5843 | CTACACGCGCAGGCGAGTATATCTTTGAGTTTCGACAAAGATGACCGCTCTCTCTGTG | 5902 | QY | 6923 | GGGCGGCGGTCTCCAGCAAGAGCAGCCACAGCCACCACTGCGAGTTCTTCTATGACAGAC | 6982 |
| Db | 5714 | CTCCATAGCCAGCGGAGTACATCTTCGAATACGACATGTGGACCGCTGTCCGCCATC | 5773 | Db | 6794 | GGAAGAGTGTCTTAGCAAAACCCAGCTGGGACAGCACCTTTCAGTTTCTACGCGGAC | 6853 |
| QY | 5903 | ACGATGCCAACTGTGGCGGCGACACCTAGACACCATCGCTCAGTGGGCTACTACAGA | 5962 | QY | 6983 | CTGACCAACCCCAACAGGTCAACCACTGTACAAACACTCCAGCTCTGAGATCACCTCC | 7042 |
| Db | 5774 | ACCATGCCAGTGTGGCTGCCACACCATGCGACACCATCGGTCCATGGCTACTACCGC | 5833 | Db | 6854 | CTGACATACCCCAAGAGAAATTAATCAGCTTACAAACCATTCAGTTTCAAGAAATCACCTCC | 6913 |
| QY | 5963 | AACATCTATCAGCCCTGAGGGCAATGCTCAGTCTATACAGGACTTCTACTGAGGATGGG | 6022 | QY | 7043 | CTCTACTACGACTTGAAGGACACCTCTTTTGCCATGGAGCTGAGCAGTGGTGTGATGATTT | 7102 |
| Db | 5834 | AACATCTACAAATCCCCAGAAAGCAATGCTCTATCATCACCGACTACAACGAGGAAGG | 5893 | Db | 6914 | CTGTACTATGACCTCCAAAGGACATCTCTTCGCCATGGAGATCAGCAGTGGGGATGAGTTC | 6973 |
| QY | 6023 | CACCTCTTCCACACTTCTACCTGGGCACTGGCGCGAGGTGATATACAAAGTATGCAAA | 6082 | QY | 7103 | TACATAGCTTGTGAACAACATCGGACCCCTCTTGTGTCTTTAGTGGACAGGTTTGTATG | 7162 |
| Db | 5894 | CTGCTTCTGCAACAGCTTCTCTGGGAAACGAGTGGAGGGTCTTATTCAGTATAGAAG | 5953 | Db | 6974 | TACATCGCTCGGACAAACACGCGGACACCGCTGCTGTTTTTTCAGCAGCAACGGGCTCATG | 7033 |
| QY | 6083 | CTGTCAAGCTGGCAGAGAGCTCTATGACACCAACCAAGTCAAGTTTCACTATGACGAG | 6142 | QY | 7163 | ATCAAGCAAAATCCTGTATACAGACCTTATGGGAGATCTACATGGATACCAACCCCACTTT | 7222 |
| Db | 5954 | CAGACCAAGGCTATCAGAAATTTTATACGACAGACAAAGTCAAGTTCAGTTTACCTACGAG | 6013 | Db | 7034 | CTGAAACAGAGCCAGTACACTGCTTATGGTGTGATCTACTTTGATCTCCCAAGTGCACATTT | 7093 |
| QY | 6143 | ACGCGAGGATGCTGAAGACCATCAACCTTACAGAAATGAGGCTTCACTGCAACATCCGC | 6202 | QY | 7223 | CAGATCATCATAGGCTACCATGGTGGCTCTTATGATCCACTCACCAAGCTGTCCACATG | 7282 |
| Db | 6014 | ACAGCGGATCTCTGAAACAGTAAACCTTCAGAGTGTGTTTATTTTCACCAATTAGA | 6073 | Db | 7094 | CAGCTGGTAAATTTGGATTCCAGGGGCTTGTATGACCGGCTCACCAAACTAATTCACATTT | 7153 |
| QY | 6203 | TACCGTCAAGTGGGCGCTGATTGACGACAGATCTTCGCTTCACTGAGGAGGCAATG | 6262 | QY | 7283 | GGCGGCGAGATTATGATGTGCTGGCGGACGCTGAGCTAGCGCCAGACCCAGAGCTGTGG | 7342 |
| Db | 6074 | TACAGGCAAAATGGTCTCCCTGATTGACAGACAGATTTTTCGCTTTCAGCGAGGATG | 6133 | Db | 7154 | GGAGAAAGAGATTATGACATTTTGGCGGGAAGATGGAACCAACCGGACATTTGAATCTGG | 7213 |
| QY | 6263 | GTCAACGCGCTTTTGACTACAACTATGACAAACAGTCTTCGGGTGACCAAGCATGACGGCT | 6322 | QY | 7343 | AAAGCACTTTAGTAGCAGCAACCGTCAATGCTCTTTTAAATCTCTATATGTTTCAAAAACAAAC | 7402 |
| Db | 6134 | GTAAATGCGAATTTGACTATAGCTACGACAAACAGCTTTCGAGTGCACAGCATGACGGT | 6193 | Db | 7214 | A---AAAGATCGGAAGGACCCCTGCTCTCTTTTAACTGTATATGTTTCGGAATAACAAC | 7270 |
| | | | | QY | 7403 | CCCATCAGCAACTCCCGAGACATCAAGTCTTCATGACAGATGTTTAAACAGCTGGCTGCTC | 7462 |

EFYIASNTGTPLAVSSNGLMLKQTOYTAYGEIYFDSNVDPOLVIFPHGLYDPLTK
LIHFGRDYDILAGRMTTPDIEIKWIKIDKDPAPFNLYMERNNNPASKIHDVKDYITDV
NSMLVTFGFLHNAIPFPVPKFDLPSPYELVKSQWEDVPPIFGVQOQVARQAKAF
LSLKGMAEVOVSRKAGAEQSWFATVLSLIGKVMYLAQSRVGTINVLINANEDCI
KVAALNNAFVLENLHFTIEGKDTHTPIKTTTPESDLGTLRLSRKALENGINVTVS
QSTTVNGRTRRRPADVEMQFALALHVRVYGTDESKARILEQARALARAWAREQQ
RVDRBEGARLNTBEXKQLLSAGKVQGYDGYVLSVEQYPELADSNANIQFURQSEI
GKR"

ORIGIN

Query Match 42.4%; Score 3544.6; DB 9; Length 8964;
Best Local Similarity 65.6%; Pred. No. 0;
Matches 5458; Conservative 0; Mismatches 2679; Indels 186; Gaps 12;

| | | | |
|----|-----|--|-----|
| Qy | 35 | ATGACGCTGAAGGAGAGAGCCTTACCGCTCGCTGACCCGGCGC---CGCGAGCCGAG | 91 |
| Db | 50 | ATGGATGTGAAGGAACGAGGCTTACTGCTCTTGACCAAGAGACAGCGGAAGAA | 109 |
| Qy | 92 | CGCCGTACACAGCTCGTCGCGACACAGCAGGAGGCAAGGCC---CGCAAAATCG | 148 |
| Db | 110 | AGGCGCTATACAAATTCGTCGCGACCAATGAGGAGTGTAGGTCGCCACGAGAATCC | 169 |
| Qy | 149 | TACAGCTCCAGCGAGACCTGAAGCGCTACGACGAGG---ACGCCGCTAGCCTATGGC | 205 |
| Db | 170 | TATAGTTCCAGTGAAACCTTGAAGCTTCGATCATGATTAATTCACGGCTGCTTATGGA | 229 |
| Qy | 206 | AGCCGCTCAAGGACATTTGTCGCGGAGGCGGAGGAATTCGCGCACAGGTGCCAAC | 265 |
| Db | 230 | AACAGAGTAAGAGATTGTGTCCAGAGAGGCGGAGGATGATACAGAGGACAGAA | 289 |
| Qy | 266 | TTCAACCTCGGGAGCTGGGGCTGGAGAAAGTAAAGCCCGCTCACGAGACCTGTACCGG | 325 |
| Db | 290 | TTTACCTAAGGCAGTTAGGAGTGTGTAATCCGAACTCGAAGAGGAGTGCGCATCTGT | 349 |
| Qy | 326 | ACAGACATTTGGCTGCGCCATCGGCTACTCATGGGGCTGGCTCTGATCCGACATG | 385 |
| Db | 350 | CGCGAAATGGGCTCCCTCACAGAGGTACTCCATCAGTGCAGGTGAGTCCGATAGC | 409 |
| Qy | 386 | GAGGCTGACACGTGTGCTCCCTGAGCACCCCGTGCCTGTGTGGGCGGAGGACACGG | 445 |
| Db | 410 | GAATAAGACAGTGTGCTCCCTGAGCATGCCATGAGACTTTGGGCGAGGGGGTCAAA | 469 |
| Qy | 446 | TCAGGGCGCAGCTCTGCTGTCAGCGCGGCAATTCNAATCTCACACTCACCGACAC | 505 |
| Db | 470 | TCGGGCGCAGTTCTGCTGTCAAGCGGTCAACTCCGCGCTCACTCCCTGACAGACG | 529 |
| Qy | 506 | GAGCATGAACACTGAGATGATCATCCGGGCGGCTGCAGAACCAACGCGGGCTCCGG | 565 |
| Db | 530 | GAGCAGAGAACAGGTGGACAGTGTAGAGCGGACCACTTCAAAACCAACCGGCAACCC | 589 |
| Qy | 566 | ACGCGCGCGCGCTCTGCGACCGCCACACCCCGAACAGCACCACGCGGCTCCATT | 625 |
| Db | 590 | ACCTCGACGCTTTGCGCCATCCACAGCAGCACCCGCGCAGCATACCCGTCATC | 649 |
| Qy | 626 | AATCCCTGAACCGGGCACTTCCAGCGGAGGACCAACCCCGCGGCTCCCGACCGGAC | 685 |
| Db | 650 | ACTTCCCTCAATAGAACTCCCTGACCAATAGAGAACACAGAGTCCGCGCGCGGCT | 709 |
| Qy | 686 | CACCTCGCTCTCGGAGAGCCCTGCGCGCGGCGCCAGGAGCTGCGCACCGCCAGGAG | 745 |
| Db | 710 | GCTTTGCGCGGAGCTGCAAC-----CACACCCGAGTCCGTCAGCTGCGGAC | 760 |
| Qy | 746 | AACTGGCTGTCAACAGCAACATCCCTCGGAGACCCAGGACCTTAGGCAAGCAGCATTC | 805 |
| Db | 761 | AGCTGGCTTGGCAGTAATGTATCCACTGTGAAGAGAGGAGCATTT----- | 804 |
| Qy | 806 | CTAGGACATTCAGGACAACTCATTTAGATGGACATTTCTCGGCGCTCCCGCATGAT | 865 |
| Db | 805 | ----- | 804 |
| Qy | 866 | GGGGCTTACAGTGACGGGCACTTCTCTTCAAGCTGGAGCACTCCCGCTCTTCTGCG | 925 |
| Db | 805 | -----CCTATTCAAAACAGGAGCAGGGACGACGCCACTGTTAGT | 844 |

| | | | |
|----|------|--|------|
| Qy | 926 | ACCACATCACAGAGGTACCCACTGACGTCAGACAGTGTACTCTCTCGCGCCCGACCC | 985 |
| Db | 845 | ACGGCAACCCCGGATACACAATGGCATCTGCTCTGTTATTCTCCGCTTACCGCGCA | 904 |
| Qy | 986 | CTGCCCGCAGACACCTTCGCCCGCGCGCTTTAACTCAAGAGCCCTCAAGTACTGT | 1045 |
| Db | 905 | CTTCTAGAAACACCCATATCAAGAGTCTTTAAATTTCAAGAGTCTTTCAAGTACTGC | 964 |
| Qy | 1046 | AACTGGAAGTGGCAGCCCTGAGCGCCATCTCATCTCAGCCACTCTGGTCATCTCGCTG | 1105 |
| Db | 965 | AGCTGGAGTGCACCGCACTGTGTGCTGTAGGGGTCTCAGTGTCTCTGGCCATTTCTCTC | 1024 |
| Qy | 1106 | GCATATTTTGGCCCATGCACTGTTTGGCTTAACTGGCACCTGCGCCAGCATGAGGGG | 1165 |
| Db | 1025 | TCTATTTTATAGCAATGCACTCTATTTGGCTCTCACTGGCACTTACAGCAGCGGAAAT | 1084 |
| Qy | 1166 | CAGATGTATGAGATCACCGAGGACACAGCAGCAGTTGGCTGTGCCAACCGACCTGCC | 1225 |
| Db | 1085 | GACACATTCGAGA-----ATGGAAGAGTGAATCTGACACCGTGCACCAACACTGTA | 1138 |
| Qy | 1226 | CTATACCTCTCAGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAGAACCA | 1285 |
| Db | 1139 | TCGTTTACCTTCTGGCGACA----- | 1157 |
| Qy | 1286 | GAAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAGTTTCAATAGATCTCGGAGAAATGAT | 1345 |
| Db | 1158 | -ATGGAATATTAGTGTGATTTACACATGAAATAAACCATAGATTCGCGAGAACTGTAT | 1216 |
| Qy | 1346 | GTGGGAAGGGAGCCTCCAGAGATTTCTCTGGCACTTTCTGGAGATCTCAAGTGTTC | 1405 |
| Db | 1217 | ATTGGCGGAGAGCAATCAAGAGGTTCCCGCGGATCTTCTGGAGATCGCAGCTCTT | 1276 |
| Qy | 1406 | ATAGACCATCTGTGATCTGAAATTTCAATGTCTCTGGGAAAGGACGCCCTGGTGGC | 1465 |
| Db | 1277 | ATTGATCAGCAAGTTCTTAAAGTTCAACATCTCTTCAGAGAGTATGATTCGGA | 1336 |
| Qy | 1466 | ATTTATCGCAAAAGGCCCTCCCTCTTCAATACACAGTTTTCAGTTTGGAGCTGCTG | 1525 |
| Db | 1337 | GTGTACGGCGGAGGGCTTACCGCTTCCCATCTACTCAGTACGACTTTTGGAACTACTG | 1396 |
| Qy | 1526 | GATGGCAGGAGCTCTTAACCCAGGAGCGCGAGCCTAGAGGGGACCCCGCGCAGTCT | 1585 |
| Db | 1397 | GATGGTAGCAGTTAATTCGAGAGAGCAGCGGAACCTGGTGGAGTCCGAAGAGCGCGG | 1456 |
| Qy | 1586 | CGGGAACTGTGCCCCCTCCAGCATGAGACAGGCTTCACTCCAGTATTTGGATTCAAG | 1645 |
| Db | 1457 | CGGCAGGCGAGATCTGTGAGCTGCAGAAAGCTGGCTTCATCCAGTACTTGGATTCTGGA | 1516 |
| Qy | 1646 | ATCTGGCACTTGGCTTTTACAATGACGGAAGAGTCAAGAGTGGTTCCTTTCTCAC | 1705 |
| Db | 1517 | ATCTGGCATCTGGCTTTTTTATAACGACGGGAAACCCAGAGAGGTCCTCTTTAAACAG | 1576 |
| Qy | 1706 | ACTGCCATTTAGTCTGGTGATAACTGCCCCAGCAACTGCTATGGCAATGGTGCATC | 1765 |
| Db | 1577 | ATCGTTATAGAGTCTGTGTGGAATGCCCCGAAATTCCTATGGAAATGGAGAGTGTGT | 1636 |
| Qy | 1766 | TCCTGGCACTGCACTGCTTCTGGGTTCTGGCCCCGAGCTGTGGCAGAGCTCTCTGC | 1825 |
| Db | 1637 | TCCTGAACTTGCATTTGTTTCCCGGGTTTCTAGTCTCGGATTTGTTCAAGAGCAGCTGT | 1696 |
| Qy | 1826 | CCGCTGCTCTGTAGCGGAAATGCGCAATACATGAAGGAGCAGATGTTGTGCCACAGTGGC | 1885 |
| Db | 1697 | CCGCTGCTCTGTAGTGGCAACGGGCAATACTCAAGGGCGCGCTGCTGTCTGCTAGTGGC | 1756 |
| Qy | 1886 | TGGAAGGCGCTGAGTGCATGTGCCACCAACCAAGTGTATCGATGTGSCCTGCGACAA | 1945 |
| Db | 1757 | TGGAAGGCGCACAGTGTGACGTGCGGACGACCAAGTGCATTTGAACCCGAGTGGGGGT | 1816 |
| Qy | 1946 | CATGGCACCTGCATCAGCGGCACTGTCATCTGCAACCTTGGCTTACAGGGCGGAGCTGT | 2005 |
| Db | 1817 | CGTGGGATTTGCATCATGCGCTCTTGGCTTGTAACTCGGATACAAAGAGAGAACTGT | 1876 |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|------|--------|-------|------|------|------|------|-----|------|------|--------|-----|------|-----|-------|------|-----|------|-----|------|-----|------|------|-----|------|------|------|----|----|----|------|----|----|------|------|------|------|-------|------|------|
| Qy | 2006 | GAGGAA | TGGA | CTGC | ATG | GCAC | CCCA | ATG | TTT | CAGG | CCCGGG | TGT | CTCG | TG | GAGAG | CGCG | AA | 2061 | | | | | | | | | | | | | | | | | | | | | | |
| Db | 1877 | GAGGAA | CGGAC | TGCT | CT | PAGA | CCCT | TGG | ATG | TTT | TAAT | CAC | CGGG | TGT | GTAT | TCC | ATG | CGG | AA | 1936 | | | | | | | | | | | | | | | | | | | | |
| Qy | 2066 | TGCAT | TGCT | TTG | TGG | ATG | CGG | AGG | CAC | CA | CTG | CG | GAG | AC | CC | C | C | CGG | CC | CA | CTG | CTTA | 2125 | | | | | | | | | | | | | | | | | |
| Db | 1937 | TGT | CAC | TG | CAAT | CC | CAG | GCT | CGGG | TGG | CAG | CA | CT | GT | GAAT | AT | CT | G | A | AG | AT | TGT | GTG | CA | 1996 | | | | | | | | | | | | | | | |
| Qy | 2126 | GACCAG | TG | TTT | CAGG | CC | CAG | AA | CTT | CT | CC | CG | G | A | C | AC | CGG | GG | CTT | T | G | C | AG | CTG | CA | 2185 | | | | | | | | | | | | | | |
| Db | 1997 | GACCAG | TGCT | CAG | CC | CAG | CC | CAG | GA | CTT | AC | TTT | CA | GA | AA | AG | CG | GC | CT | T | G | C | AG | CTT | CG | CA | 2056 | | | | | | | | | | | | | |
| Qy | 2186 | AGCTG | GA | CTG | GA | C | AG | CA | CTG | TTT | CT | AT | CG | AG | AT | CT | GT | CT | C | CG | A | CT | TGT | TGT | GC | AT | 2245 | | | | | | | | | | | | | |
| Db | 2057 | AA | TTG | GA | CT | TG | CCCC | CG | CA | CTG | CT | CA | AA | T | GA | AA | T | AT | T | G | T | C | AG | TG | GA | CT | C | CA | CG | GC | 2116 | | | | | | | | | |
| Qy | 2246 | GTG | TG | CG | CT | PAG | GGG | CA | CT | C | CG | CT | CG | G | AG | AG | TG | CG | T | G | GA | TG | GGG | CAG | CT | C | CG | AC | CG | AG | 2305 | | | | | | | | | |
| Db | 2117 | GT | CT | TG | CA | TGG | GGG | G | CT | C | T | G | T | C | G | T | G | A | A | G | G | CT | G | GA | C | CG | G | CT | G | T | AT | CT | AG | 2176 | | | | | | |
| Qy | 2306 | CGG | GC | CT | GC | CA | CC | CG | CG | CT | G | T | G | C | G | A | CT | G | G | A | CT | G | G | CA | CT | G | C | G | CA | CT | G | AG | T | GC | 2365 | | | | | |
| Db | 2177 | AG | AG | CT | T | GC | CA | CC | CT | C | G | CT | G | T | G | CT | G | A | C | CG | G | AG | CT | G | C | G | AG | T | G | C | AG | T | GC | 2236 | | | | | | |
| Qy | 2366 | AG | CC | CT | GG | CT | G | GA | AT | TG | CG | AA | C | AG | CT | G | CA | CT | AT | CT | T | G | GA | T | AG | GG | T | AG | T | T | A | A | A | 2425 | | | | | | |
| Db | 2237 | AG | CC | AA | G | TG | GA | AC | CG | G | A | CA | CT | G | C | A | AA | T | T | G | C | T | C | A | T | T | T | G | GA | T | A | GA | T | AG | T | T | AA | 2296 | | |
| Qy | 2426 | GAG | GG | T | T | GC | AT | TG | GC | AA | TG | GC | AA | CG | G | CAG | AT | G | T | AC | CT | T | AG | AC | CT | G | GA | CT | G | GA | T | GT | TG | G | 2485 | | | | | |
| Db | 2297 | GAG | GG | T | T | GC | CC | CG | CT | T | G | T | G | CA | CAG | CA | AT | TG | GG | AG | A | T | G | C | A | CT | T | G | G | A | A | A | A | A | CG | CT | G | 2356 | | |
| Qy | 2486 | CAC | T | GC | CT | T | GC | CA | AG | CT | G | GG | CT | G | G | A | G | AG | AG | CT | T | G | G | CT | G | T | G | C | A | CT | T | CC | A | T | G | G | A | CT | GC | 2545 |
| Db | 2357 | CAC | T | GC | CT | T | T | GC | CA | CG | CC | AG | GG | T | G | A | G | AG | AG | CAG | GG | CT | T | G | CA | OG | T | AG | CC | A | T | G | G | A | CC | CT | C | 2416 | | |
| Qy | 2546 | TG | CG | GT | G | A | C | A | G | A | A | G | A | CA | AT | GA | TG | GG | CT | T | G | T | G | G | A | CT | G | C | A | T | G | G | A | CC | CT | G | A | CT | GC | 2605 |
| Db | 2417 | TG | T | A | C | A | G | A | C | A | A | G | A | CA | CA | AG | G | A | G | A | CG | GA | CT | C | A | T | T | G | A | CT | G | A | T | G | GA | CC | CT | G | A | 2476 |
| Qy | 2606 | TGC | CT | C | A | G | CC | CT | T | G | CC | A | T | A | CA | CC | CG | CT | G | T | GC | CT | T | GG | CT | CC | CT | A | CC | CT | A | CC | CT | C | T | G | GA | C | 2665 | |
| Db | 2477 | TGC | CT | C | A | G | AG | CT | C | CT | GC | CA | AA | C | AG | CC | CT | A | CT | G | T | GC | T | GG | CT | G | A | CT | C | T | G | A | CT | C | T | G | AG | A | 2536 | |
| Qy | 2666 | AT | CA | T | C | AG | G | A | G | A | C | A | G | G | T | CT | CT | C | A | C | A | G | A | A | C | CT | A | C | CT | T | CT | A | T | G | A | C | CG | C | 2725 | |
| Db | 2337 | AT | CA | T | T | AG | CC | AA | AG | CC | TT | C | A | G | A | C | CA | CT | C | A | G | A | AG | CT | G | CC | A | G | CT | G | CC | A | G | T | G | A | CC | G | A | 2596 |
| Qy | 2726 | AT | CA | G | T | T | CT | CT | G | G | G | CAG | GGA | CAG | CA | CG | CA | TA | AT | T | CC | CC | GG | G | A | GA | A | CC | CC | CT | T | T | G | A | T | 2785 | | | | |
| Db | 2597 | AT | CA | G | T | T | CT | CT | G | A | T | CG | A | T | AG | CA | CC | CA | CG | CT | CC | CT | G | G | A | AA | AG | T | CC | GG | T | T | CA | A | T | 2656 | | | | |
| Qy | 2786 | GG | AG | GC | AT | TG | CT | TG | T | AT | T | CG | T | GG | CC | AG | T | GA | T | GA | CA | T | CAG | AT | G | GA | A | CC | CC | CC | CT | GG | T | T | 2845 | | | | | |
| Db | 2657 | AAG | AG | T | CT | T | GG | CT | CC | G | CT | CA | T | CAG | AG | GC | CA | AG | T | ACT | AA | CAG | CT | G | AT | G | GA | A | CC | CA | CT | T | AT | T | 2716 | | | | | |
| Qy | 2846 | GG | T | G | TA | CA | CT | CAG | T | TTT | TG | T | CA | A | A | CC | CT | CT | CT | TT | TG | GA | T | A | CA | AT | C | A | AT | C | A | G | A | CG | CA | AG | A | 2905 | | |
| Db | 2717 | GG | CG | T | CA | AG | CT | G | T | CT | TTT | T | A | CT | A | CT | A | CT | A | CT | A | CT | A | CT | A | CT | A | CT | A | CT | A | CT | A | CT | A | CT | A | 2776 | | |
| Qy | 2906 | GG | C | AG | CT | T | T | G | A | CA | AA | T | G | G | CG | GC | AT | CT | CC | A | CT | CA | T | CT | CT | CA | CT | CT | CT | CT | CT | CT | CT | CT | CT | CT | CT | 2965 | | |
| Db | 2777 | GG | AA | T | GT | T | G | A | CT | TT | GG | CA | AA | T | GG | T | GG | CG | CT | CT | CT | GA | CT | TT | T | GG | T | AT | TT | G | A | G | CG | T | CT | C | 2836 | | | |
| Qy | 2966 | C | T | T | T | C | A | C | A | G | G | A | G | C | A | C | A | C | CT | T | G | G | CT | G | C | CA | T | G | G | GA | T | G | G | GA | T | G | CA | 23025 | | |
| Db | 2837 | C | A | T | T | CT | C | A | C | T | AG | T | CC | A | C | A | C | A | C | T | G | T | G | G | A | T | CC | CT | G | SA | A | T | G | T | AT | G | A | T | 2896 | |
| Qy | 3026 | ACC | A | T | C | A | T | C | A | T | G | A | G | A | A | T | G | A | G | A | T | T | C | C | C | A | G | T | G | T | G | A | C | C | T | G | A | C | A | 3085 |
| Db | 2897 | ACC | T | T | G | T | C | A | T | GA | AA | AA | AG | AG | GA | AA | CG | A | AT | T | CC | AG | CT | G | T | GA | CT | C | AG | T | G | CC | T | T | G | T | G | 2956 | | |
| Qy | 3086 | CG | C | C | C | C | AA | C | C | C | AG | T | CT | CT | CT | CA | T | C | C | CA | C | AG | CT | G | A | CT | G | C | T | T | C | G | C | CA | G | A | G | 3145 | | |

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|------|----|--|------|
| 2957 | Db | AGGCCAAGTCCCATCATGTGTCTTACCAGTTATCCACCTTCTTTCAGGCTCTTCCCCTGAG | 3016 |
| 3146 | Qy | AAAGGGCCCATTTGTGCGGAAATTCAGGCTTTTGCAGAGGAAATCTCTATCTCTGCGCTGC | 3205 |
| 3017 | Db | GACAGCCCATCATCCCGAGACACAGGTCCTGCATGAAGAAACCAATTCACAGGAACA | 3076 |
| 3206 | Qy | AAGATGAGGTGAGCTTACCTTGAGAGCGGACCCCTGGCTTACAANAATGTCTCTGAGGATC | 3265 |
| 3077 | Db | GATTTGAAACTTTCTTCACTACCTGAGTTCCAGAGCGGCAAGGTTCACAGTCAGTTCTTAAAGATT | 3136 |
| 3266 | Qy | AGCTCACCCACCGACCATCCCTTCAACCTCATGAAGGTGCACCTCATGTGTAGCGGTG | 3325 |
| 3137 | Db | ACCATGACCCAGCGGCTCATACCGTTTAAACCTCATGAAGTCCATCTGATGGTGGCCGTG | 3196 |
| 3326 | Qy | GAGGGCCGCTCTTTCAGGAAATGGTTGGCTGCAGCCCCAGACCTGTCTTATTTTCATT | 3385 |
| 3197 | Db | GTTTGGGAGACTCTTCCAGAAGTGGTTCTTCTGCCTCGCCAAATCTGGCCTACACGTTTCATC | 3256 |
| 3386 | Qy | TGGGACAAGACAGAGCTTACAACCGAAGGTGTTTGGGCTTTCAGAAAGCCTTTGTTTCC | 3445 |
| 3257 | Db | TGGGATAAGACGGACGCATATAATACGAAAGTCTTACGGCTTGTTCAGAGGCAGTTGTGTCC | 3316 |
| 3446 | Qy | GTGGTTATGAATATGAATCTCTGCCAGATCTAATCTGTGGGAAAGAAACAACACAGTG | 3505 |
| 3317 | Db | GTGGATACAGGATACGAGTCGTGCTTGGACCTGACTCTCTGGGAAAGAGACATGCCGTT | 3376 |
| 3506 | Qy | CTGCAGGGCTATGAAATTTGACGGCTCCAAGCTTGGAGGATGGAGCCTTAGACAAACATCAT | 3565 |
| 3377 | Db | TTGCAAGGCTATGATTTGGATGCTTCGAAATCATGGCGCTGGAGCTTTGGACAGCACCAT | 3436 |
| 3566 | Qy | GCCTCAACATTCAAAGTGTATCTTGCACAAAAGGGAATGGGAGAAACCAAGTTTGTGTCT | 3625 |
| 3437 | Db | GTACTGACCGTTCAGAAACGGTATACTATACAAGGAAATGGAGAAATCAGTTTCATCTCT | 3496 |
| 3626 | Qy | CAGCAGCTCTGTCTATTTGGAGCATCATCGGCAATGGGCGCGGAGAACATCTCTCTGC | 3685 |
| 3497 | Db | CAGCAGCCTCCGGTGGTCAGCAGCATCATGGGTAATGGTCGGAGCGTAGCATCTCATGC | 3556 |
| 3686 | Qy | CCAGCTGCAACGGCCTTGCTGACGGCAACAAGCTCTCTGCCCCAGGTGGCCCTCACCTGT | 3745 |
| 3557 | Db | CCAAGTTGCAATGGTCAAGCTGACGGGAAACAATCTCTGACCCGTGGCGCTGCTGT | 3616 |
| 3746 | Qy | GGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAACTACATTAAGAGGATCTTCCCTCT | 3805 |
| 3617 | Db | GGGATCGACGGCAGTCTATACGTAGGGGATTTCAAATTAACGTCCGGCGGATATTCCTGT | 3676 |
| 3806 | Qy | GGAAATGTCACCAACATCCTTAGAGCTGAGGAAATAAGATTTTCAGACATAGTCACAGTCCA | 3865 |
| 3677 | Db | GGGAATGTGCAAGTGTTTTAGAACTAAGAAATAAGATTTTAGACATAGTAGCAACCCA | 3736 |
| 3866 | Qy | GCACAAATACTACCTTGGCCACAGACCCCATGAGTGGGCGGTCTTCTTTTCTGACAGC | 3925 |
| 3737 | Db | GCTCACAGATACTACCTTGGCTACGGACCCAGTCACCGAGATTTGTACGCTCTGTACT | 3796 |
| 3926 | Qy | AACAGCGGCGGTCTTTAAAAATCAAGTCCACTGTGTGTGTGAGGACCTTGTGCAAGAAC | 3985 |
| 3797 | Db | AACACCGCAGAACTATTCGGCCGAAATCACTCACGGGAGCCAAAGACCTGACTAAAAAC | 3856 |
| 3986 | Qy | TCTGAGTGGTTGGGGGACAGGTGACAGTGTCTCCCTTGTATGACATCTCGCTGCGGG | 4045 |
| 3857 | Db | GCTGAAGTGGTGGCAGGACCGGGGAACAGTGCCCTTCCCTTTGACGAGGCCAGGTGTGGG | 3916 |
| 4046 | Qy | GATGGTGGGAAGGCCACAGAAGCCACACTCAACAAATCCCAGGGGTATTAACAGTGGACAAG | 4105 |
| 3917 | Db | GATGGAGCAAGGCTGTGGAAAGCAACGCTCATGATGCCAAAGGAATGGCAATCGATAAG | 3976 |
| 4106 | Qy | TTTGGGCTGATCTACTTTCGTGGATGGCAACCATGATCAGACGCAATCGATCAGAAATGGGATC | 4165 |
| 3977 | Db | AACGGACTGATCTACTTTTGTGTGATGGAAACCATGATCAGAAAGGTTGATCAAAATGGGAATC | 4036 |
| 4166 | Qy | ATCTCCACCTGTCTGCGCTCTAATGATCTCACATCAGCCGGCCACTCAGCTGTGATTCT | 4225 |

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|----|------|--|------|----|------|---|------|
| Db | 4037 | ATATCAACTCTCTCTGGGCTCCACAGACCTCACGTACGCTCGACCTTTAACTGTGATACT | 4096 | Qy | 5303 | CGGAACAGCTACTACATCGGGCCGATGGCTCTTTCGGCGCTGTGCTGGCCAAACCGCATG | 5362 |
| Qy | 4226 | GTCAATGATATTTCCCAAGGTAAGACTGGAATGGGCCACAGACTTAGCCATCAACCCCAATG | 4285 | Db | 5174 | AGAAACAGTTTACCAAGATTGGGTATGATGGCTCCCTTAGAATCTTCTATGCCAGTGGTCTG | 5233 |
| Db | 4097 | AGCATGATATCAGCCAGGTGGCTTTGGAAATGGCCCACTGACCTCGCGATCAACCCCAATG | 4156 | Qy | 5363 | GAGGTGGCGCTGCAGACTGAGCCCCACATTTGTGGCTGGCAACGTCACACCCACCGTGGGC | 5422 |
| Qy | 4286 | GACAACTCATTTTATGTCCTGCACAAACAATGTGGTCTTGCAAAATCTCTGAAAACCAACAG | 4345 | Db | 5234 | GACTCTCACTACCAGACAGAGCCCCACGTTCTGGCTGGCACCGCGCAATCCACAGTAGCC | 5293 |
| Db | 4157 | GATAACTCCATCTACGTCCTGGATATAACAGTAGTTTATACAGATCACTGAAAACCGTCA | 4216 | Qy | 5423 | AAAGAGAAATGTCAACGCTGCCCATTCGAACACGSCCTCAACCTGGTGGAGTGGCGCCAGCGC | 5482 |
| Qy | 4346 | GTGGCATTTGTCGGGAGGCCCATGCACTGCAGGTCCCTGGCATTTGACCACTTCTCTG | 4405 | Db | 5294 | AAAAGAAAATGACTCTTCCCGGTGAGAACGGGCAAGATCTGGTGGAGTGGAGATTCGGA | 5353 |
| Db | 4217 | GTCCGATCGTGTCCGGGCGGCCCATGCACTGTCAAGTCTCCCTGGAGTGG---AATACCG | 4273 | Qy | 5483 | AAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGCGCGCGCTCGCGGTGGGTGCAACCCGA | 5542 |
| Qy | 4406 | CTAAGCAAGGTGGCCATCCACGCAACCTTGGAGTCAAGCCACCGCTTTGGCTGTTTTCACAC | 4465 | Db | 5354 | AAAGAAACAAGCCAGGCAAGGTCAAACGTAATTCGGCGGCAAGCTCAGGGTCAATGGGCGC | 5413 |
| Db | 4274 | GTGGGAAGCAGCGGGTTTCAGACCAACCTTGAGTCAAGCCACCGCCATTTGCTGTCTTAC | 4333 | Qy | 5543 | AAATCTCTATCTCTGGACTTTTGTATCGCGTAAACGACGACAGAGAGATCTATGATGACCAC | 5602 |
| Qy | 4466 | AATGGGTCTCTGATATTTCTGAGACTGATGAGAAAAGATCAACCGCATCAGCAGGTC | 4525 | Db | 5414 | AACCTACTCTCAGTGGACTTTTGTATCGGACCAACCAAGACGGAAGATCTATGATGACCAC | 5473 |
| Db | 4334 | ACGGGGTCTTTTACATCAGGAACTGATGAGAAGAGATCAACCGAATAAGCAGGTC | 4393 | Qy | 5603 | CGCAAGTTTCAACCTTCCGATTTCTGTACGACACGCGGGCGGCCCAAGCCTCTGGTCCCG | 5662 |
| Qy | 4526 | ACCACTAGTGGAGAGATCTCACTCGTTGTCTGGGGCCCCAGTGGCTGTGACTGTAAAAAT | 4585 | Db | 5474 | CGGAAATTTTCTCTGAGGATCGCTTACGACACGTCGCGGGCACCCGACTCTCTGGTCCCG | 5533 |
| Db | 4394 | ACGACAGCGGGAGATCTCTTAGTGGCTGGGATACCTTCGGAATGTGACTGCAAGAAC | 4453 | Qy | 5663 | AGCAGCAGGCTGAATGGTGTCAACGCTGACATATCTCCCTGGGGGTTACATTTGCTGGCATC | 5722 |
| Qy | 4586 | GATGCCAACTGTGATTTTCTGAGACGATGGTGTATGCCAAGATGCAAAAGTTAAAT | 4645 | Db | 5534 | AGTAGCAAGCTAATGGCAGTGAAGCTCACCTACTCATCCACCGGTCAAAATGGCAGCATC | 5593 |
| Db | 4454 | GACGCCAACTGTGATCTGTACCAAGCGGAGACGGCTACGCCAAGATGCCAAACTCAAT | 4513 | Qy | 5723 | CAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACAGCGGGCGGCCGATCATCATCAGG | 5782 |
| Qy | 4646 | ACCCACTCTCTTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACCTTGGGAAC | 4705 | Db | 5594 | CAGAGGGGACCAAGCAGCGGAAAAGGTGGACTATGACAGCCAGGGGAGGATCGTATCTCGG | 5653 |
| Db | 4514 | GGCGGCTCTCTGGCGCCCTCGCAGATGGCACTCTGTACTATGCAAGTCTGGGAAAT | 4573 | Qy | 5783 | ATCTTCGCTGATGGGAAGACATGGAGCTTACACATCTTATAGAGAAAGTCCATGGTCTGCTA | 5842 |
| Qy | 4706 | ATCCGAATTCGGTTTATCCGAGAGAACAGGCTTCTCTCAACACCCAGCAACATGATGAG | 4765 | Db | 5654 | GTCTTTGCCATGGGAAAACATGGAGTTACAGTACTTTGGAAGAGTCCATGGTCTTCTG | 5713 |
| Db | 4574 | ATCAGGATCCGGGCGGTTTCGAAGAAATAAACCTTTACTGAACTCAATGAACTTTACGAA | 4633 | Qy | 5843 | CTACACAGCCAGAGGCAAGTATATCTTTGAGTTTCGAAGAATGACCCGCTCTCTCTGTG | 5902 |
| Qy | 4766 | CTGTCTTCAACAAATGACAGGAGCTCTATCTGTTTGTATACCAACCGCAAGCACTGTATC | 4825 | Db | 5714 | CTCCATAGCCAGCGCAGTACATCTTCGAATACGACATGTGGGACCCGCTGTCCGCCATC | 5773 |
| Db | 4634 | GTTCGCTCTCCAACTGATCAAGAGCTCTACATCTTTGACATCAACGGTACTCACCAGTAC | 4693 | Qy | 5903 | ACGATGCCAACCTGGCGCGCAGACACTAGAGACCATCCGCTCAGTGGGCTACTTACAGA | 5962 |
| Qy | 4826 | ACCCAAAGCTGCCACAGGAGACTACCTGTACAACTTCCCTACACTACCTGGGACGCGAC | 4885 | Db | 5774 | ACCATGCCAGTGTGGCTCGCCACACCATGACAGACCATCCGCTCAATTTGGCTACTTACCGC | 5833 |
| Db | 4694 | ACCGTAGCCTGTGTCAGGGTACTACCTATATAATTTAGTTACGAATGACATGAC | 4753 | Qy | 5963 | AACATCTATCAGCCCCCTGAGGGCAATGCCCTCATCATCACCGACTACAAAGGAAGGG | 6022 |
| Qy | 4886 | ATCACACTATCACAGAACAAATGGCAACATGGTAAATGTCCCGCGAGACTCTACTGGG | 4945 | Db | 5834 | AAATCTACAATCCCCCAGAAAAGCAATGCCCTCATCATCACCGACTACAAAGGAAGGG | 5893 |
| Db | 4754 | GTACCGCTGTAACTGACAGCAATGGCAACACCCCTCGAATCCGAAGGATCCGAATCGG | 4813 | Qy | 6023 | CACCTCTTTCACACCTTCTACTGGGCATCTGGCGCAGGCTGATATACAAGTATGGCAAA | 6082 |
| Qy | 4946 | ATGCCCCCTCTGGCTGGTCCAGATGGCCAGGTGTACTGGGTGACCATGGGCAACCAAC | 5005 | Db | 5894 | CTGCTTCTGCAAAACAGCTTTCCTGGGAACGAGTCGGAGGGTCTTATTCAGTATAGAAG | 5953 |
| Db | 4814 | ATGCGGTGCGGGTGGTGTCTCTGTATAACAGGTGATATGGTTGACCATAGGCAACCAAC | 4873 | Qy | 6083 | CTGTCAAAAGCTGGCAGAGACGCTCTATGACACCAACCAAGGTCAGTTTCACTTATGACGAG | 6142 |
| Qy | 5006 | AGTGCACTCAAGAGTGTACCAACAGGACACGAGTTGGCCATGATGACATACCATGGC | 5065 | Db | 5954 | CAGACAGGCTATCAGAAATTTTATACGACAGCAACAGAGTCAGTTTACCTACGACGAA | 6013 |
| Db | 4874 | GGGTGTCTGAAAAGCATGACCGCTCAGGGCTCGAAGTGGTTTGTACTTTACCATGGC | 4933 | Qy | 6143 | ACGGCAGGCACTGCTGAAGACCATCAACCTACAGATGAGGGCTTCCACCTGCACCATCCGC | 6202 |
| Qy | 5066 | AATTCGGGCTCTTGGCAACCAAAAAGCAATGAAAACGAGTGGACCAACATTTTATGATAC | 5125 | Db | 6014 | ACAGCGGAGTCTCTGAAAACAGTAAACCTTCAGAGTGTGTTTATTTTGACCAATTAGA | 6073 |
| Db | 4934 | AAACAGTGGGCTTTTAGCCACCAAAAGTGACGAAACTGGATGGACAAACATTTTGTGACTAT | 4993 | Qy | 6203 | TACCGTCAGATTTGGGCCCCCTGATTGACCGACAGATCTTCCGCTTCACTGAGGAAGCATG | 6262 |
| Qy | 5126 | GACAGTTTGGCCGCTTGACAAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCCGA | 5185 | Db | 6074 | TACAGGCAAAATTTGGTCCCCCTGATTGACAGACAGATTTTCCGCTTCAGCGAGGATGAAATG | 6133 |
| Db | 4994 | GACAGTGAAGGTGCGCTGACGAATGTTACTTCCCACCTGGGGTGGTTTACAACCTGCAC | 5053 | Qy | 6263 | GTCAACCGCCGTTTTGACTTACAACTATGACAAACAGCTTCCGGGTGACAGCATGCAAGCT | 6322 |
| Qy | 5186 | AGTGATACAGACAGTTTCAGTGCAATGTCAGGTAGAGACTCCAGCA---AGGATGATGTC | 5242 | Db | 6134 | GTAAATGCGAGATTTGACTATAGCTACGCAACAGCTTTCGAGTGAACAGCATGCAAGGT | 6193 |
| Db | 5054 | GGGACATGGACAGGCTATCACCGTGGACATCGAGTCACTCCAGCAGAGAGGAAGATGTC | 5113 | Qy | 6323 | GTGATCAACAGAGACCCCACTGCCATTGATCTCTATCGCTATGATGATGTGTGAGCAAG | 6382 |
| Qy | 5243 | ACCATAACCAACCACTGTCTGCTCAGGGCCCTTCTACACACTGCTGCAAGACCAAGTC | 5302 | Db | 6194 | GTCAATCAATGAAACACCACTGCCCATTTGATCTATACCAAGTTTGTGATGACATCTCTGGCAAA | 6253 |
| Db | 5114 | AGCATCACTTCGAACTTGTCTCCATCGATTTCTTCTACACCAATGGTCCAAAGCCAGTTA | 5173 | | | | |

6383 ACAGACAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATTAACACAGATCATCAACCA 6442
|||||
6254 GTGAGCAGTTTGGAAAATTCGAGTGATATACTACGACATCAACCAATCAATTCACAG 6313
|||||
6443 GCTGTCAATGACCAACCAAGCAATTTTGATGATATGCGAGGATGAAGAAAGTGCAGTAT 6502
|||||
6314 GCCGTGATGACTTATACAAAGCACTTTGATGCTCATGGCGCATCAAGGAGATCCAAATAT 6373
|||||
6503 GAGATCTTCGGCTCGCTCATGTACTGATGACCGTCCAGTATGATACATATGAGAGTGA 6562
|||||
6374 GAGATATTTAGGTCACCTCATGTACTGATGATCAATTAATATGATATGAGGCGGGTA 6433
|||||
6563 GTCAAGAAGAGCTGAAGGTAGGACCTACGCCAAATACCACTCGCTACTCTATGAGTAT 6622
|||||
6434 ACCAAGAGAGATTAAATTTGGGCTTTTGGCCAACTACCAAAATACGGTACGAGTAC 6493
|||||
6623 GATGCTGAAGCGGCTGCGAGACAGTCTCCATCAATGACAAAGCCATCTGCGGCTACAGC 6682
|||||
6494 GACGTGATGACAGCTCCAAACAGTTTACCTAAACGAAAGATCATGTGGCGGTACAAC 6553
|||||
6683 TAGACCTCAATGGGAACCTGCACTTACTGAGCCCTGGGAACAGTGCAGGCTCACACCA 6742
|||||
6554 TAGACCTAAATGGAACCTCCACTTGTCTCAACCCAGCAGCGCGCCCTGACCCCT 6613
|||||
6743 CTACGGTATGACATCCGCGACCGCATCATCTCGGCTGGGTGACGTGCAATACAAAGATGGAT 6802
|||||
6614 CTGGCTATGACCTGCGGACAGAAATCACCCGCTGGGCGATGTTCAATACCGGCTGGAT 6673
|||||
6803 GAGGATGGCTTCTGAGGACAGCGGCGGTGATATCTTTGAGTACAACTCAGCTGCGCTG 6862
|||||
6674 GAAGATGGTTTCTGCGTCAGAGGGGCACTGAAATTTTGAATACAGCTCCAAAGGGCTT 6733
|||||
6863 CTATCAAGGCTTACAAACCGGCTGCGAGCTGGAGTGCAGGTACCGCTACGATGCGCTG 6922
|||||
6734 CTGACTCGAGTCTACAGTAAAGGCGAGTGGCTGACAGTGTATCTATCGGTACGACGGCTG 6793
|||||
6923 GGGCGGCGGTGTCAGCAAGAGCAGCCACAGCCACCACTGCGAGTTCTTCTATGACAGAC 6982
|||||
6794 GGAAGAGCTGTTCTAGCAAAACAGCGCTGGGACAGCACCTTCAGTTTTCTACGCGGAC 6953
|||||
6983 CTGACCAACCCCAAGAGTCAACCACTGTACAACTCCAGCTCTGAGATCACTCC 7042
6854 CTGACATACCCACAGAAATTACTACGCTCTACAACTTCCAGTTTCAGAAATCACTCC 6913
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7043 CTCTACTACACTTGCAGAGACACCTTTTGGCATGAGAGTGCAGAGTGGTGTAGTTT 7102
6914 CTGTACTATGACCTTCAAGGACATCTCTTCGCCATGGAGATCAGAGTGGGGATGATTC 6973
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7103 TACATAGCTTGTGACAAACATCGGACCCCTCTTGTCTCTTTAGTGAACAGAGTTTGATG 7162
7094 TACATCGCTCGGACAAACAGGGGACACCGCTGGCTGTTTTCAGCAACAGGGCTCATG 7033
|||||
7163 ATCAAGCAAAATCTGTACACAGCCTATGGGAGATCTACATGGATACCAACCCCACTTT 7222
7034 CTGAAACAGACCCAGTACATGCTATGGTGAGATCTACTTGACTCCAACGTCGACTTT 7093
|||||
7223 CAGATCATATAGGCTACCATGTTGGCTCTATGATCCACTCACCAGCTTGTGCCATG 7282
7094 CAGCTGGTAAATGGATTTCCAGGGGGCTTGTATGACCCGCTCACCACCAATATCCACTTT 7153
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7283 GGGCGGAGATATGATGTGTCGGCGGACGCTGGAGCTAGCCAGACACAGAGCTGTGG 7342
7154 GGAGAAAGAGATTATGACATTTTGGCGGGAAGATGGACCAACCGGACATTTGAATCTGG 7213
|||||
7343 AAGCACCTTAGTAGCAGCAACGTCATGCTTTTAACTCTATATGTTTCAAAAAACAAC 7402
7214 A---AAGGATCGAAAGGACCTGCTCTTTTAACTGTATATGTTTCGGAATAACAAC 7270
|||||
7403 CCCATCAGCAACTCCAGGACATCAAGTGTCTATGACAGATGTTTAACTGCTGCTGCTC 7462
7271 CCCCGAGCAAAATCCATGATGTGAAAGATTACATCACGGATTTAACTGCTGCTGCTG 7330
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7463 ACCTTTGGATTCAGCTACACAACTGATCCCTGGTTATCCCAACACAGACATGGATGCC 7522

7331 ACCTTTGGCTTCCATCTGCACAAATGCTATTCCTGGAATTCCTGTTCCTCCAAATTTGATT 7390
|||||
7523 ATGGAACCTCTCTACGAGCTCATCACACACAGATGAATAACAGAGTGGGACAAACAGC 7582
7391 ACTGAGCCTTCTCTATGAGCT-----TGTAAGAGTCAACAGTGGAGATGTG 7438
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7583 AAGTCTATCTCTCGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGGCTTTGTTCACCTTT 7642
7439 CCGCCATCTTTGGAGTTTTCAGCAGCAAGTGGCAAGCAAGCAAGGCTTCTTGTCCCTG 7498
|||||
7643 GAACGGTTTGAACAGCTCTATGGCTTCAATCACAGCTGCCAGCAGGCTCAAAGACC 7702
7499 GGGAAAGTGGCGGAGTGCAGGTGAGCCGACCAAGCTGGCGCCGAG---CAGTCGTGG 7555
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|||||

RESULT 12

AX662355
LOCUS AX662355
DEFINITION Sequence 37 from Patent WO02062999.
ACCESSION AX662355
VERSION AX662355.1 GI:29163217
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1

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Mon Dec 12 08:09:40 2005

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| Db | 4078 | GGAAATGGCAGTTGATAAGAATGGATTAATCTACTTTTGTGATGGAAACCATGATTAGAAA | 4137 | Qy | 5228 | AGC---AAGAGTATGATGTACCAATAAACCAACCTGTCTGCTCAGGGCCCTTCTACACA | 5284 |
| Qy | 4148 | ATCGATCAGAAATGGATCATCTCACCCCTGCTCGGCTCTAATGATCTCACATCAGCCCGG | 4207 | Db | 5215 | AGCCGAGAAGAAGATGTGAGCATCACTTTCAAATCTGTCTCGATCGATCTTTCTACACC | 5274 |
| Db | 4138 | GTGACCAAAATGGAAATCATATCAACTCTTCTGGCTCTAACGATTTGACTTCAGCCAGA | 4197 | Qy | 5285 | CTGCTGGAAGACCAAGTCCGGNACAGCTACTACATCGGGGCCGATGGCTCTCTGGCGGTG | 5344 |
| Qy | 4208 | CCACTCAGCTGTGATTTCTCATGGATATTTCCAGGTAAGATGGAGTGGCCACAGAC | 4267 | Db | 5275 | ATGGTTCAAGATCAAGTTAAGAAACAGCTACCAAGTTGGTTATGACGGCTCTCCTCAGAATT | 5334 |
| Db | 4198 | CTTTTAACTTGTGACACCAGCATGCACATCAGCAGGTACGCTCTGGAATGGCCACTGAC | 4257 | Qy | 5345 | CTGCTGGCCAAACCGCATGGAGTGGCGCTGCAGACTGAGCCCCACTTCTGCTGGTGGAC | 5404 |
| Qy | 4268 | TTAGCCATCAACCAATGGCAACTCACTTTATGTCTCGACAAACAATGTGGTCTCTGCAA | 4327 | Db | 5335 | ATCTACGCCAGTGGCTGGACTCACACTACAAACAGAGCCGACGTTCTGGCTGGCACC | 5394 |
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| Qy | 4328 | ATCTCTGAAACACACAGGTGGCAATGTGCGCGGAGGCCCATGCACTGCCAGTCCCT | 4387 | Db | 5395 | GCTAATCCGACGTTTCCCAAAAGAACATGATCTTTCCTGGGAGAACGGTCAAACTTG | 5454 |
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| Qy | 4388 | GGCATTTGACCACTTCTGCTAAGCAAGTGGCCATCCACGCAACCTCGAGTCAGCCACC | 4447 | Db | 5455 | GTGGAAATGGAGATTCGAAAGAGGCAAGCCCAAGGGAAGTCAATGTCTTTGGCCGCAAG | 5514 |
| Db | 4378 | GGAGTGG---AATATCTCTGTGGGAAGCAGCGGTGCGACAACTGGAATCAGCCACT | 4434 | Qy | 5525 | CTGCGGGTGCAACAACCGAAATCTCTATCTCTGGACTTTGATCGCGTAACACGACAGAG | 5584 |
| Qy | 4448 | GCCTTGGCTGTTTCAACAATGGGGTCTGTATATTGCTGAGACTGATGAGAAAAGATC | 4507 | Db | 5515 | CTCAGGGTTAAATGGCAGAAAACCTCTTTTCAGTTGACTTTGATCGAAACAACAAGACAGAA | 5574 |
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| Db | 4495 | AACCGGATAGGCAGGTCAACAAGATGGAGAAATCTCTTAGTGGCCGGAATACCTTCA | 4554 | Qy | 5645 | CCACAGCTCTGGTCAACCAGCAGCAGCGGTGAATGTGTCAACGTGACATATCCCTGGG | 5704 |
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| Db | 4855 | TACAGCAATGACATGATATTTACTGCTGTACAGACAGCAATGGCAACACCCCTTAGAAAT | 4914 | Qy | 6005 | GACTTCACTGAGGATGGCACTCTCTTCCACACTTCTACCTGGGCACCTTGGCGCAGGGTG | 6064 |
| Qy | 4928 | CGCCGAGACTTACTGGGATGCCCTCTGGCTGTGTGCTCCAGATGCCAGGTGTACTGG | 4987 | Db | 5995 | GACTCAACAGGAAGGGCTGCTCTACAACAGCTTTCTTTGGGTACAAGTCGGAGGGTC | 6054 |
| Db | 4915 | AGACGGGACCAATCGCATGCCAGTTTCGAGTGGTGTCTCTGTATACCAAGTATAGG | 4974 | Qy | 6065 | ATATACAAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACCAAGTTC | 6124 |
| Qy | 4988 | GTGACCATGGGCACCAACAGTGCATCAAGAGTGTGACCAACAAGGACACGAGTTGGCC | 5047 | Db | 6055 | TTATTCAAATAACAGAGGCAGACTAGGCTCTCAGAAATTTTATATGATAGCAACAGATC | 6114 |
| Db | 4975 | TTGACAAATAGGAACAAATGGATGTTTGAAGGCATGACTGCTCAAGGACTGGAATTAGTT | 5034 | Qy | 6125 | AGTTTCACTTATGACGAGAGCGCAGCATGCTGGAAGCCATCAACCTACAGAAATCAGGGC | 6184 |
| Qy | 5048 | ATGATGACATACCATGGCAATTCGGCTTCTGGCAACCAAAAGCAATGAAACGGATGG | 5107 | Db | 6115 | AGTTTATACCTATGATGAAACACAGCAGATCTCTTAAGACAGTAAACCTCCAGAGTATGAT | 6174 |
| Db | 5035 | TTGTTTACTTACATGGCAATAGTGGCCTTTTAGCCACTTAAAGTATGAAACTGGATGG | 5094 | Qy | 6185 | TTCACTGCACCATCCGCTACCGTACAGATTTGGGCCCTGATTTGAACGACAGATCTCCGC | 6244 |
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AX662353
LOCUS

8675 bp DNA linear PAT 22-MAR-2003

DEFINITION Sequence 35 from Patent WO02062999.
ACCESSION AX62253
VERSION AX62253.1 GI:29163216
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Spytek,K.A., Li,L., Wolenc,A.R., Vernet,C.A., Eisen,A., Liu,X.,
Malyankar,U., Shimkets,R.A., Tchernev,V.I., Spaderma,S.K.,
Gorman,L., Kekuda,R., Patturajan,M., Gusev,V., Gangolli,E.A.,
Guo,X., Shenoy,S., Rastelli,L., Casman,S.J., Boldog,F.,
Burgess,C.E., Edinger,S., Ellerman,K., Gunther,E., Smithson,G.,
Millett,I. and Macdougall,J.R.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 02062999-A 35 15-AUG-2002;
Curagen Corporation (US)
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Best Local Similarity 65.2%; Pred. No. 0;
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RESULT 14

AX662357

LOCUS AX662357 8473 bp DNA linear PAT 22-MAR-2003

DEFINITION Sequence 39 from Patent WO02062999.

ACCESSION AX662357

VERSION AX662357.1 GI:29163218

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

1

REFERENCE

AUTHORS Spytek, K.A., Li, L., Wolenc, A.R., Vernet, C.A., Eisen, A., Liu, X., Malyan, U., Shinkets, R.A., Tchernev, V.T., Spaderna, S.K., Gorman, L., Kekuda, R., Patturajan, M., Gusev, V., Gangolli, E.A., Guo, X., Shenoy, S., Rastelli, L., Casman, S.J., Boldog, F., Burgess, C.E., Edinger, S., Ellerman, K., Gunther, E., Smithson, G., Millet, I. and Macdougall, J.R.

TITLE Proteins and nucleic acids encoding same

JOURNAL Patent: WO 02062999-A 39 15-AUG-2002;

Curagen Corporation (US)

FEATURES

source 1. .8473

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Best Local Similarity 67.1%; Pred. No. 0;

Matches 5027; Conservative 0; Mismatches 2370; Indels 93; Gaps 9;

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Qy 1297 CAGTAGTTCTTTCCAGAGGACAGTTTCATAGATTCTGGGAAATTTGATGTGGGAGCGC 1356

Db 1097 AGGTGGATTATAGCAGGAAATATACACCATAGATTCCGGGAACTTTGATATGGCCGAG 1156

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ACCESSION AX662359
VERSION AX662359.1 GI:29163219
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ORGANISM Homo sapiens
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Homnidae; Homo.

REFERENCE 1

SPYTEK, K.A., LI, L., WOLENC, A.R., VERNET, C.A., EISEN, A., LIU, X.,
MALYANKAR, U., SHINKETA, R.A., TCHERNEV, V.T., SPADERNA, S.K.,
GORMAN, L., KEKUDA, R., PATTURAJAN, M., GUSEV, V., GANGOLLI, E.A.,
GUO, X., SHENOY, S., RAETELLI, L., CASMAN, S.J., BOLDIG, F.,
BURGESS, C.E., EDINGER, S., ELLERMAN, K., GUNTHER, E., SMITHSON, G.,
MILLET, I. and MACDOUGALL, J.R.
Proteins and nucleic acids encoding same

PATENT: WO 02062999-A 41 15-AUG-2002;
Curagen Corporation (US)

FEATURES

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5374 QY GCAGACTGAGCCCACTTGTGCTGGCTCGCTCAACCCCAACCGTGGGCAAGGAAATGT 5433
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 19:04:25 ; Search time 29280 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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4: gb_est4.*
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9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 13 | 646.8 | 7.7 | 762 | 7 CV559879 | CV559879 UI-M-H2O- |
| 14 | 630.8 | 7.6 | 827 | 3 BM947883 | BM947883 UI-M-EGOp |
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| 26 | 560.6 | 6.7 | 815 | 8 CX901050 | CX901050 JGI_CAAM9 |
| 27 | 558.2 | 6.7 | 1125 | 10 CL649832 | CL649832 CH213-255 |
| 28 | 544.8 | 6.5 | 694 | 6 CF723353 | CF723353 UI-M-GV0- |
| 29 | 539.4 | 6.5 | 545 | 7 CN358072 | CN358072 170005999 |
| 30 | 536.8 | 6.4 | 1214 | 8 DN736264 | DN736264 CNB85-H08 |
| 31 | 534.6 | 6.4 | 637 | 6 CF171639 | CF171639 B0845C10- |
| 32 | 533.8 | 6.4 | 786 | 8 CX801335 | CX801335 JGI_CAAM1 |
| 33 | 532.2 | 6.4 | 834 | 8 CX892816 | CX892816 JGI_CAAM4 |
| 34 | 531.6 | 6.4 | 890 | 10 CZ923788 | CZ923788 109841592 |
| 35 | 531.2 | 6.4 | 798 | 2 BF144774 | BF144774 601791454 |
| 36 | 528.6 | 6.3 | 632 | 2 BB655038 | BB655038 BB655038 |
| 37 | 525 | 6.3 | 621 | 6 CF182790 | CF182790 UI-M-EY0- |
| 38 | 518.6 | 6.2 | 525 | 1 AL046228 | AL046228 DKFZp434E |
| 39 | 514 | 6.2 | 592 | 2 BF349559 | BF349559 MRO-HT015 |
| 40 | 507 | 6.1 | 1173 | 8 DN705156 | DN705156 CBJ57-G03 |
| 41 | 506.4 | 6.1 | 533 | 7 CR548033 | CR548033 DKFZp459D |
| 42 | 497 | 5.9 | 693 | 3 BQ210132 | BQ210132 UI-R-EP0- |
| 43 | 494.2 | 5.9 | 620 | 6 CB532612 | CB532612 757081 MA |
| 44 | 491 | 5.9 | 620 | 6 CB532245 | CB532245 756697 MA |
| 45 | 489.4 | 5.9 | 566 | 5 BU072782 | BU072782 im47902.Y |

ALIGNMENTS

RESULT 1
AY413475
LOCUS Homo sapiens HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence, 6246 bp DNA linear GSS 12-DEC-2003
DEFINITION genomic survey sequence.
ACCESSION AY413475
VERSION AY413475.1 GI:39769437
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 6246)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrieria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 6246)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrieria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>6246
/locus_tag="HCM4903"

Query Match 70.1%; Score 5857.4; DB 10; Length 6246;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 6006; Conservative 0; Mismatches 233; Indels 57; Gaps 4;

| | | | | | | | |
|----|------|--|------|----|------|--|------|
| QY | 2055 | TGAGAGCGAATGCAATGCTTTGTGGGATGGGAGGCGACCAACTGGGAGACCCCGAGG | 2114 | Db | 1052 | CTGTGCAGAGAAAGGCCCATTTGTGCGGAAATTCAGGCTTTGCAGGAGAAATCTCTA | 1111 |
| Db | 2 | TGAAAGCGAGATCTTGTGCGACAGATGGCTGGAAAGCGCTGAGTGCGATGTGCCACCA | 61 | QY | 3195 | TCTCTGGCTGCAAGATAGGCTGAGCTACTGAGAGCGGACCCCTGGCTACAAATCTG | 3254 |
| QY | 2115 | CCACATGCTTAGACCACTGTTCAGGCCACGAACTTCTTCCGCGACACCGGCTTTTGA | 2174 | Db | 1112 | TCTCTGGCTGCAAGATAGGCTGAGCTACTGAGCAGCGGACCCCTGGCTACAAATCTG | 1171 |
| Db | 62 | ACCAAGTGTATCGATGTGGCTGCGAGCAACCATGGCACTGC--ATCAGGGCACCTGCA | 118 | QY | 3255 | TCCTGAGATACGCTTACCCACCGGACCATCCCTTCAACTCATGAAGGTGACCTCA | 3314 |
| QY | 2175 | GCTGTGACCCAAAGCTGGACTGGACACGACTTCTATCGAGATCTGTGCTGCCACTGTG | 2234 | Db | 1172 | TCCTGAGGATCAGCTTACCCACCGGACCATCCCTTCAACTCATGAAGGTGACCTCA | 1231 |
| Db | 119 | TCTGCAACCTTGGCTTACAAGGGGAGAGCTGTGAGGAAGAGATCTGTGCTGCCACTGTG | 178 | QY | 3315 | TGGTAGCGGTGAGGGCGCGCTTTCAGGAAAGTGGTTCGCTGCAGCCCGACCTGTCT | 3374 |
| QY | 2235 | GTGGCCATGGCGTGTGCTAGGGGGCACCTGCCCTCGAGGATGGCTGGATGGGGGCGAG | 2294 | Db | 1232 | TGGTAGCGGTGAGGGCGCGCTTTCAGGAAAGTGGTTCGCTGCAGCCCGACCTGTCT | 1291 |
| Db | 179 | GTGGCCATGGCGTGTGCTAGGGGGCACCTGCCCTCGAGGATGGCTGGATGGGGGCGAG | 238 | QY | 3375 | ATTATTTTCATTTGGGACAAAGACAGACAGCTCTCAACACAGAGGTGTTTGGGCTTTCAGAAAG | 3434 |
| QY | 2295 | CCTGGACACAGGGGCTGCCACCGCGCTGTGCGAGCATTGGACCTTGGCGGACGCGCA | 2354 | Db | 1292 | ATTATTTTCATTTGGGACAAAGACAGACAGCTCTCAACACAGAGGTGTTTGGGCTTTCAGAAAG | 1351 |
| Db | 239 | CCTGGACACAGGGGCTGCCACCGCGCTGTGCGAGCATTGGACCTTGGCGGACGCGCA | 298 | QY | 3435 | CCTTTGTTTCCGTTGGGTTATGAATCTCTGCCCGAGATCTAATCTCTGTGGGAAAAA | 3494 |
| QY | 2355 | AGTGCAGTGCAGCCCTGGCTGGAAATGGCGAACACTGCACCATCGCTATCTGGATA | 2414 | Db | 1352 | CCTTTGTTTCCGTTGGGTTATGAATCTCTGCCCGAGATCTAATCTCTGTGGGAAAAA | 1411 |
| Db | 299 | AGTGCAGTGCAGCCCTGGCTGGAAATGGCGAACACTGCACCATC-----342 | 342 | QY | 3495 | GAACAAAGTGTGCGAGGCTATGAAATTTGACGCGCTCAAGCTTGGAGATGGAGCTAG | 3554 |
| QY | 2415 | GGGTAGTTAAAGAGGGTTGCCCTGGCTTGTGCAATGGCAACGGCAGATGTACCTTAGACC | 2474 | Db | 1412 | GAACAAAGTGTGCGAGGCTATGAAATTTGACGCGCTCAAGCTTGGAGATGGAGCTAG | 1471 |
| Db | 343 | -----GNN | 391 | QY | 3555 | ACAAACATCATGCCCTCAACATTTCAAGTGGTATCTCTGCACAAAGGGAATGGGGAGAAC | 3614 |
| QY | 2475 | TGAATGTTGGCACTGCGCTGCCAGCTGGCGCTGGAGAGGAGCTGGCTGTGACACTTCCA | 2534 | Db | 1472 | ACAAACATCATGCCCTCAACATTTCAAGTGGGAGCATCTATGGGCAATGGGCGCGAGAA | 1531 |
| Db | 392 | NN | 451 | QY | 3615 | AGTTTGTGCTCAGCAGCCTCTCTGTCAITTTGGGAGCATATGGGCAATGGGCGCGAGAA | 3674 |
| QY | 2535 | TGGAGACTGCTGCGGTGACAGCAAGACAAATGATGGAGATGGCTGTGGAGCTGCATGG | 2594 | Db | 1532 | AGTTTGTGCTCAGCAGCCTCTCTGTCAITTTGGGAGCATATGGGCAATGGGCGCGAGAA | 1591 |
| Db | 452 | NN | 511 | QY | 3675 | GCATCTCTCTCCAGCTGCAACGGCTTGTCTGACGCGCAACAGCTCTTGGCCCGCAGTGG | 3734 |
| QY | 2595 | ACCCTGACTGCTGCTTCCAGCCCTGTGTGCCATATCAACCCGCTGTGCTTGGCTCCCTTA | 2654 | Db | 1592 | GCATCTCTCTCCAGCTGCAACGGCTTGTCTGACGCGCAACAGCTCTTGGCCCGCAGTGG | 1651 |
| Db | 512 | ACCCTGACTGCTGCTTCCAGCCCTGTGTGCCATATCAACCCGCTGTGCTTGGCTCCCTTA | 571 | QY | 3735 | CCCTCAGCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCACTACATTAGAAGGA | 3794 |
| QY | 2655 | ACCCTCTGGACATCATCAGGAGACACAGTCCCTGTGTGACAGAGAACCTTACACTCTCT | 2714 | Db | 1652 | CCCTCAGCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCACTACATTAGAAGGA | 1711 |
| Db | 572 | ACCCTCTGGACATCATCAGGAGACACAGTCCCTGTGTGACAGAGAACCTTACACTCTCT | 631 | QY | 3795 | TCCTTCCCTCTGGAAATGTCAACAACTCTTAGAGCTGAGGAATAAAGATTTACAGACATA | 3854 |
| QY | 2715 | TCTATGACCATCAAGTTCTCTGCGGAGGAGACAGCACATATATCCCGGGGAGA | 2774 | Db | 1712 | TCCTTCCCTCTGGAAATGTCAACAACTCTTAGAGCTG-----A | 1750 |
| Db | 632 | TCTATGACCATCAAGTTCTCTGCGGAGGAGACAGCACATATATCCCGGGGAGA | 691 | QY | 3855 | GTGACAGTCCAGCACACAAATACTACTCTGGCCACAGACCCCATGAGTGGGCGCGCTTCC | 3914 |
| QY | 2775 | ACCCCTTTGATGAGGGCATGCTTGTGTTATTCGTGGCCAAGTGATGACATCAGATGGAA | 2834 | Db | 1751 | GTGACAGTCCAGCACACAAATACTACTCTGGCCACAGACCCCATGAGTGGGCGCGCTTCC | 1810 |
| Db | 692 | ACCCCTTTGATGAGGGCATGCTTGTGTTATTCGTGGCCAAGTGATGACATCAGATGGAA | 751 | QY | 3915 | TTTCTGACAGCAACAGCGCGGCTTTTAAATCAAGTCCACTGTGGTGGTGAAGGACC | 3974 |
| QY | 2835 | CCCCCTGTTGTTGCAACATCAGTTTGTCAATAACCCCTCTCTTTGGATATACAAATCA | 2894 | Db | 1811 | TTTCTGACAGCAACAGCGCGGCTTTTAAATCAAGTCCACTGTGGTGGTGAAGGACC | 1870 |
| Db | 752 | CCCCCTGTTGTTGCAACATCAGTTTGTCAATAACCCCTCTCTTTGGATATACAAATCA | 811 | QY | 3975 | TTGTCAGAACTCTGAGTGGTTCGGGGACAGGTGACCACTGCTCCCTTTTGTATGACA | 4034 |
| QY | 2895 | GCAGGCAAGATGGCAGCTTTGACTGTGTGACAAATGGCGGCATCTCCATCATCTCGGCT | 2954 | Db | 1871 | TTGTCAGAACTCTGAGTGGTTCGGGGACAGGTGACCACTGCTCCCTTTTGTATGACA | 1930 |
| Db | 812 | GCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCTCGGCT | 871 | QY | 4035 | CTCGCTGCGGGATGGTGGGAAAGGCCACAGAAAGCCACACTCAACATCCAGGGGTATTA | 4094 |
| QY | 2955 | TCGAGCGGGACCTTTTATCACAGAGGACACCTGTGGCTGCCATGGGATCGCTTCT | 3014 | Db | 1931 | CTCGCTGCGGGATGGTGGGAAAGGCCACAGAAAGCCACACTCAACATCCAGGGGTATTA | 1990 |
| Db | 872 | TCGAGCGGGACCTTTTATCACAGAGGACACCTGTGGCTGCCATGGGATCGCTTCT | 931 | QY | 4095 | CAGTGGACAAAGTTTGGGCTGATCTACTTTCGTGGATGGCACCATGATCAGACGCTCGATC | 4154 |
| QY | 3015 | TTGTCATGGAACCATCATCATGAGACATGAGGAGATGAGATTTCCAGCTGTGACTTGA | 3074 | Db | 1991 | CAGTGGACAAAGTTTGGGCTGATCTACTTTCGTGGATGGCACCATGATCAGACGCTCGATC | 2050 |
| Db | 932 | TTGTCATGGAACCATCATCATGAGACATGAGGAGATGAGATTTCCAGCTGTGACTTGA | 991 | QY | 4155 | AGAAATGGGATCATCTCCACCTGCTCGGCTCTAAATGATCTCATACGCGGCGCACTCA | 4214 |
| QY | 3075 | GCAATTTTGGCGGCGGCGGCTCTCTCCATCCCACTGACGCTCTTTCGCCAGCT | 3134 | Db | 2051 | AGAAATGGGATCATCTCCACCTGCTCGGCTCTAAATGATCTCATACGCGGCGCACTCA | 2110 |
| Db | 992 | GCAATTTTGGCGGCGGCGGCTCTCTCCATCCCACTGACGCTCTTTCGCCAGCT | 1051 | QY | 4215 | GCTGTGATTTCTGTATGGATATTTCCAGGTAAAGTGGAGTGGCCACAGACTTAGCCA | 4274 |
| QY | 3135 | CCTGTGCAGAGAAAGGCCCATTTGTGCGGAAATTCAGGCTTTGCAGGAGGAAATCTCTA | 3194 | | | | |

| | | | | | | |
|----|------|-----------------|------------------|------------------|-------------------|------|
| Db | 2111 | GCTGTGATTCTGTCA | TGGATATTTCCAGGTT | CACCTGGAGTGGCCCA | CAGACCTTAGCCA | 2170 |
| Qy | 4275 | TCAAACCAATGGGAC | ACTCTATTTATGTCT | CCGACCAACATGTGG | CTCGCAATCTCTG | 4334 |
| Db | 2171 | TCAAACCAATGGGAC | ACTCTATTTATGTCT | CCGACCAACATGTGG | CTCGCAATCTCTG | 2230 |
| Qy | 4335 | AAAAACCAAGGTGCG | CAATTTGTCCCGGAGG | CCCATGCACTGCCAGG | TCCCTGGCAATG | 4394 |
| Db | 2231 | AAAAACCAAGGTGCG | CAATTTGTCCCGGAGG | CCCATGCACTGCCAGG | TCCCTGGCAATG | 2290 |
| Qy | 4395 | ACCACTTCCTGCTAA | GGAAGTGGCCATCC | ACGCAACCTTGAGT | AGCCACCGCTTTGG | 4454 |
| Db | 2291 | ACCACTTCCTGCTAA | GGAAGTGGCCATCC | ACGCAACCTTGAGT | AGCCACCGCTTTGG | 2350 |
| Qy | 4455 | CTGTTTACACAATGG | GGTCTCTGTATTTCT | CGAGCTGATGAGAAA | AGATCAACCGCA | 4514 |
| Db | 2351 | CTGTTTACACAATGG | GGTCTCTGTATTTCT | CGAGCTGATGAGAAA | AGATCAACCGCA | 2410 |
| Qy | 4515 | TCAGGCAAGGTCA | CCACTAGTGGAGAG | ATCTCACTCGTTTGT | CGGGCCCCCAGTGG | 4574 |
| Db | 2411 | TCAGGCAAGGTCA | CCACTAGTGGAGAG | ATCTCACTCGTTTGT | CGGGCCCCCAGTGG | 2470 |
| Qy | 4575 | ACTGTAAAAATGAT | GCACCTGTGATTTT | CTGGAGACGATGGT | TATGCAAGATG | 4634 |
| Db | 2471 | ACTGTAAAAATGAT | GCACCTGTGATTTT | CTGGAGACGATGGT | TATGCAAGATG | 2530 |
| Qy | 4635 | CAAAAGTTAAATAC | CCCACTCTTCTTGG | CTGTGTGTGATGGG | AGCTTACGTGGCCG | 4694 |
| Db | 2531 | CAAAAGTTAAATAC | CCCACTCTTCTTGG | CTGTGTGTGATGGG | AGCTTACGTGGCCG | 2590 |
| Qy | 4695 | ACCTTGGGAACAT | CCGAATTCGGTTAT | CCGGAAGAACAGC | CTTCTCAACCCAGA | 4754 |
| Db | 2591 | ACCTTGGGAACAT | CCGAATTCGGTTAT | CCGGAAGAACAGC | CTTCTCAACCCAGA | 2650 |
| Qy | 4755 | ACATGTATGAGTGT | CTTCAACCAATGCA | CCAGGAGCTCTAT | CTGTGTTTGTATG | 4814 |
| Db | 2651 | ACATGTATGAGTGT | CTTCAACCAATGCA | CCAGGAGCTCTAT | CTGTGTTTGTATG | 2710 |
| Qy | 4815 | AGCACTGTACACCA | AGGCTGCCACAGG | AGACTACCTGTACA | AGCTTCACTTACACTG | 4874 |
| Db | 2711 | AGCACTGTACACCA | AGGCTGCCACAGG | AGACTACCTGTACA | AGCTTCACTTACACTG | 2770 |
| Qy | 4875 | GGGACGGCAGATCA | CACACTATACACACA | CAACATGGTAAATG | TGTCGGCCGAG | 4934 |
| Db | 2771 | GGGACGGCAGATCA | CACACTATACACACA | CAACATGGTAAATG | TGTCGGCCGAG | 2830 |
| Qy | 4935 | ACTCTACTGGGATG | CCCTCTGGCTGTGT | GTGTCAGATGGCC | AGGTGTACTGGGTG | 4994 |
| Db | 2831 | ACTCTACTGGGATG | CCCTCTGGCTGTGT | GTGTCAGATGGCC | AGGTGTACTGGGTG | 2890 |
| Qy | 4995 | TGGGCAACACAGTG | CACTCAAGAGTGTGA | CCACCAAGGACAGG | TGTCGCATGATGA | 5054 |
| Db | 2891 | TGGGCAACACAGTG | CACTCAAGAGTGTGA | CCACCAAGGACAGG | TGTCGCATGATGA | 2950 |
| Qy | 5055 | CATACCAATGGCA | ATTCGGCCCTCTGG | CAACCAAAAGCAAT | GGAATGGAACACAT | 5114 |
| Db | 2951 | CATACCAATGGCA | ATTCGGCCCTCTGG | CAACCAAAAGCAAT | GGAATGGAACACAT | 3010 |
| Qy | 5115 | TTTATGAGTACGAC | GTGTCGCGCCCTG | CAAAATGTGACCTT | CCCTACTGGCCAGTGA | 5174 |
| Db | 3011 | TTTATGAGTACGAC | GTGTCGCGCCCTG | CAAAATGTGACCTT | CCCTACTGGCCAGTGA | 3070 |
| Qy | 5175 | GCAGTTTCCGAAGT | GTATACAGAGTTCA | GATGTGATGTCCAGG | TAGAGACCTCCAGCAAG | 5234 |
| Db | 3071 | GCAGTTTCCGAAGT | GTATACAGAGTTCA | GATGTGATGTCCAGG | TAGAGACCTCCAGCAAG | 3130 |
| Qy | 5235 | ATGATGTACCAAT | AACCAACCTGTCTG | CTCAGGCGCTTCT | TACACACTGCTGCAAG | 5294 |
| Db | 3131 | ATGATGTACCAAT | AACCAACCTGTCTG | CTCAGGCGCTTCT | TACACACTGCTGCAAG | 3190 |
| Qy | 5295 | ACCAAGTCCGGA | ACAGCTACTACAT | CGGGGCGGATGG | CTCTTGGGCTGCTG | 5354 |
| Db | 3191 | ACCAAGTCCGGA | ACAGCTACTACAT | CGGGGCGGATGG | CTCTTGGGCTGCTG | 5414 |
| Qy | 5355 | ACGGCATGAGGTGG | CGCTGCGAGCTGAG | CCCCACCTTGTG | TGGTGGCACCGTCA | 5414 |
| Db | 3251 | ACGGCATGAGGTGG | CGCTGCGAGCTGAG | CCCCACCTTGTG | TGGTGGCACCGTCA | 3310 |
| Qy | 5415 | CGTGGGCAAGAG | GAATGTACGCTGCC | ATCGAACCGGCTCA | ACCTGGTGGAGTGG | 5474 |
| Db | 3311 | CGTGGGCAAGAG | GAATGTACGCTGCC | ATCGAACCGGCTCA | ACCTGGTGGAGTGG | 3370 |
| Qy | 5475 | GCAGCGCAAGAG | GAGGCTCGGGGCG | AGGTCACTCTTTT | TGGGCGCCGCGGTG | 5534 |
| Db | 3371 | GCAGCGCAAGAG | GAGGCTCGGGGCG | AGGTCACTCTTTT | TGGGCGCCGCGGTG | 3430 |
| Qy | 5535 | ACAAACCGAAATCT | CTCTATCTCTGGA | CTTTGATCGCGTAA | CAGCAAGAGATCTATG | 5594 |
| Db | 3431 | ACAAACCGAAATCT | CTCTATCTCTGGA | CTTTGATCGCGTAA | CAGCAAGAGATCTATG | 3490 |
| Qy | 5595 | ATGACACCGCAAG | TTCACCCCTTCG | GAATTCGATACCA | CGGCGGCGCCAGCTCT | 5654 |
| Db | 3491 | ATGACACCGCAAG | TTCACCCCTTCG | GAATTCGATACCA | CGGCGGCGCCAGCTCT | 3550 |
| Qy | 5655 | GGTACCCAGCAG | CGGCTGAATGTT | CAAACTGACATCT | CCCTGGGGTTACATG | 5714 |
| Db | 3551 | GGTACCCAGCAG | CGGCTGAATGTT | CAAACTGACATCT | CCCTGGGGTTACATG | 3610 |
| Qy | 5715 | CTGGCATCCAG | AGGGCATCATGTCT | GAAAGATGGAAT | ACGACCGGCGCGCATCA | 5774 |
| Db | 3611 | CTGGCATCCAG | AGGGCATCATGTCT | GAAAGATGGAAT | ACGACCGGCGCGCATCA | 3670 |
| Qy | 5775 | CAATCAGGATCT | TCGTGATGGGAA | GCATGAGCTAC | ATCTTAGAGAAG | 5828 |
| Db | 3671 | CAATCAGGATCT | TCGTGATGGGAA | GCATGAGCTAC | ATCTTAGAGAAG | 3730 |
| Qy | 5829 | CCATGTGTCTGT | CTACTACAGC | CGGCGAGTATAT | CTTTGAGTTTCG | 5888 |
| Db | 3731 | CCATGTGTCTGT | CTACTACAGC | CGGCGAGTATAT | CTTTGAGTTTCG | 3790 |
| Qy | 5889 | GCCTCTCTTCTG | TGACGATGCC | CAACGTGGCGG | CAGACACTAGAG | 5948 |
| Db | 3791 | GCCTCTCTTCTG | TGACGATGCC | CAACGTGGCGG | CAGACACTAGAG | 3850 |
| Qy | 5949 | TGGGCTACTAC | AGAAATCATCTAT | CAGCCCTCAG | GGGCAATGCTCAG | 6008 |
| Db | 3851 | TGGGCTACTAC | AGAAATCATCTAT | CAGCCCTCAG | GGGCAATGCTCAG | 3910 |
| Qy | 6009 | TCATCAGGATGG | CACTCTTACAC | CTTCTACCTT | CGGCGAGGTTGAT | 6068 |
| Db | 3911 | TCATCAGGATGG | CACTCTTACAC | CTTCTACCTT | CGGCGAGGTTGAT | 3970 |
| Qy | 6069 | ACAAAGTATGG | CAAACTGTCAA | AGCTGGCAG | AGACGCTTATG | 6128 |
| Db | 3971 | ACAAAGTATGG | CAAACTGTCAA | AGCTGGCAG | AGACGCTTATG | 4030 |
| Qy | 6129 | TCACCTATGAC | GAGACGGCATG | CTGAAGACCAT | CAACCTACAG | 6188 |
| Db | 4031 | TCACCTATGAC | GAGACGGCATG | CTGAAGACCAT | CAACCTACAG | 4090 |
| Qy | 6189 | CCTGCAACCAT | CCGCTACCGT | CAGATTTGGG | CCCTGATTCG | 6248 |
| Db | 4091 | CCTGCAACCAT | CCGCTACCGT | CAGATTTGGG | CCCTGATTCG | 4150 |
| Qy | 6249 | CTGAGGAAGCA | TGGTCAACG | CCGCTTGTG | ACTTATGAC | 6308 |
| Db | 4151 | CTGAGGAAGCA | TGGTCAACG | CCGCTTGTG | ACTTATGAC | 4210 |
| Qy | 6309 | CCAGCATGCA | GGTGTGATCA | ACGACCCCA | CTGCGCATGATG | 6368 |
| Db | 4211 | CCAGCATGCA | GGTGTGATCA | ACGACCCCA | CTGCGCATGATG | 4270 |
| Qy | 6369 | ATGTGTGAG | CAAGACAG | AGCAGTTTGG | GAGTTTGGTGT | 6428 |
| Db | 4271 | ATGTGTGAG | CAAGACAG | AGCAGTTTGG | GAGTTTGGTGT | 4330 |

| | | | | | | | | | |
|----|------|--------------|-------------|-----------|------------|----------|----------|-------------|------|
| QY | 6429 | AGATCATCACCA | AGCTGTCTATG | ATGACCCCA | CCCAAGCA | TTTTGAT | GCATATG | CGCAGGATGA | 6488 |
| DB | 4331 | AGATCATCATCA | CCACAGCTG | TCATGACCC | CAACCAAGCA | TTTTTGAT | GCATATG | CGCAGGATGA | 4390 |
| QY | 6489 | AGGAAGTGCAG | TATAGATCT | TTCCCGT | CGCTCATG | TACTG | GATGACCG | TCCAGTATCAT | 6548 |
| DB | 4391 | AGGAAGTGCAG | TATAGATCT | TTCCCGT | CGCTCATG | TACTG | GATGACCG | TCCAGTATCAT | 4450 |
| QY | 6549 | ACATGGGGCGA | GTAAGAGGAG | CTGAAGCT | AGGACCT | TACGCC | CAATAC | CTCGCT | 6608 |
| DB | 4451 | ACATGGGGCGA | GTAAGAGGAG | CTGAAGCT | AGGACCT | TACGCC | CAATAC | CTCGCT | 4510 |
| QY | 6609 | ACTCCTATGAT | GATGATGCT | GACGGC | AGCTGC | AGACAGT | CTCCAT | CAATGAC | 6668 |
| DB | 4511 | ACTCCTATGAT | GATGATGCT | GACGGC | AGCTGC | AGACAGT | CTCCAT | CAATGAC | 4570 |
| QY | 6669 | TCTGGCGCTAC | AGCTACGAC | CTCAATGG | GAACTG | CACCTT | ACTG | AGCCCTGG | 6728 |
| DB | 4571 | TCTGGCGCTAC | AGCTACGAC | CTCAATGG | GAACTG | CACCTT | ACTG | AGCCCTGG | 4630 |
| QY | 6729 | CACGGCTCACA | CCACTACG | TATGACAT | CCGGAC | CGCATCT | CGGCTGG | GTTGAC | 6788 |
| DB | 4631 | CACGGCTCACA | CCACTACG | TATGACAT | CCGGAC | CGCATCT | CGGCTGG | GTTGAC | 4690 |
| QY | 6789 | AATACAAGATG | GATGAGGAT | GGCTTCT | TGAGGC | AGCGGGCG | TGATATCT | TTTGGATACA | 6848 |
| DB | 4691 | AATACAAGATG | GATGAGGAT | GGCTTCT | TGAGGC | AGCGGGCG | TGATATCT | TTTGGATACA | 4750 |
| QY | 6849 | ACTCAGCTGG | CTGCTCAT | CAAGGC | CTTACA | ACCGGGCT | GGCAGCT | GGAGTGT | 6908 |
| DB | 4751 | ACTCAGCTGG | CTGCTCAT | CAAGGC | CTTACA | ACCGGGCT | GGCAGCT | GGAGTGT | 4810 |
| QY | 6909 | GCTACGATGG | CGCTGGGCG | GGGTG | CTCAG | AGAGCAG | CCACAG | CCACCTGC | 6968 |
| DB | 4811 | GCTACGATGG | CGCTGGGCG | GGGTG | CTCAG | AGAGCAG | CCACAG | CCACCTGC | 4870 |
| QY | 6969 | TCTTCTATG | CAGACTG | ACCAACCC | CAACAG | GTGACCC | ACTGTACA | CCACTCC | 7028 |
| DB | 4871 | TCTTCTATG | CAGACTG | ACCAACCC | CAACAG | GTGACCC | ACTGTACA | CCACTCC | 4930 |
| QY | 7029 | CTGAGATCAC | CTCCCTCT | ACTAC | AGTTC | CAAGGAC | ACCTCT | TTTGC | 7088 |
| DB | 4931 | CTGAGATCAC | CTCCCTCT | ACTAC | AGTTC | CAAGGAC | ACCTCT | TTTGC | 4990 |
| QY | 7089 | GTGGTGATG | AGTTTTTAC | ATAGCTT | GTGAC | AACATCG | GGACCCCT | CTTGTCT | 7148 |
| DB | 4991 | GTGGTGATG | AGTTTTTAC | ATAGCTT | GTGAC | AACATCG | GGACCCCT | CTTGTCT | 5050 |
| QY | 7149 | GAACAGGTTG | ATGATCAAG | CAAAATCT | TGTAC | AGCCT | TATGGG | AGATCTA | 7208 |
| DB | 5051 | GAACAGGTTG | ATGATCAAG | CAAAATCT | TGTAC | AGCCT | TATGGG | AGATCTA | 5110 |
| QY | 7209 | CCAAACCCAA | CTTTTCAG | ATCATAG | CTAC | TAGGCT | ACCACT | TATGATCC | 7268 |
| DB | 5111 | CCAAACCCAA | CTTTTCAG | ATCATAG | CTAC | TAGGCT | ACCACT | TATGATCC | 5170 |
| QY | 7269 | AGCTTGTCCA | TATGGCGG | AGAGATT | ATGAT | GTGCT | GGCCG | AGCTAG | 7328 |
| DB | 5171 | AGCTTGTCCA | TATGGCGG | AGAGATT | ATGAT | GTGCT | GGCCG | AGCTAG | 5230 |
| QY | 7329 | ACCACGAG | CTGTGG | AGACCTTT | AGT | AGC | CACTAT | CTATATGT | 7388 |
| DB | 5231 | ACCACGAG | CTGTGG | AGACCTTT | AGT | AGC | CACTAT | CTATATGT | 5290 |
| QY | 7389 | TCAAAAACA | CAACCCCAT | CAGCACT | CCCGAG | CACTCA | AGTGCT | TATGAC | 7448 |
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| QY | 7449 | ACAGCTGG | GTGCTCAC | CTTTTGG | ATTTCC | AGTACA | CAAGCT | GATCCCT | 7508 |
| DB | 5351 | ACAGCTGG | GTGCTCAC | CTTTTGG | ATTTCC | AGTACA | CAAGCT | GATCCCT | 5410 |
| QY | 7509 | CAGACATGG | ATGCCATGG | GAACCTCT | CTAC | AGCTCAT | CCACAC | ACAGATG | 7568 |

[illegible]

Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 5970)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source location/Qualifiers
1..5970
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..5970
/locus_tag="HCM4903"
ORIGIN
Query Match 60.4%; Score 5045.8; DB 10; Length 5970;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 5149; Conservative 0; Mismatches 815; Indels 54; Gaps 3;
Qy 2333 CATGGGACCTGCCGCGAGCGCAAGTGCAGTGCAGCCCTGGCTGGAATGCGAACACTGC 2392
Db 1 CATGGGACCTGCCGCGAGCGCAAGTGCAGTGCAGTCTGGCTGGAATGCGAACACTGC 60
Qy 2393 ACCATCCTCCTATCTCGTAGGTAGTTAAAGAGGGTGGCCCTGGTGTGCAATGGC 2452
Db 61 ACCATCGNN 112
Qy 2453 AACGGCAGATGTACTTTAGACCTGAATGGTTGGCACTCGCTGCCAGCTGGGCTGGAGA 2512
Db 113 -----NN 153
Qy 2513 GGAGCTGGCTGTGACACTTCATCGGAGACTGCCTGGGTGACAGCAAGAACAATGATGGA 2572
Db 154 NNN 213
Qy 2573 GATGGCTGTGGACTGACAGGACCTGACTGCTGCTCCAGCCCTGCGCCATATCAAC 2632
Db 214 NATGGCTGTGGACTGACAGGACCTGACTGCTGCTCCAGCCCTGCGCCATATCAAC 273
Qy 2633 CCGCTGTGCTTGGCTCCCTTAACTTGGACATCATCCAGGAGACACAGGTCCCTGTG 2692
Db 274 CCGCTGTGCTTGGCTCCCTTAACTTGGACATCATCCAGGAGACACAGGTCCCTGTG 333
Qy 2693 TCACAGCAGAACCTTACACTCTCTTATGACCGCATCAAGTTCTCTGTTGGGAGGACAGC 2752
Db 334 TCACAGCAGAACCTTACACTCTCTTATGACCGCATCAAGTTCTCTGTTGGGAGGACAGC 393
Qy 2753 ACGCACATAATCCCGGGGAGAACCCCTTTGATCGAGGACATGCTGTATTCTGTTGGC 2812
Db 394 ACGCACATAATCCCGGGGAGAACCCCTTTGATCGAGGACATGCTGTATTCTGTTGGC 453
Qy 2813 CAAGTGATGACATCAGATGGAACCCCTGGTGTGATGGAACATCAGTTTGTCAATAAC 2872
Db 454 NNN 513
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1474 -----AGNN 1512
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 Db 5953 GAGATGGCGGAGGTGA 5970

RESULT 3
 CR936703
 LOCUS
 DEFINITION Homo sapiens mRNA; cDNA DKF2p686A1568 (from clone DKF2p686A1568).
 ACCESSION CR936703

8027 bp mRNA linear HTC 23-FEB-2005

| | | | | | |
|-----------|---|--|------|--|------|
| VERSION | CR936703.1 | GI:60219614 | 1797 | TGGGCCCCGAGCTGTGGCAGAGCCTCTCTGCCCGTCTCTGTAGCGGAAATGGCCAAATACA | 1856 |
| KEYWORDS | HTC. | | 1148 | TAGGAGCAGACTGTCTAAAGCTGCTGCTCTGTGCGAGTGGGAATGGACAATATT | 1207 |
| SOURCE | Homo sapiens (human) | | 1857 | TGAAAGGCGAGATGCTTTGTGCCACAGTGGCTGGAAGGCGCTGAGTGCATGTGCCACCA | 1916 |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. | | 1208 | CTAAAGGACGTGTCAGTGTCTACAGCGGTGGAAGGTGCAGAGTGCACGTCGCCATGA | 1267 |
| REFERENCE | 1 (bases 1 to 8027) | | 1917 | ACAGTGTATCATGTGGCTTGCAGCAACCATGGCACCTGTGCATCACGGGCACCTGCATCT | 1976 |
| AUTHORS | Ottenwaelder,B.; Obermaier,B.; Deutschenbaur,S.; Schaipp,A.; Mewes,H.W.; Weill,B.; Amid,C.; Osanger,A.; Fobo,G.; Han,M. and Wiemann,S. | | 1268 | ATCAGTGCATTCGATCTCTCTCGGGGGCCACGGCTCTTCGCAATTGATGGAACTGTGTCT | 1327 |
| CONSTRM | The German cDNA Consortium | | 1977 | GCAACCTCGCTACAGGGCGAGAGCTGTGAGGAAGTGGACTGCAATGACACCCACATGTT | 2036 |
| TITLE | Direct Submission | | 1328 | GCTCTGCTGGCTACAAAGCGGAGCACTGTGAGGAAGTTGATTTGCTTGGATCCCACCTGCT | 1387 |
| JOURNAL | Submitted (22-FEB-2005) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY | | 2037 | CAGGCGGGGTGTCTGCTGAGAGGGAATGCCATTTGTTGGATGGGAGGACCA | 2096 |
| COMMENT | Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martinried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686A1568) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686A1568 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/. | | 1388 | CCAGCCACGGAGTCTGTGTAAATGGAGAAATGCTGTGCAGCCCTGGCTGGGTCTGA | 1447 |
| FEATURES | Location/Qualifiers | | 2097 | ACTGCGAGACCCCCAGGGCCACATGTTAGACCAGTGTTCAGGCCACCGAAACCTTCCTCC | 2156 |
| source | 1..8027 | /organism="Homo sapiens" | 1448 | ACTGTGAGCTGGCGAGGGTCCAGTGCACAGCAGTGCGAGTGGGCATGCGACGTACTGC | 1507 |
| | | /mcl_type="mRNA" | 2157 | CGGACACCGGGCTTTGACGTGTGACCCAAAGCTGGACTGGAACAGACTGTTCTATCGAGA | 2216 |
| | | /db_xref="taxon:9606" | 1508 | CTGACACGGGCTCTGCAGCTGCGATCCCAATCGGATGGGTCCCGACTGCTGTGTGAAG | 1567 |
| | | /clone="DKFZp686A1568" | 2217 | TCTGTGCTGCCGACTGTGGTGGCCATGGCGTGTGGCGGCGACCTGCCGTGGGAGG | 2276 |
| | | /issue_type="endometrium carcinoma cell line" | 1568 | TGTGCTCAGTAGACTGTGGCATTGCGGCGCTCTGCATCGGGGAGGCTGCCCGTGTGAAG | 1627 |
| | | /clone_lib="686 (synonym: hicc3). Vector pSport1_Sfi; host DH10B; sites SfiIA + SfiIB" | 2277 | ATGCTCGAATGGGGGAGCCTGCGACAGCGGGCCTGCCACCCGCGTGTGCCAGCATG | 2336 |
| | | /dev_stage="adult" | 1628 | AGGCTGGACAGGCGCAGCTGTGTACCAGCGCTGTGCCACCCCGCTGCTATTTGAGCAG | 1687 |
| ORIGIN | | | 2337 | GGACCTCCCGCAGCGGCAAGTGGAGTGCAGCCCTGGCTGGATGGGAACTGCACTGCA | 2396 |
| | Query Match 39.4%; Score 3289; DB 4; Length 8027; | | 1688 | GGACCTGTAAGATGGCAATGTGAATGCGGAGGGCTGGAATGGTGAACACTGCACTCA | 1747 |
| | Best Local Similarity 67.8%; Pred. No. 0; | | 2397 | TCGCTCACTATCTGGATAGGTTAGTTAAAGAGGGTGTCCCTGGGGTGTGCAATGGCAACG | 2456 |
| | Matches 4781; Conservative 0; Mismatches 2185; Indels 81; Gaps 10; | | 1748 | TTGTTAGGCAAAACCGGAGGACCGAAGCAGATGGCTGCCCTGACTTGTGCAACGGTAACG | 1807 |
| QY | 1317 | ACAGTTTCATAGATTCTGGAGAAATTGATGTGGAGGCGAGCCTCCAGAGAGATTCTCTC | 2457 | GCAGATGTACCTTAGACCTTGAATGGTTGGCACTGCTGCTGTGCGACCTGGCTGGAGAGAG | 2516 |
| DB | 683 | ACAGCAGCATAGACAGTGGTGAAGCAGAAAGTTGGTCGGCGGTAAACAAGAAAGTCCAC | 1808 | GGAGATGCACACTGGGTGAGAAACAGCTGGCAGTGTGTGCGCAGACCGCGCTGGAGAGGGC | 1867 |
| QY | 1377 | CTGGCACTTCTGGAGATCTCAAGTGTTCATGACCATCTGTGCACTCTGGAATTCGAATG | 2517 | CTGGCTGTGACACTTCCATGGAGACTGCTGCGGTGACAGCAAGACAATGATGGAGATG | 2576 |
| DB | 743 | CAGGGGTGTTTGGAGTGCACAAATTCGCATCAGTCAGCCCCCAGTTCTTTAAAGTTCAACA | 1868 | CCGATGCAACGTTGCCATGGAAACTTCTCTGTGCTGATACAGAGATAATGAGGGAGATG | 1927 |
| QY | 1437 | TGCTCTGGGAAAGGCGCCCTGGTTGGCATTTATGGCAGAAAGCCCTCCCTCTTCAC | 2577 | GCCTGGTGACTGATGGACCCCTGACTGCTGCTCCAGCCCTGTGCATATCAACCCGC | 2636 |
| DB | 803 | TCTCCCTCGGGAAGGACGCTCTCTTTGGTGTTCATAGAAGAGGACTTCCACCATCTC | 1928 | GCCTGGTGAGTTGTTGGACCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 1987 |
| QY | 1497 | ATACAGATTGACTTTGTGGAGCTGCTGGATGGCAGAGGGCTCTTAACCCAGGAGGCGC | 2637 | TGTGCTTTGGTTCCTTAAACCTCTGAGACATCTCCAGGAGACACAGGTCCCTCTGTGTAC | 2696 |
| DB | 863 | ATGCCCCAGTATGACTTCATGGAACGCTTGACCGGA-----AGGAGAAGT | 1988 | TCTGCGGGGGTCCCGGAGCCACTGGGACATCATTTAG-----CAGGGCCAGACGGATT | 2041 |
| QY | 1557 | GGAGCCTAGAGGGGACCCCGCGCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAGA | 2697 | AGCAGAACTACACTCTCTTCTATGACCGCATCAAGTTCTCTGTGGGAGGAGGACAGCAGC | 2756 |
| DB | 908 | GGAGTGTGTTGAGTCTCCAGGGAACCGCGGAGCATACAGACTTGGTTTCAGAAATGAAG | 2042 | GCCCCGCGAGTGAAGTCTCTATGACCGTATCAGCTCTTGCGAGGCAAGGATAGCACCC | 2101 |
| QY | 1617 | CAGGCTTATCCAGTATTTGGATTCAGGAATCTGGCACTTGGCTTTTACAATGACGGAA | 2757 | ACATAATCCCGGGGAGAACCCCTTTGATGAGGGGCAATGCTTGTGTTTATGTTGGCCGAG | 2816 |
| DB | 968 | CCGTGTTTGTGCTAGTACCTGGATGTGGCCCTGTGGCATCTGGCTTCTACATGATGGA | 2102 | ACATCATTTCTGGAGAGAACCCCTTTCAACAGCAGCTTGTGTTTCTCTCATCCGAGGCCAAG | 2161 |
| QY | 1677 | AGGAGTCAGAAAGTGGTTTCTCTTCTCACCAATGCAATGAGTGGTGGATTAATCTGCCCA | 2817 | TGATGACATCAGATGGAACCCCTTGGTTGGTGTGAACATCAGTTTGTCAATAACCCCTC | 2876 |
| DB | 1028 | AAGACAAAGAGATGGTTTCTTCAATCTGTTGCTCTAGATTCAAGTGCAGGACTGTCCAC | 2162 | TAGTAACATACAGATGGAATCTCCCTGGTGGTGTGAACGTGTCTTTTGTCAAGTACCCAA | 2221 |
| QY | 1737 | GCAACTGCTATGGCAATGGTGAATCTCTGGGACCTGGCACTGCTCTGGGTTTCC | 2877 | TCTTTGGATATACAATCAGAGGCAAGATGGCAGCTTTTGTGTTGTTGTTGTTGTTGTTGTTG | 2936 |
| DB | 1088 | GTAACGCAATGGGAATGGTGAATGTGTGTCGGGGGTGTGTCACTGTTTCCAGGATTTC | | | |

| | | | |
|----|------|--|------|
| Db | 1421 | ATTGCTGCTGGACGGCCCACTGCACTGTTCAGGTTCCTCCGAGTGG--AAATATCTGTGTGGG | 1477 |
| Qy | 4412 | AAGGTGGCCATCCACGGCAACCTGGAGTCAGCCACCGCTTTGGCTGTGTTCACACAATGGG | 4471 |
| Db | 1478 | AAGCAACGGGGTCAGACAACTGGAATCAGCCACTGCGCATTTGCTGTCTCTACAGTGGG | 1537 |
| Qy | 4472 | GTCTCTGATATTTGCTGAGACTGATGAGAAAAAGATCAAACCGCATCAGGACAGTCACTACT | 4531 |
| Db | 1538 | GTCTCTGATATTTGCTGAGACTGATGAGAAAAAGATCAAACCGCATCAGGACAGTCACTACT | 1597 |
| Qy | 4532 | AGTGAGAGATCTACTCGTTGCTGGGGCCCGAGTGGCTGTGACTGTGTAATAAATGATGCC | 4591 |
| Db | 1598 | GATGAGAAAACTCTCTTAGTGGCCGGAATACCTTCAGAGTGTGACTGCAAAAATGATGCC | 1657 |
| Qy | 4592 | AACTGTGATGTTTCTTCTGGAGACGATGGTTATGCAAGGATGCAAAAGTAAATACCCCA | 4651 |
| Db | 1658 | AACTGTGATGTTTCTTCTGGAGACGATGGTTATGCAAGGATGCAAAAGTAAATACCCCA | 1717 |
| Qy | 4652 | TTCTTCTTGGCTGTGTGTCTGATGGGAGCTCTATCTGTGTTGATACACCGGCAAGCACCTGTACACCCAA | 4711 |
| Db | 1718 | TTCTTCTTGGCTGTGTGTCTGATGGGAGCTCTATCTGTGTTGATACACCGGCAAGCACCTGTACACCCAA | 1777 |
| Qy | 4712 | ATTCGGTTTATCCGGNAGAACAGCCTTTCTCAACACCGCAAGCATGTATGAGCTGTCT | 4771 |
| Db | 1778 | ATCCGGCTGTGTCAAAGAAATAGCCTTTTACTTAACTCTTGAAGTGTGCG | 1837 |
| Qy | 4772 | TCACCAATTTGACCAGGAGCTCTATCTGTGTTGATACACCGGCAAGCACCTGTACACCCAA | 4831 |
| Db | 1838 | TTCTTCTTGGCTGTGTGTCTGATGGGAGCTCTATCTGTGTTGATACACCGGCAAGCACCTGTACACCCAA | 1897 |
| Qy | 4832 | AGCTGCCCCCAGGAGACTACCTGTGTAACCTTTACCTACACTGGGACCGCGACATCACA | 4891 |
| Db | 1898 | AGTTTGTGCTGCTGATTAACCTTTTAACTTTAGCTACAGCAATGCAATGATATTA | 1957 |
| Qy | 4892 | CTCATCACACACAAATGGAACATGGAACATGTAATGTCCTGGAGACTCTACTGGGATGCCC | 4951 |
| Db | 1958 | GCTGTGACACAGCAATGGAACATGGAACATGTAATGTCCTGGAGACTCTACTGGGATGCCC | 2017 |
| Qy | 4952 | CTCTGGCTGTGTGTCAGATGCGGAGTGTACTGGGTGACCTGGGACCGCAACAGTGCA | 5011 |
| Db | 2018 | GTTCGAGTGTGTCTCTGATTAACCAAGTGTATGTTGTAATAGAGCAAAATGCAATGATGT | 2077 |
| Qy | 5012 | CTCAAGAGTGTGACCAACAGGACAGAGTGTGCGCATGATGACATACCATGCAATTC | 5071 |
| Db | 2078 | TTGAAAAGCATGACTGTCTCAAGGACTGGAATTTAGTTTGTACTTACCATGCAATGT | 2137 |
| Qy | 5072 | GGCCTTCTGGCAACCAAAAGCAATGAAACCGATGGAACAATTTTATGATGACGACG | 5131 |
| Db | 2138 | GGCCTTCTGGCAACCAAAAGCAATGGAACCGATGGAACAATTTTATGATGACGACG | 2197 |
| Qy | 5132 | TTTGGCGCTGACAAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCCGAGGTGAT | 5191 |
| Db | 2198 | GAAAGTGTGTGACAAATTTTACGTTTCCAACTGGAGTGTGACAAACCTGCAATGGGAC | 2257 |
| Qy | 5192 | ACAGACAGTTTCAGTGTGATGTCAGGTAGAGACCTCCAGC---AAGGATGATGTCAACNTA | 5248 |
| Db | 2258 | ATGGAACAGGCTATCAACAGTGGACATTTAGTGTCTAGCCGAGAGAAAGATGTGAGCATC | 2317 |
| Qy | 5249 | ACCAACCAACCTGTGTGCTCAGGCGCTTCTACACACTGCTGCAAGACCAAGTCCGGAAC | 5308 |
| Db | 2318 | ACTTCAAAATCTCTCTCATCGATCGATTTCTTTCTACACCATGGTTCAAGATCAGTTAAGAAC | 2377 |
| Qy | 5309 | AGCTACTACATCGGGCGGATGGCTCTTGGCGGTGCTGTGTCGGCCAAACCGCATGGAGGTG | 5368 |
| Db | 2378 | AGCTACCAAGATTTGTTATGACGGCTCTCTCAGAAATTAATCTAGCCAGTGGCTGACATCA | 2437 |
| Qy | 5369 | GGCTGTGACACTGAGCCCCACTTGTGCTGGCACCGCTCAACCCCAACCGTGGGCAAGAGG | 5428 |
| Db | 2438 | CACCTACCAACACAGACCGCACGTTCTGGCTGGCACCGCTTAATCCGACCGTTGCCAAAAGA | 2497 |
| Qy | 5429 | AATGTCAACGCTGCCATCGACAAACCGCTCAACCTGTGGAGTGGCGGCGAGCCAAAGAG | 5488 |
| Db | 2498 | AACATGACTTTTCCCTGGGAGAACCGTCAAAACTTTGGTGGATGGAGATTCGCAAAAGAG | 2557 |

| | | | | | | | |
|----|------|---|------|----|------|--|------|
| QY | 5489 | CAGGCTCGGGCCAGGTCACTGTCTTTTGGCGCGCTGCGGTGCACAACCGAAATCTC | 5548 | QY | 6569 | AAGAGCTGAAGGTAGGACCCCTTACGCCAATATACCACTCGCTACTCTTATGAGTATGATGCT | 6628 |
| DB | 2558 | CAAGCCCAAGGGAAGTCAATGTCTTTGGCCGCAAGCTCAGGGTTAATGGCAGAAACCTC | 2617 | DB | 3638 | AGAGAGATTTAAATAGGGCCCTTTGCCAACAACCACTATGCTTTATGAATATGATGT | 3697 |
| QY | 5549 | CTATCTCTGGACTTTGATCGCGTAAACGACACAGAGAAAGATCTATGATGACCAACCGCAAG | 5608 | QY | 6629 | GAGGCCAGCTCGACAGCTCTCAATCAATGACAGCACTCTGGGCTTACAGCTACGAC | 6688 |
| DB | 2618 | CTTTCAGTTGACTTTGATCGAAACAAACAAAGACAGAAAGATCTATGACGACCAACCGTAAA | 2677 | DB | 3698 | GATGACAGCTCCAAACAGTTTACCTCAATGAAAAGATTAATGTGGCGGTACAACTACGAT | 3757 |
| QY | 5609 | TTCAACCTTCGGATTCTGACGACAGGCGGGGGCCAGCCTCTGFTCACCCAGCAGC | 5668 | QY | 6689 | CTCAATGGGAACCTGCACCTTACTGAGCCCTGGGAAACAGTGCACGGCTCACACCCTACCGG | 6748 |
| DB | 2678 | TTTCTACTAGGATCGCTACGACACGCTCTGGGCACCCGACTCTCTGGCTGCCAAGCAGC | 2737 | DB | 3758 | CTGAATGGNAACCTCCATTTACTGAAACCAAGTNACAGTGCAGCTGCACACCCCTTCGC | 3817 |
| QY | 5669 | AGGCTGAATGGTGTCAACGTGACATATCTCCCTGGGGGTTACATTCGTGCGATCCAGAGG | 5728 | QY | 6749 | TATGACATCCGGACCGCATCACTCGGCTGGGTGAGTGCATACAAAGATGGATAGGAT | 6808 |
| DB | 2738 | AGCTGATGCCGTCAATGTCACTATTATCATCAGAGTCAATTCGACGATCCAGCGA | 2797 | DB | 3818 | TATGACCTCGAGACAGAAATCACTCGACTGGGTGATTTCAATATCGTGGATGAAGAT | 3877 |
| QY | 5729 | GGCATCATGTCTGAAGAAATGGAATACGACAGCGCGCGCATCAATCCAGGATCTTC | 5788 | QY | 6809 | GGCTTCTGAGCAGCGGGCGGTGATATCTTTTGATGACAACTCAGCTGCGCTGCTCATC | 6868 |
| DB | 2798 | GGCACCACTAGCGAGAAAGTAGATTATGACGGACAGGGAGGATCGTGTCTCGGGTCTTT | 2857 | DB | 3878 | GGTTTCTTACGTCAAAGGGGCGACGGAAATCTTTTGAATATAGCTCCAAGGGGCTTCTA | 3937 |
| QY | 5789 | GCTGATGGNAGACATGGAGCTACATATCTTAGAGAGTCCATGGTGTGCTACTACAC | 5848 | QY | 6869 | AAGGCCCTCAACCGGGCTGGCAGCTGGAGTGTCAAGTACCGCTACGATGGCTTGGGCGG | 6928 |
| DB | 2858 | GCTGATGGTAAACATGGAGTTACATATTTAGAAAAGTCCATGGTCTTCTGCTTCAT | 2917 | DB | 3938 | CGAGTTTACAGTAAAGGAGTGGCTGGACAGTGATCTACCGTTATGACGGCTTGGNAGG | 3997 |
| QY | 5849 | AGCCAGAGGCAATATCTTTTGAAGTTCGACAAAGATGACCGCCTCTCTTCTGTGACGATG | 5908 | QY | 6929 | CGCGTGTCCAGCAAGAGCAGCCACAGCCACCTGCGATCTTCTTATGACAGCTTGACC | 6988 |
| DB | 2918 | AGCCAGGGCAGTACATCTTCGAAATAGATATGTGGACCGCTGTCTGCCATCACATG | 2977 | DB | 3998 | CGTGTCTTCTAGCAAAACCACTGTAGGACAGCACTGCAGTCTTTTATGCTGACTTAACT | 4057 |
| QY | 5909 | CCCAAGTGGCGGGCGGACACTAGAGACCATCCGCTCAGTGGGCTACTACAGAAACATC | 5968 | QY | 6989 | AACCCCAACCAAGTCAACCACTGTACAAACCACTCAGCTCTGAGATCACTCCCTCTAC | 7048 |
| DB | 2978 | CCCAGTGGCTCGCCACACCATGCGAGCCATCCGATCCATTTGGCTACTACCGCAACATA | 3037 | DB | 4058 | TATCCCACTAGGATTACTCATGTCTACAAACCAATTCAGTTCAGAAATTAACCTCCCTGT | 4117 |
| QY | 5969 | TATCAGCCCTCAGGGCAATGCTCAGTCAATACAGGACTTCACTGAGGATGGGCACTC | 6028 | QY | 7049 | TAGCACTTCAAGGACACCTCTTTTGGCATGGAGCTGAGCAGTGGTGTATGAGTTTACATA | 7108 |
| DB | 3038 | TACAACCCCGGAAAGCAACGCTCCATCATCACGCACTACAAACGAGGAAGGGCTGCT | 3097 | DB | 4118 | TATGATCTCAAGGACATCTTTTGGCATGGAAATCAGCAGTGGGATGAAATCTATATT | 4177 |
| QY | 6029 | CTTTCACACCTTCTACCTGGGCACTGGCGCAGAGGTGATATACAAAGTATGCCAACTGTCA | 6088 | QY | 7109 | GCTTGTGACAACATCGGACCCCTCTTGTGTCTTTTGTAGTGGAAACAGGTTTGTATCAAG | 7168 |
| DB | 3098 | CTAACAACAGCTTTCTTGGGTACAAGTCGGAGGGTCTTATTCAAATACAGAAAGGCACT | 3157 | DB | 4178 | GCATCGGATAACACAGGGACACCACTGGCTGTTCAGTAGCAATGGGCTTATGCTGAAA | 4237 |
| QY | 6089 | AAGCTGGCAGAGCGCTCTATGACACCAACCAAGGTGAGTTTCACTATGACAGACGGCA | 6148 | QY | 7169 | CAAACTCTGTACACAGCTTATGGGAGATCTACATGGATACCAACCCCACTTTCAGATC | 7228 |
| DB | 3158 | AGGCTCTCAGAAATTTATATGATAGCACAAAGAGTCAGTTTACCTATGATGAAACAGCA | 3217 | DB | 4238 | CAGATTCAGTACACTGTCATATGGGAAATCTATTTTGACTCTAATATGACTTTCACACTG | 4297 |
| QY | 6149 | GGCATGCTGAAGACCATCAACCTTACAGAAATGAGGGCTTACCTGCAACCATCCCTACCGT | 6208 | QY | 7229 | ATCATAGGCTACCATGGTGGCTCTATGATCCACTCACAAGCTGTGCACATGGGCGCG | 7288 |
| DB | 3218 | GGAGTCTTAAAGACAGTAAACCTCCAGAGTGTGGTTTATTTTGCACCATTTAGATACAGG | 3277 | DB | 4298 | GTAATTTGGAATTCATGTGGCTGTATGACCCACTCACCAATTAATCCACTTGGAGAA | 4357 |
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| DB | 3278 | CAAAATTTGGTCCCTGATTTGACGAGAGATTTCCGCTTTTGTAGTGAAGATGGATGGTAAT | 3337 | DB | 4358 | AGAGATTATGACATTTTGGCAGGAGCGTGACAAACACCTGACATAGAAATCTGGA---AA | 4414 |
| QY | 6269 | GCCTGTTTGTACTACAACTATGACAAACAGCTTCCGGGTGACCAAGCATGAGGCTGTGATC | 6328 | QY | 7349 | CTTAGTAGAGCAAGCTCATGCTTTTAACTCTATATGTTTCAAAAACAAACACCCCATC | 7408 |
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| QY | 6329 | AACGAGACCCACTGCCCATTGATCTCTATCGCTATGATGATGTGTGAGGCAACAGAG | 6388 | QY | 7409 | AGCACTCCCGAGACATCAAGTGTTCATGACAGATGTTTAAACAGCTGGCTGCACCTTT | 7468 |
| DB | 3398 | AATGAAACGCACTGCTTATGATCTGTATCAGTTTGTATGACATTTCTGGCAAGTTGAG | 3457 | DB | 4475 | AGCAAAATCCATGACGTGAAGATTACATCAGATGTTTAAACAGCTGGCTGTGACATTT | 4534 |
| QY | 6389 | CAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATTAACCAAGATCATCACAGCTGTC | 6448 | QY | 7469 | GGATTCACGACTACAACCGTGTATCCCTGGTTATCCCAACACAGACATGGATGCCATGGAA | 7528 |
| DB | 3458 | CAGTTTGGGAAGTTTGGAGTTATATATATGATATTAACCAAGATCATTTCTACAGCTGTA | 3517 | DB | 4535 | GGTTTCCATCTGCACAAATGCTATTCTCTGGATTCCCTGTTCCCAAAATTTGATTTAAACAGAA | 4594 |
| QY | 6449 | ATGACCCACCAAGCAATTTTGTATGATATGGCAGGATGAAGGATGACAGTATGAGATC | 6508 | QY | 7529 | CCCTCTCAGAGTCAACACAGATGAAACCGCAGGAGTGGGACAAACAGCAAGTCT | 7588 |
| DB | 3518 | ATGACCTTACGAGCACTTTGATGCTCATGGCCGTATCAAGGATTTCAATATGAGATA | 3577 | DB | 4595 | CTTCTCTACGA-----ACTTGTGAAGAGTCAGCAGTGGGATGATATACCGCCC | 4642 |
| QY | 6509 | TTCCGCTCGCTCATGTACTGGATGACCGCTCCAGTATGATTAACATGGGGCGAGTAGTGAAG | 6568 | QY | 7589 | ATCTCGGGGTACAGTGTGNAGTACAGAGCAGCTCAAGSCCTTTGTCACCTTTAGAACCG | 7648 |
| DB | 3578 | TTCAGGCTCGCTCATGTACTGGATTACAAATTCAGTATGATAAATTCAGTGGGTCCGGTAAACCAAG | 3637 | DB | 4643 | ATCTTCGGAGTCAGCAGCAAGGTGGCGCGCAGGCCCAAGGCCCTTCTCTGTCGCTGGGNAAG | 4702 |
| | | | | QY | 7649 | TTTGACCAAGCTCTATGGCTCCACAAATCAACGAGTGCACAGGCTCTCCAAAGACCAAGAG | 7708 |

VERSION AV405421.1 GI:39761395
 KEYWORDS GSS. pan troglodytes (chimpanzee)
 SOURCE Pan troglodytes
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.
 REFERENCE 1 (bases 1 to 5069)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 5069)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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|----|------|---|------|------|---|------|
| Qy | 4532 | AGTGGAGAGATCTCACTCGTTGCTGGGGCCCCAGTGGCTGTGACTGTAATAATGATGCC | 4591 | 5609 | TTCAACCTTCGGATTCTGTACGACGAGGGGGGGCCGACCGCTCTGGTCAACCCAGCAGC | 5668 |
| Dd | 1598 | GATGGAGAAATCTCTTAGTGGCGGAATACCTTCAGAGTGTGACTGCAAAAATGATGCC | 1657 | Dd | TTTCTACTGAGGATCGCTACGACACGTCCTGGSCACCCGACTCTCTGGCTGCCAAGCAGC | 2737 |
| Qy | 4592 | AACGTGATGTTTTCTCGAGAGCATGGTTATGCGCAAGATGCAAAAGTTAAATACCCCA | 4651 | Qy | AGGCTGAATGGTGTCAACGTGACATACTCCCTGGGGGTTTACATTGCTGGCATCCAGAGG | 5728 |
| Dd | 1658 | AACGTGACTGTTACCAAGATGGAGATGGCTAAGCCAAAGATGCCAACTCAGTGCCCA | 1717 | Dd | AGCTGATGGCCGTCAATGTCACTATTATCCACAGGTCAAAATGCCAGCATCCAGCGA | 2797 |
| Qy | 4652 | TCTTCCTTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACCTTGGGACATCCGA | 4711 | Qy | GGCATCATGTCTGAAAGAAATGGAATACGACAGCGGGCGGCATCATCATCCAGATCTTC | 5788 |
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| Qy | 4712 | ATTCCGGTTTATCCGAAAGAAACAGCCCTTCTCAACACCCAGCAATCATGTATGAGCTGTCT | 4771 | Qy | GCTGATGGGAAGACATGGAGCTACACATATTAGAGAAGTCCATGGTGTCTACTACAC | 5848 |
| Dd | 1778 | ATCCGGCTGTGCAAGAAATAGCCCTTACTTAACTCTATGAACCTCTATGAAGTTGCG | 1837 | Dd | GCTGATGGTAAACATGGAGTTACACATATTTAGAAAAGTCCATGGTTCTTCTGCTTCAT | 2917 |
| Qy | 4772 | TCACCAATTAACCAAGGAGCTCTATCTGTTTTGATACCAACCGGCAAGCACTGTACACCAA | 4831 | Qy | AGCCAGAGGAGTATATCTTTGAGTTGCGACAAATGACCGCTCTCTTCTGTGACCATG | 5908 |
| Dd | 1838 | TCTCCAACTGATCAAGAACTCTACATCTTTGACATCAATGGTACTCACCAATATCTGTA | 1897 | Dd | AGCCAGCGGAGTACATCTTTCGAATACGATATGTGGACCGCTGTCTGCCATCACCATG | 2977 |
| Qy | 4832 | AGCTGCCACAGGAGACTACTGTACAACTTACCTACACTGGGAGCGGACATCACA | 4891 | Qy | CCCAACGTGGCGGCGAGACACTAGACCATCCGCTCAGTGGGCTACTACAGAAAATC | 5968 |
| Dd | 1898 | AGTTAGTCACTGGTGAATACCTTTACAAATTTTAGCTTACAGCAATGACAAATGATTA | 1957 | Dd | CCGAGTGGCTCGCCACACCATGCGACCATCCGATCCATTTGGCTACTACCGCAATAT | 3037 |
| Qy | 4892 | CTCATCACAGACAAATGSCAACATGTTAAATGTCCGCGAGACTCTACTGGGATGCC | 4951 | Qy | TATCAGCCCCCTGAGGGCAATGCTCAGTCTATACAGGACTTCTACTGAGGATGGGACCTC | 6028 |
| Dd | 1958 | GCTGTGACAGACAGCAATGGCAACACCTTTAGAAATAGAGGGACCCAAATCGCATGCCA | 2017 | Dd | TACAAACCCCGGAAAGCAACGCTCCATCATCACGGACTTACAACGAGGAGGGCTGCTT | 3097 |
| Qy | 4952 | CTCTGGCTGGTGGTCCAGATGGCCAGGTGTACTGGGTGACCACTGGGCACCAACAGTGCA | 5011 | Qy | CTTCAACCTTCTACTCTGGGCACTGGCGGAGGGTGATATACAAATGAGCAAACTGTCA | 6088 |
| Dd | 2018 | GTTCGAGTGGTCTCCCGATAACCAAGTATGATGGTTGACATAGGAAACAAATGGATGT | 2077 | Dd | CTGCAAAACAGCTTCTTGGGTACAAGTCGGAGGGTCTTATTCAAAATACAGAAAGCAGACT | 3157 |
| Qy | 5012 | CTCAAGAGTGTACCAACAAAGACACGAGTGTGGCCATGATGACATACCAATGCAATTC | 5071 | Qy | AGCTGGCAGAGACGCTCTATGACACCAACCAAGTCAGTTTACCTATGACGAGACGGCA | 6148 |
| Dd | 2078 | TTGAAAAGCATGACTGTCAAGGACTGGAATTAGTTNNGTTTACTTANNNNNNNNNNNN | 2137 | Dd | AGGCTCTCAGAAATTTTATGATAGCACGAGTCAAGTTTACCTACGATGAACAGCA | 3217 |
| Qy | 5072 | GGCCTTCTGGCAACCAAAAGCAATGAAACCGATGGACAACATTTTATGATGACGACGC | 5131 | Qy | GGCATGCTGAAGACCATCAACCTACAGAAATGAGGGCTTCACTGCCACCATCCGCTACCGT | 6208 |
| Dd | 2138 | NN | 2197 | Dd | GGAGTCTTAAGACAGTAAACCTCCAGAGTGACGGTTTTTATTTGCAACCATTAGATACAGG | 3277 |
| Qy | 5132 | TTTGGCGCCTGACAAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTGAT | 5191 | Qy | CAGATTGGGCCCCTGATTGACCGACAGATCTTCCGCTTCACTGAGGAGGATGCTCAAC | 6268 |
| Dd | 2198 | GAAGTGTCTGACAAATGTTACGTTTCCAACCTGGAGTGTCAAAACCTGCTATGGGAC | 2257 | Dd | CAAAATTTGGTCCCCTGATTGACAGGCAGATTTTCCGCTTTAGTGAAGATGGGATGTAAT | 3337 |
| Qy | 5192 | ACAGACAGTTCAAGTGCATGTCAGGTAGAGACCTCCAGC---AAGGATGATGCACATA | 5248 | Qy | GCCCGTTTGTGACTACAACTATGACAAACAGCTTCCGGGTGACCAAGTGCAGGCTGTGATC | 6328 |
| Dd | 2258 | ATGGACAAGGCTATCACAGTGGACATTSAGTCTATCTAGCCGAGAGGAAGATGTCA | 5317 | Dd | GCAAGATTTGACTATAGCTATGACACAGCTTTCGGAGTGACCAAGATGCAAGGGTGTGATC | 3397 |
| Qy | 5249 | ACCACCAACCTGTCTGCTCAGGCGCTTCTACACACTGTGCAAGACCAAGTCCCGAAC | 5308 | Qy | AACGAGACCCCACTGGCCATTTGATCTCTATCGCTATGATGATGTGTGTCAGGCAAGACAGAG | 6388 |
| Dd | 2318 | ACTTCAATCTGTCTCGATCGATTCTTTCTACACCATGGTTCAAGATCAGTTAAGNAAC | 2377 | Dd | AATGAACTCCACTGCTATTGATCTGTATCAGTTTGTATGACATTTCTGGCAAAAGTTGAG | 3457 |
| Qy | 5309 | AGCTACTACATCGGGCGCATGGCTCTCTGGCGTCTGCTGGCCCAACGGCATGGAGGTG | 5368 | Qy | CAGTTTGGGAAGTTTGGAGTTATATATATGATATTAACCCAGATCATTTCTACAGCTGTN | 3517 |
| Dd | 2378 | AGCTACAGATTGGTTATAGCGCTCCCTCAGAAATTAATCTACGCCAGCGGCTGGACTCA | 2437 | Qy | ATGACCCCAACCAAGCATTTTGGATGATATGGCAGGATGAAGAGTGCAGTATGAGATC | 6508 |
| Qy | 5369 | GGCTGCAGACTGAGCCCACTTGTCTGGCTGGGCAACCGTCAACCCACCGTGGGCAAGAGG | 5428 | Dd | ATGACCTATACGAAGACATTTGATGTCTATGCTGTCATGGCCGATCAAGGAGATTCAATATGAGATA | 3577 |
| Dd | 2438 | CATTACCAAAACAGAGCGGCATTTCTGGCTGGCATCTGCTAATCCAAACCGTTGCCAAAAGA | 2497 | Qy | TTCCGCTCGCTCATGTACTGAGTACCGCTCCAGTATGATGATAACATGGGGCGAGTAGTGAAG | 6568 |
| Qy | 5429 | AATGTACGCTGCCCATCGAACACCGGCTCAACCTGGTGGAGTGGCGCCAGCGCAAGAG | 5488 | Dd | TTGAGTCTGCTCATGTACTGGAATTACAAATTCAGTATGATGAATACATGGGTCGGGTAACCAAG | 3637 |
| Dd | 2498 | AACATGACGTTGCTGTGTGAGAACGGTCAAACTTTGGTGGAAATGGAATTCGGAANAAG | 2557 | Qy | AAGGAGCTGAAGGTAGAGACCTTACAGGCAATACCTCGCTACTCTCTATGATGATGATGCT | 6628 |
| Qy | 5489 | CAGGCTCGGGCCAGGTCACCTGTCTTTGGCGCGCGCTGGGGTGGCAACACCGAAATCTC | 5548 | Dd | AGAGAGATTAAAAATAGGGCCCTTTGGCAACACCAACCAAAATATGCTTATGATGATGATGTT | 3697 |
| Dd | 2558 | CAAGCCCAAGGGAAGTCAATGTCTTTGGCGCAAGCTCAGGGTTAATGCGAAGAACTCTC | 2617 | Qy | GACGGCAGCTGACAGACGCTCCATCAATGACAGCCCATCTCTGGCGCTACACCTAGCAC | 6688 |
| Qy | 5549 | CTATCTCGGATTTGATCGGGTAAACAGCAACAGAGAAAGATCTATGATGATCCACCGCAAG | 5608 | Dd | GATGGAACGCTCCAAACAGTTTACCTCAATGAAAAGATATATGTGGGGGTACAACTACGAT | 3757 |
| Dd | 2618 | CTTTCAGTTGACTTTGATCGAAACAAACAAAGACAGAAAAGATCTATGACGACCAACCGTAAA | 2677 | Qy | CTCAATGGGAACTCTGCACTTTACTGAGCCCTGGGAAACAGTGCACGGGCTCACACCACTACGG | 6748 |

| | | | | | | |
|------------|---|---|------|------|--|------|
| Db | 3758 | CTGAATGGAAACCTCCATTTACTGAAACCCCAAGTAAACAGTGGCGGTCTGACACCCCTTCGC | 3817 | 4820 | GTGAGAGCAACGCTGCTCAACATCGCCAAACGAGGACTGCATCAAGGTGGCGCGCTGCTC | 4879 |
| Qy | 6749 | TATGACATCCGCGACCGCATCCTCGCTGGGTGAGCGTGAACATACAAAGATGGATGAGGAT | 6808 | 7829 | AAACCATGCCCACTACTAGAGAACTTGACATTCACCATTTGATGGGTGATACCCATTAC | 7888 |
| Db | 3818 | TATGACCTGCGAGACAGAACTCACTCGACTGGGTGATGTTCAATATATCGTTGGTGAAGAT | 3877 | 4880 | AACAACGCGCTTCTACCTGGAGAACTTGACATTCACCATCGAGGGAAGACACGCACTAC | 4939 |
| Qy | 6809 | GGCTTCCTGAGGACGCGGGGGGTGATATCTTTGAGTACAACTCAGCTGCCTGCTCATC | 6868 | 7889 | TTTGTGAACACGAGACCTTTCAGAAAGTGCACCTGGGCCATCCTGGGCTCAGTGGGGGGCGG | 7948 |
| Db | 3878 | GGTTTCTTACGTCAAAGGGGACGGAATCTTTGAAATATAGCTCAAAGGGGCTTCTAACT | 3937 | 4940 | TTTCATCAAGACACACACGCCCGAGAGCGACCTGGGCGCTGCGGCTGACGAGCGCGCG | 4999 |
| Qy | 6869 | AAGGCTTACACCGGGCTGGCAGCTGGAGTGTCAAGTACCGCTACGATGCGCTGGGCGG | 6928 | 7949 | CGAACCTCTGGAGATGGGGTCAACGTCACTGTGTCCAGATCAACACAGTACTTAAATGCG | 8008 |
| Db | 3938 | CGAGTTTACAGTAAAGGAGTGGCTGGACAGTGANNACCGTTATGACGGCGCTGGGAAG | 3997 | 5000 | AAGGCGCTGGAGAACGGCATCAACGTGACGCGTGTGCGAGTCCACCAAGTGGTGAACGCG | 5059 |
| Qy | 6929 | CGCGTGTCCAGCAGAGAGCCACAGCCACCACTGCACTGAGTGTGAGTGGTGTGAGTGGT | 6988 | 8009 | AGGAC 8013 | |
| Db | 3998 | CGTGTNNNAGCAAAACCAAGTCTAGGACAGCACCTGCGAGTTTATGCTGACTTAACT | 4057 | 5060 | AGGAC 5064 | |
| Qy | 6989 | AACCCACCAAGGTCAACCACTGTACAAACCACTCCAGCTCTGAGATCACCTCCCTCTAC | 7048 | | | |
| Db | 4058 | TATCCCACTAGGATTACTCATGCTTACAAACCAATTCGATTCAGAAATTTACCTCCCTGTAN | 4117 | | | |
| Qy | 7049 | TACGACTTGCAGAGCACCTCTTTGCCATGGAGCTGAGCAGTGGTGTGAGTGGTGTACATA | 7108 | | | |
| Db | 4118 | NTGATCTCCAGGACATCTTTTGGCATGGAAATCAGCAGTGGGGATGAATTTCTATAT | 4177 | | | |
| Qy | 7109 | GCTTGTGACAACTCGGACCCCTCTTGTCTTTAGTGGAAACAGGTTTGTATGATCAAG | 7168 | | | |
| Db | 4178 | GCATCAGATAACACAGGACACCACTGGCTGTGTTCAAGTAGCATGGCTTATGCTGAA | 4237 | | | |
| Qy | 7169 | CAAACTCTGACAGACCTTATGGGAGATCTACATGGATACCAACCCCAACTTTCCAGATC | 7228 | | | |
| Db | 4238 | CAGATTCACTGACTGATATGGTGAATCTATTTTGACTCTAATATGACTTTCAACTG | 4297 | | | |
| Qy | 7229 | ATCATAGGTACCATGGTGGCTTATGATCACTACCAAGCTTGTCCACATGGGCGCG | 7288 | | | |
| Db | 4298 | GTAATTTGGATTTTCATGGTGGCTGTATGACCCACTCACCAAAATTAATCCACTNNNNNN | 4357 | | | |
| Qy | 7289 | CGAGATTATGATGTGCTGGCGGACGCTGGACTAGCCAGACCAAGCTGTGGAAGCAC | 7348 | | | |
| Db | 4358 | NN | 4414 | | | |
| Qy | 7349 | CTTAGTAGCAGCAACGTCATGCTTTTAACTCTATATGTTTCAAAACCAACACCCATC | 7408 | | | |
| Db | 4415 | AGAATCGGAAGACCCAGCTCTCTTTAACTTGATCATGTTTGAAGATTAACAAACCTGCA | 4474 | | | |
| Qy | 7409 | AGCAATCCAGGACATCAAGTCTTCATGACAGATGTTAAACAGCTGGCTGCTCACTTT | 7468 | | | |
| Db | 4475 | AGCAAAATCCATGACGCTGAAGATTTATCATCAGATGTTAACAGCTGGCTGGTGAATTT | 4534 | | | |
| Qy | 7469 | GGATTCAGCTTACAAACGTCATCCCTGGTTATCCCAACACAGATGGATGCCATGGAA | 7528 | | | |
| Db | 4535 | GGTTTCCATCTGCACATGCTATTCCTGGATTCCTGTTCCCAAAATTTGATTTAAACAGAA | 4594 | | | |
| Qy | 7529 | CCCTCTCAACGAGCTCATCCACACAGATGAAGACGAGAGTGGGACACAGCAAGTCT | 7588 | | | |
| Db | 4595 | CTTCTTACGA-----ACTTGTGAAGAGTCAGCAGTGGGATGATGATACCGCC | 4642 | | | |
| Qy | 7589 | ATCCTCGGGTACAGTGTGAGTACAGAAGCAGCTCAAGGCTTTGTCACTTTAGAACGG | 7648 | | | |
| Db | 4643 | ATCTTCGGAGTCCAGCAGCAGTGGCGGCGCAGCGCTTCCTGCTCGCTGGGGAAG | 4702 | | | |
| Qy | 7649 | TTTGACCAAGCTTATGGCTCCACAATCACAGCTGCCAGCAGGCTCCAAAGACCAAGAG | 7708 | | | |
| Db | 4703 | ATGCGCGAGGTGCAGTGTGAGCGCGCGCGCGCGCGC-----GGCGCGCAGTCTTGCTGTG | 4759 | | | |
| Qy | 7709 | TTTGATCCAGGGCTCAGTCTTTGGCAAGGGGTCAAGTTTGGCTTTGAAGATGGCCGA | 7768 | | | |
| Db | 4760 | TTTCGCCACCGGTCAAGTGCCTGATCGGCAAGGGCGGTCTGCTGGCGGTGACCCAGGCGCG | 4819 | | | |
| Qy | 7769 | GTGACCACACAGATCATCAGTGTGGCCAAATGAGGATGGCGAAAGGTTGTGCCATCTTG | 7828 | | | |
| LOCUS | AY405422 Mus musculus HMM218 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. 5087 bp DNA linear GSS 12-DEC-2003 | | | | | |
| DEFINITION | AY405422 Mus musculus (house mouse) | | | | | |
| ACCESSION | AY405422.1 GI:39761396 | | | | | |
| VERSION | GSS. | | | | | |
| KEYWORDS | Mus musculus (house mouse) | | | | | |
| SOURCE | Mus musculus | | | | | |
| ORGANISM | Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. | | | | | |
| REFERENCE | 1 (bases 1 to 5087) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003) | | | | | |
| AUTHORS | 14671302 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. | | | | | |
| TITLE | Direct Submission | | | | | |
| JOURNAL | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA | | | | | |
| PUBMED | This sequence was made by sequencing genomic exons and ordering them based on alignment. | | | | | |
| REFERENCE | Location/Qualifiers | | | | | |
| AUTHORS | 1..5087 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1..>5087 /locus_tag="HMM218" | | | | | |
| TITLE | source | | | | | |
| JOURNAL | gene | | | | | |
| COMMENT | ORIGIN | | | | | |
| FEATURES | Query Match 26.7%; Score 2232.8; DB 10; Length 5087; Best Local Similarity 68.4%; Pred. No. 0; Matches 3178; Conservative 0; Mismatches 1432; Indels 36; Gaps 5; | | | | | |
| source | Qy 2912 TTTGACTTGGTGACAAATGGCGGCATCTCCATCATCTCGGTTTCGAGGGGACCTTTC 2971 | | | | | |
| gene | Db 1 TTTGACTTGGTGACAAATGGCGGCATCTCTGACTTTTGGTATTTGAGGGTTCCTCCATTC 60 | | | | | |
| ORIGIN | Qy 2972 ATCACACAGGACACACCTCTGGCTGGCTGCCATCGGATCGCTTCTTGTCTCATGGAACCATC 3031 | | | | | |
| | Db 61 CTCACTCAGTACCACTGTGTGGATTCCTGGATTCCTTGTATGATGATACCTT 120 | | | | | |
| | Qy 3032 ATCATGAGACATGAGGAGAAATGAGATTCCAGCTGTGACCTGAGCAATTTTGGCCGCC 3091 | | | | | |

| | | | | | | |
|----|------|---|------|------|---|------|
| QY | 5249 | ACACCAACCTGCTGCTCAGGCGCCTCTACACACTGCTGCAAGACCAAGTCCGGAAC | 5308 | 1329 | AACGAGACCCACCTGCCATTGATCTCTATCGCTATGATGATGTTGTGACGACAGAC | 6388 |
| DB | 2311 | ACTTCGAACCTTGTCTCCATCGATTCCTTCTACACCATGCTCCAGACCAAGTTAAGAAC | 2370 | 1391 | AATGAAACACCACTGCCCATTTGATCTATACCACTTTGATGACATCTCTGGCAAGATCGC | 3450 |
| QY | 5309 | AGCTACTACATCGGGGCGGATGCTCTTCCGCTGCTGCTGCGCAACGGCATGGAGTG | 5368 | 6389 | CAGTTTGGGAAGTTTGGTGTCACTTATGACATTAACAGATCATCACCACTGCTC | 6448 |
| DB | 2371 | AGTTACCAAGTTGGTATGATGCTCTTCTAGAAATCTTATGCACTGCTGCTGCTCT | 2430 | 3451 | CAGTTTGGGAATTCGGAGTGATATACGACATCAACCAAAATCAITTTCCAGCGCGTG | 3510 |
| QY | 5369 | CGCTGCGAGATGAGCCCACTTCTGCTGGCTGGACCTCAACCCACCGTGGCAAGG | 5428 | 6449 | ATGACCCACACCAAGCATTTTGTATGTCATATGGCAGATGAAGAGTGCAGTATGATC | 6508 |
| DB | 2431 | CACCTACCAAG | 2490 | 3511 | ATGACCTTATACAAAGCATTTTGTATGCTCATGGGCGCATCAAGAGATCCAATATGATA | 3570 |
| QY | 5429 | AATGTCAGCTGCCATCGAACAGGCTCAACCTGGTGGAGTGGCGCCAGCGCAAGAG | 5488 | 6509 | TTCCGCTCGCTCATGTACTGTGATGACCGTCCAGTATGATAATCATGGGCGGATGAG | 6568 |
| DB | 2491 | AACATGATCTTCCCGGTGAGAACGGGCGAGATCTGGTGGAGTGGAGATTCCGAAAGAA | 2550 | 3571 | TTTAGGTCACTCATGTACTGTGATTAACAATTAATATGATATATATGGGCGGATTAACCAAG | 3630 |
| QY | 5489 | CAGGCTCGGGGCGAGGTCACTGTCTTTGGGCGCGGCTGCGGGTGCAACCCGAATCTC | 5548 | 6569 | AAGGAGCTGAAGGTAGGACCTTACCGCAATACCACTCGCTACTCTCTATGATGATGATCT | 6628 |
| DB | 2551 | CAAGCCAGGCGAAAGTCAAGTATTCGGCGCGAAGCTCAGGGTCAATGGGCGCAACCTA | 2610 | 3631 | AGAGAGATTAAATTTGGGCTTTTGGCAACACTCAAAATACGCGTACGAGTACGACGTC | 3690 |
| QY | 5549 | CTATCTCTGGACTTGTATCGGTACACGACAGAGAGATCTATGATGACCAACCGCAAG | 5608 | 6629 | GACGGCAGCTGCAGACAGTCTCCATCAATGACAAAGCCACTCTGGCGCTACAGCTACGAC | 6688 |
| DB | 2611 | CTCTCAGTGAATCTTGTATCGGACCAACAGACGGAAGATCTATGATGACCAACCGGAA | 2670 | 3691 | GATGGACAGCTCCAAACAGTTTACCTTAACGAAAGATCATGTGGCGGTACAACTACGAC | 3750 |
| QY | 5609 | TTTACCCTTCGGATTCGTGACACAGGCGGGGCGGCGGCTCTGTGTACCCAGGAGC | 5668 | 6689 | CTCAATGGGAACCTGCACCTTACGTAGCCCTGGGAACAGTGCACGCTCACACCTACCG | 6748 |
| DB | 2671 | TTTCTCTGAGGATCGCTTACGACAGCTCGGGGCAACCGGCTCTCTGGCTCGGAGTAGC | 2730 | 3751 | CTAAATGGAAACCTCCACTTTGCTCAACCCGACGACGCGCGCTGACCCCTCTGCGC | 3810 |
| QY | 5669 | AGGCTGAATGGTGTCAAGTGAATCTCCCTCGGGGTTCATTTGCTGGCATCAGAGG | 5728 | 6749 | TATGACATCCGGACCGCATCACTCGGCTGGGTGAGCTGCAATACAAAGATGATGATGAT | 6808 |
| DB | 2731 | AAGCTAATGGAGTGAATCTACCTACTCATCCAGGTCMAATTTGCCAGATCCAGAGA | 2790 | 3811 | TATGACCTGCGCAGCAAGATCAACCCCTGGGCGATGTTTCAGTACCGGTGGATGAAGAT | 3870 |
| QY | 5729 | GGCATCATCTCTGAAAGATGAATACGACAGGCGGGCGGATCACAATCCAGGATCTTC | 5788 | 6809 | GGCTTCTGAGGCGGGGCGGTGATATCTTTTGTAGTACAACTCAGCTGGCTGCTCATC | 6868 |
| DB | 2791 | GGGACCAAGCGAAAGTGGACTATGACGCGGGGAGGATCGTATCTCGGCTCTTT | 2850 | 3871 | GGTTTCTCGCTCAGAGGGGCACTGAAATTTTGAATACAGCTCCAAAGGGCTTCTGACT | 3930 |
| QY | 5789 | GCTGATGGGAAGACATGGAGCTACATATTTAGAGAGTCCATGGTGTCTACTACAC | 5848 | 6869 | AAGCCTTAACCGGGCTGCGAGCTGGAGTGCAGGTACCGTACGATGGCTGGGCGCG | 6928 |
| DB | 2851 | GCCGATGGGAAACATGGAGTTACAGTACTTTGGAAAGTTCATGGTTCTTCTGCTCCAT | 2910 | 3931 | CGAGTCTACAGTAAAGCGAGTGGCTGGACAGTGTCTATCGGTACGACGGCTTGGGAAGA | 3990 |
| QY | 5849 | AGCCAGGCGAGTATCTTTGAGTTCGACAAAGATGACCGCTCTCTTCTGTGACGATG | 5908 | 6929 | CGGTGTCCAGCAAGAGCAGCCACAGCCACCTGCGAGTTCCTATGAGACAGCTGACC | 6988 |
| DB | 2911 | AGCCAGGCGAGTACATCTTCGAATACGACATGTGGGACCGGCTGTCCGCCATCACCATG | 2970 | 3991 | CGTGTCTTACGAAACACCGCTGGGACAGCACCTTCAGTTTTTCTACGCGGACCTGACA | 4050 |
| QY | 5909 | CCCAAGTGGCGGGCGAGACCTAGAGACATCCGCTCAGTGGGCTACTACAGAAACATC | 5968 | 6989 | AACCCCAACCAAGGTCAACCACTGTGTACAACTCCAGCTCTGAGATCACTCCCTCTAC | 7048 |
| DB | 2971 | CCCAAGTGGCTCGCCACACCATGACAGCCATCCGCTCCATTTGGCTACTACCGCAACATC | 3030 | 4051 | TACCCCAAGAAATTACTACGCTACAACTTCAGTTCCAGTTTCAGAAATCACCTCCCTGTAC | 4110 |
| QY | 5969 | TATCAGCCCTCGAGGCAATGCTCAGTCATACAGGACTTCACTGAGATGGGCACTTC | 6028 | 7049 | TACGACTGCAAGGACACCTCTTTGCCATGGAGCTGAGCAGTGGTGTATGATTTTACATA | 7108 |
| DB | 3031 | TACAAATCCCGAGAAAGCAATGCTCTATCATCACCACTACAAAGAGTGGTGTCTT | 3090 | 4111 | TATGACCTCCAGGACATCTCTCGCCATGGAGATCAGCAGTGGGATGAGTTCTACATC | 4170 |
| QY | 6029 | CTTCACACCTTCTACCTGGGCACTGGCGCGAGGGTGATATACAAAGTATGGCAACTGTCA | 6088 | 7109 | CGTTGTGACAAACATCGGGACCCCTCTTGTGTCTTTTATAGTGGACAGGTTTGTATGATCAAG | 7168 |
| DB | 3091 | CTGCAACAGCTTCTCTGGGACGAGTGGGAGGTCTTATTAAGTATAGAAAGGACAGCC | 3150 | 4171 | GCCTCGGACACACGGGACACCGCTGGCTGTTTTTTCAGCAGCAACCGGCTCATGCTGAAA | 4230 |
| QY | 6089 | AAGCTGGCAGAGCGCTCTATGACACCAAGTCAAGTTTCACTTACCTATGAGAGCGGA | 6148 | 7169 | CAATCTGTGTACAGCCTATGGGAGATCTACATGATGATACCAACCCCACTTTTCAGATC | 7228 |
| DB | 3151 | AGGCTATCAGAAATTTTATACGACAGCAAGAGTCAAGTTTACCTACGACGAAACAGCG | 3210 | 4231 | CAGATCCAGTACACTGCTTATGGTGAGATCTACTTTGACTCCAGCTGCAGCTTTTCAGCTG | 4290 |
| QY | 6149 | GGCATGCTGAGACCATCACTACAGATGAGGGCTTCACTGCAACCATCCGCTACCGT | 6208 | 7229 | ATCATAGGCTACCAATGGTGGCTCTCTATGATCCACTCACCAAGCTTGTCCATATGGGCGCG | 7288 |
| DB | 3211 | GGAGTCTGAAACAGTAAACCTTCAGATGATGTTTATTTTGCACCATTAGATACAGG | 3270 | 4291 | GTAATTTGATTCACGGGGCTTGTATGACCGCTCACCAAACTAATCCACTTTTGGAGAA | 4350 |
| QY | 6209 | CAGATTGGGCGCTGATTGACCGACAGATCTTCCGCTTCTCTGAGGAGGATGCTCAAC | 6268 | 7289 | CGAGATTAATGATGCTCGCGGAGCGCTGGAGTAGCCAGACCAAGCTGTGGAGAGAC | 7348 |
| DB | 3271 | CAATTTGCTCCCTGATTGACAGACAGATTTCCGCTTTCAGCGAGGATGAAATGGTAAAT | 3330 | 4351 | AGAGATTATGACATTTTGGCGGGAAGATGGACCAACCGGACATTTGAAATCTGGA--NA | 4407 |
| QY | 6269 | GCCCGTTTGTATACATATGACACAGCTTCCGGGTGACAGCATGACAGGCTGTGATC | 6328 | 7349 | CTTAGTAGCAGCAACGTATGCTTTTAACTCTCTATATGTTTCAAAAACAAACCCCATC | 7408 |
| DB | 3331 | CGGAGATTGACTATAGCTACGACAAACAGCTTTTCAAGTGACAGATGTTTAAACAGCTGGCTGCTCATT | 3390 | 4408 | AGGATCGGAAAGAGCCCTGCTCTTTTAACTGTATATGTTTTCGGAATAACAAACCCCGG | 4467 |
| QY | | | | 7409 | AGCAACTCCAGGACATCAAGTGTCTCATGACAGATGTTTAAACAGCTGGCTGCTCATT | 7468 |

| | | | | | | | |
|----|------|--|------|----|------|---|------|
| Db | 182 | AAACCTACTTCCATTGATTTTGATCATATGACCGGCACCGGTAAAGATCTATGATGACCA | 241 | Db | 1259 | TGATGCTGATGGCAACTTCAAACCTGTTTCTGTGAATGACAAAAATCCAGTGGCGGTATAG | 1318 |
| Qy | 5602 | CCGAAAGTTACCCCTTCGGATTCTGTAGCACCAGGCGGGGCGCCACCGCTCTGGTCACC | 5661 | Qy | 6682 | CTACGACCTCAATGGGAACCTGCACTTACTGAGCCCTGGGAACAGTGCACGGCTCACACC | 6741 |
| Db | 242 | CCGAAAATTCACCTCTCGAATTTCTTATGACCAGACCGGGGCGACCTTATCTGTGGTCTCC | 301 | Db | 1319 | TTATGATCTGAATGGAAACATCAACCTTTTGGGCCATGGGAATAGTGTCTGTACTTACC | 1378 |
| Qy | 5662 | CAGCAGAGGCTGAATGCTGTCAACGTGACATATCTCCCTTGGGGGTTTACATTCCTGGCAT | 5721 | Qy | 6742 | ACTACGGTATGACATCCCGCAGCCGACATCACTCGGCTGGGTGACGTGCAATCAAGATGGA | 6801 |
| Db | 302 | TGTGAGCAGATATTAATGAGTGAACATCAGTATTCACCTTCAGGATTAGTCAATTTAT | 361 | Db | 1379 | TCCTCGATATGACCTCCGAGACCGCATCACTAGACTAGGGGAAATTCAGTATAAATGGA | 1438 |
| Qy | 5722 | CCAGAGGGCATATGCTCTGAAAGAAATGGAATACGACGCGGGCGGCATCATCCAG | 5781 | Qy | 6802 | TCAGGATGCTTCCTGAGGACGCGGGGGGTGATATCTTTGAGTACAACTCAGCTGGGCT | 6861 |
| Db | 362 | TCAAGAGGAACCTTGAATGAAAAGATGGAGTATGACCAGAGTGGAAAATAATCTCAAG | 421 | Db | 1439 | TCGAAGACGGTTTCTGAGACAGAGGGGAAATGATATATTTGAGTATAATTTCTAATGGTCT | 1498 |
| Qy | 5782 | GATCTTCGCTGATGGGAGACATGGAGCTACACATATCTTAGAGAAAGTCCATGGTGTGCT | 5841 | Qy | 6862 | GCTCATCAAGGCTCAAAACCGGCTGGCAGCTGGAGTGTCAAGGTACCGCTACGATGGGCT | 6921 |
| Db | 422 | AACTTGGGCGGATGGGAAAATTTGGAGCTATACCTATTAGAAAAGTCTGTGATGCTTCT | 481 | Db | 1499 | GCTGCGAAGGCTTACATTAAGTTCCTGGCTGGACTGTACAGTATTACTATGATGGGCT | 1558 |
| Qy | 5842 | ACTACACAGCCAGAGCGAGTATATCTTTTGGTTCGACAAGAAATGACCGCCTCTCTTCTGT | 5901 | Qy | 6922 | GGGGCGGCGGTGTCCAGCAAGAGCAGCAGCAGCCACCTGTACAAACCACTCCAGCTCTGAGATCACCTC | 7041 |
| Db | 482 | GTTACACAGTCAGCGCGTTACATCTTTGAGTATGACCAATCAGATTGCTGCTCAGT | 541 | Db | 1559 | TGGGCGACGGTTGCCAGTAACTCCAGCTAGGACAGCATCTCCAATTCCTTTATGCGAGA | 1618 |
| Qy | 5902 | GACGATGCCCAAGCTGGCGGCGCAGACACTAGAGACCATCCGCTCAGTGGGCTACTACAG | 5961 | Qy | 6982 | CCTGACCAACCCCAACCAAGGTCACCCACCTGTACAAACCACTCCAGCTCTGAGATCACCTC | 7041 |
| Db | 542 | TACCATGCTAGCATGCTGCGCCACAGCTTTACAAACCATGCTTTCAHTGGGCTACTACCG | 601 | Db | 1619 | CCTGGCCAAACCTTATAAGAGTTACTCATCTGTACAACCAACAGCGCAGAGATTACATC | 1678 |
| Qy | 5962 | AAACATCTATACGCCCTTGAGGGCAATGCCCTCAGTCAATACAGGACTTCACTGAGGATGG | 6021 | Qy | 7042 | CCTCTACTACGACTTGCAAGGACACCTCTTTGCCATGGAGCTGAGCAGTGGTGTGATGAGTT | 7101 |
| Db | 602 | TTAATATCTACCCNACCAGACAGCAGCACCTCTTTTATCCAAGACTACAGTCGAGATGG | 661 | Db | 1679 | TCCTTATATGATCTCCAAGGTCACCTTATGCGCATGGAGCTAAGCAGTGGTGAGGAATA | 1738 |
| Qy | 6022 | GCACCTCTTTCACACCTTCTA CTGGGCACTGGCGGAGGGTGTATACAAAGTATGGCAA | 6081 | Qy | 7102 | TTACATAGCTTTGTGACAAACATCGGGACCCCTCTGTGCTGCTTTAGTGGAAACAGGTTTGAT | 7161 |
| Db | 662 | CCGACTGTTTACAGACTCTGCATCTAGGGACTGGGCGCAGAGTTTATACAAGTACACANA | 721 | Db | 1739 | TTATGTAGCCTGTGTATAATATGGGCACTCCATTAGCTGTGTTTCAGCAGTCGGGTCAGGT | 1798 |
| Qy | 6082 | ACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACCAAGGTCAGTTTCACTATGACGA | 6141 | Qy | 7162 | GATCAAGCAAACTCCTGTACACAGCCTATGGGGAGATCTACATGGATACCAACCCCAACTT | 7221 |
| Db | 722 | GCAAGCAAGACTGTCTGAGATTCTCTATGACACCACTCAGTCACTTAACATATGAAGA | 781 | Db | 1799 | CATAAAGAGATTCTGTATACACCTTATGCTGATCACTACCATGATACATACCCTGACTT | 1858 |
| Qy | 6142 | GACGGCAGGCATCTCTGAAGACCATCAACCTACAGAAATGAGGCTTCACTGACCATCGG | 6201 | Qy | 7222 | TCAGATCATCATAGGCTACCATGTGGGCTCTATATGATCCACTCACCAGGCTTGTCCACAT | 7281 |
| Db | 782 | GTCTTCTGGAGTAAATTAAGACAAATACACCTGTATGATGACGGATTCATCTGCACATCAG | 841 | Db | 1859 | TGAGGTCATCATTTGGTTTTTCATGGAGGACTCTATGATTTTCTTACTAAACTAGTGCATCT | 1918 |
| Qy | 6202 | CTACCGTCAAGTTGGGCCCTGATTGACGACAGATCTTCCGCTTCACTGAGGAAGGAT | 6261 | Qy | 7282 | GGGCGGCGAGATTATGATGTGCTGGCGGACGCTGGACTAGCCAGACACCAAGCTGTG | 7341 |
| Db | 842 | ATACAGCAAAACAGGACCTCTCAATTGGAGCTCAGATTTTCCGATTCACTGGAAGGTTCT | 901 | Db | 1919 | AGGCAAAAGAGATTATGATGTTGTTGCTGSCAGATGGACAACGCCTAATCATCACATATG | 1978 |
| Qy | 6262 | GGTCAACGCCGTTTTTGACTACAACTATGACAAAGCTTCCGGGTGACCCAGCATGAGGC | 6321 | Qy | 7342 | GAAGCACTTAGTAGCAGCAACGTCATGCGCTTTTAAATCTCTATATGTTTCAAABACACAA | 7401 |
| Db | 902 | TGTGAATGCAAGGTTTGACTACA- --GTTACAACTTTTCGTTGTCACCGCATGCAAGC | 958 | Db | 1979 | GAACAGTTGA- --ACCTTCTTCTTAAACCAATTCACCTCTCTCTTTTGAGAAATACTA | 2035 |
| Qy | 6322 | TGTGATCAACGAGACCCCATGCCCCATTGATCTCTATCGCTATGATGATGTGTCAGGCAA | 6381 | Qy | 7402 | CCCCATCAGCAACTCCCGGACATCAAGTGTTCATGACAGATGTTAAACAGCTGGCTGCT | 7461 |
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| Qy | 6382 | GACAGCAGTTTGGGAAGTTTGGTGCAATTTACTATGACATTAACAGATATCACTACCAC | 6441 | Qy | 7462 | CACCTTTGGATTTCAGGCTACACAAAGTATCCCTGGTTTATCCCAAAACAGACATGGATGC | 7521 |
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| Qy | 6502 | TGAGATCTTCGCTCGCTCATGTACTGGATGACCGCTCCAGTATGATTAACATGGGCGAGT | 6561 | Qy | 7582 | CHAAGTCTATCTCCGGGTACAGTGTGAAGTACAGAAAGCAGCTCAAGGCTTTGTCACTT | 7641 |
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DEFINITION AL137500
ACCESSION AL137500
VERSION AL137500.1 GI:6808144
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 2926)
AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaidp,A.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
The German cDNA Consortium
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinried/Germany) within the cDNA
sequencing consortium of the German Genome Project.
This clone (DKFp761F171) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFp761F171
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
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ORIGIN

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Best Local Similarity 68.6%; Pred. No. 2.9e-297;
Matches 1766; Conservative 0; Mismatches 776; Indels 33; Gaps 5;
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FEATURES

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RESULT 10
AK039472 1284 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus adult male spinal cord cDNA, RIKEN full-length
DEFINITION enriched library, clone:A330048C04 product:neuregulin 1, full

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| Qy | 3095 | CCAGTGTCTCTCCATCCCACTGAGCTCTCTCGCAGCTCTCTGTGCAGAGAAAGGCCCC | 3154 |
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| RESULT 11 | | | |
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| DEFINITION | DKFZp343F206 r1 434 (synonym: htes3) Homo sapiens cDNA clone | | |
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| VERSION | AL045768.1 GI:5433880 | | |
| KEYWORDS | EST. | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | | |
| | Hominidae; Homo. | | |
| REFERENCE | 1 (bases 1 to 718) | | |
| AUTHORS | Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S. | | |
| TITLE | EST (Koehler, et al.) | | |
| JOURNAL | Unpublished (1999) | | |
| COMMENT | Contact: MIPS | | |
| | MIPS | | |
| | Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany | | |
| | This is the 5' sequence of the clone insert | | |
| | Clone from S. Wiemann, Molecular Genome Analysis, German Cancer | | |
| | Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; | | |
| | sequenced by BMFZ (Biomedical Research Center at the Charite, | | |
| | Berlin/Germany) within the cDNA sequencing consortium of the German | | |
| | Genome Project. | | |
| | sl sequence also available. | | |
| | This clone (DKFZp343F206) is available at the RZPD in Berlin. | | |
| | Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 | | |
| | Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. | | |
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| Db | 61 | TCCCTGGTTATCCCAAAACACAGATGGATGCGCATGGAAACCTCTACGAGCTTATCCACA | 120 |
| Qy | 7551 | CACAGATGAAAACGAGGAGTGGGACAAACAGCAAGTCTTCTCTCGGGGTACAGTGTGAAG | 7610 |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| 121 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|

| |
|--|
| RESULT 13 |
| CV559879 |
| LOCUS |
| DEFINITION |
| CV559879 762 bp mRNA linear EST 22-OCT-2004 |
| UI-M-HZO-ctk-j-07-0-UI.r1 NTH_BNAP_HZO Mus musculus cDNA clone |
| IMAGE:30692478 5' , mRNA sequence. |

| | |
|-----------|--|
| SOURCE | Mus musculus (house mouse) |
| ORGANISM | Mus musculus |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 762) |
| AUTHORS | NIH-MGC http://mgc.nci.nih.gov/ . |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) |
| JOURNAL | Unpublished (1999) |
| COMMENT | Contact: Robert Strausberg, Ph.D. |

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 762)
N1H-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, ph.D.

NATIONAL INSTITUTE OF HEALTH, HUMANOMICS CORE COLLABORATION (NIH)
 UNPUBLISHED (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-x@mail.nih.gov
 Tissue Procurement: Dr. James Lin University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

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Seq primer: pyx-5.
Location/Qualifiers
1..762
source
FEATURES

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"

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/clone="IMAGE:30692478"
/tissue_type="whole eye"
/dev_stage="newborn 1,5,15 and embryos 15,16,17,18 dpc"

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/clone.lib="NIH_BMAP_H20"  
  
/note="Organ: Eye; Vector: pyx-Asc; Site_1: EcoR I;  
Site 2: Not I; The library was constructed according
```

1996). Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-Asc vector. The library tag sequence located between the NotI site and the polyA tail

This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National

| ORIGIN | Query Match | 7.7% | Score 646.8 | DB 7 | Length 762 |
|--------|-------------|------|-------------|------|------------|
|--------|-------------|------|-------------|------|------------|

| | | | |
|-----------------------|--------------|------------|----|
| Best Local Similarity | 70.00 | Indels | 0 |
| Matches | 690 | Mismatches | 72 |
| | Conservative | | |

| | | | | |
|-----------------------|--------------|---------------------|----------------|-------------|
| Query Match | 7.7%; | Score 646.8; | DB 7; | Length 762; |
| Best Local Similarity | 90.6%; | Pred. No. 2.1e-152; | | |
| Matches 690; | Conservative | 0; | Mismatches 72; | Indels 0 |

5833 GGTGCTGCTACTACACAGCCAGAGCGAGTATATCTTTGAGTTTCGACAAAGATGACCGCCT 5892
1 GGTGCTTCATCTCCACAGCCAGAGCGAGTATATCTTTGAGTTTCGACAAAGATGACCGCCT 60
5893 CTCCTCTGTGACGATGCCCAACGTCGGCGCGCAGACACTAGAGACCAATCCGCTCAGTGGG 5952
61 CTCCTCTGTGACGATGCCCAACGTCGGCGCGCAGAGCGCTGGAGACCAATCCGCTCAGTGGG 120
5953 CTACTACAGAAACATCTATACAGCCCTTCGAGGCAATGCCTCACTATACAGGACTTTCAC 6012
121 CTACTACAGAAACATCTATACAGCCCTTCGAGGCAATGCCTCACTATACAGGACTTTCAC 180
6013 TGAGGATGGGACCTCTCTACACCTTCTACTGGGCACTGGCGGCACTGGGCTGATATACAA 6072
181 TGAGGATGGGACCTCTCTACACCTTCTACTGGGCACTGGCGGCACTGGGCTGATATACAA 240
6073 GTATGGCAAACTGTCAAAGCTGGGAGAGACGCTCTATGACACCAACCAAGGCTTTCAC 6132
241 GTATGGCAAACTGTCAAAGCTGGGAGAGACGCTCTATGACACCAACCAAGGCTTTCAC 300
6133 CTATGACGAGCGGAGGATGCTGAAGACCAATCAACCTACAGATGAGGCTTTCACCTG 6192
301 CTATGACGAGCGGAGGATGCTGAAGACCAATGCTCAACCTACAGATGAGGCTTTCACCTG 360
6193 CACCATCCGCTACCGTCAAGTGGGCGGCTGATGACCGACAGATCTTCCGCTTCACTGA 6252
361 CACCATCCGCTACCGTCAAGTGGGCGGCTGATGACCGACAGATCTTCCGCTTCACTGA 420
6253 GGAAGGATGGTCAACCGCGCTTTGACTCAACTATGACACAGCTTCCGGGTCACGAG 6312
421 AGAAGGATGGTCAACCGCGCTTTGATTAACAACCTATGACACAGCTTCCGGGTCACGAG 480
6313 CATGAGGCTGTGATCAACGAGACCCACTGCGCCATGATCTCTATCGCTATGATGATGT 6372
481 CATGAGGCTGTGATCAACGAGACCCACTGCGCCATGATCTCTATCGCTATGATGATGT 540
6373 GTCAGGCAAGACAGAGCAGTTGGGAAGTTTGGTGTCTATTTACTATGACATTAACAGAT 6432
541 GTCAGGCAAGACAGAGCAGTTGGGAAGTTTGGTGTCTATTTACTATGACATTAACAGAT 600
6433 CATCACACAGCTGTATGACACCCACACCAAGCAATTTGATGATGATGATGATGATGATGAT 6492
601 CATTACACAGCGCTCATGACACCCACACCAAGCAATTTGATGATGATGATGATGATGATGAT 660
6493 AGTGAGTATGATCTTCCGCTCGCTCATGATGATGATGATGATGATGATGATGATGATGAT 6552
661 AGTGAGTATGATCTTCCGCTCGCTCATGATGATGATGATGATGATGATGATGATGATGAT 720
6553 GGGGCGGATGATGAAGAGGAGCTGAAGGTAGGACCTTACGC 6594
721 GGGGCGGATGATGAAGAGGAGCTGAAGGTAGGACCTTATGC 762

RESULT 14
BM947883
LOCUS
DEFINITION
IMAGE:5690214 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM947883 827 bp mRNA linear EST 14-MAR-2002
UI-M-EG0p-bvc-j-07-0-UI.r1 NIH_BMAP_EG0p Mus musculus cDNA clone
IMAGE:5690214 5', mRNA sequence.
BM947883
BM947883.1 GI:19431473
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 827)
NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.
Location/Qualifiers
1. .827
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5690214"
/issue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EG0p"
/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is CAGCCAGCAGC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP). 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institute of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 7.6%; Score 630.8; DB 3; Length 827;
Best Local Similarity 89.3%; Pred. No. 2.6e-148;
Matches 734; Conservative 0; Mismatches 81; Indels 7; Gaps 5;
QY 6504 AGATCTTCGGCTCCTCATGTACTGGATGACCGTCCAGTATGATAAATGGGCGAGTAG 6563
DB 1 AGATCTTCGGCTCCTCATGTACTGGATGACCTGTTTCAGTATGATTAATGGGCGGATG 60
QY 6564 TGAAGAGGAGCTGAAGTGAAGCTTACGCAATACCACTTCGCTACTCTCTATGAGTATG 6623
DB 61 TGAAGAGGAGCTGAAGTGAAGCTTACGCAATACCACTTCGCTACTCTCTATGAGTATG 120
QY 6624 ATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGACACCCACTCTGGCGCTACAGCT 6683
DB 121 ATGCTGATGGCCAGCTGCAGACAGTCTCCATCAATGACACCCACTCTGGCGCTACAGCT 180
QY 6684 AGGACTCAATGGGNAACCTGCACCTTACTGAGCCCTGGGAAACAGTGCAGCGCTACACAC 6743
DB 181 ATGACTCAATGGGNAACCTGCACCTTACTGAGCCCTGGGAAACAGTGCAGCGCTACACAC 240
QY 6744 TACGCTATGACATCCGCGACCGCATCACTCCGCTGGGTGAGCGTCAATACAGATGGATG 6803
DB 241 TACGCTATGACATCCGCGACCGCATCACTCCGCTGGGTGAGCGTCAATACAGATGGATG 300
QY 6804 AGGATGGCTTCTGAGGAGCGGGCGGTGATATCTTTGAGTACAACTCAGCTGGCGCTGC 6863
DB 301 AGGATGGCTTCTGAGGAGCGGGCGGTGATATCTTTGAGTACAACTCAGCTGGCGCTGC 360
QY 6864 TCATCAAGGCTTACAAACCGGCTGGCAGCTGGAGTGTTCAGGTACCGCTACAGATGGCTGG 6923
DB 361 TCATCAAGGCTTACAAACCGGCTGGCAGCTGGAGTGTTCAGGTACCGCTACAGATGGCTGG 420
QY 6924 GCGCGCGCTGTCCAGCAAGAGCAGCCACAGCCACCTGAGTCTTCTATGAGAGCC 6983
DB 421 GACGCCGAGTATCCAGCAAGAGCAGCCACAGCCACCTGAGTCTTCTTACGAGACC 480

QY 6984 TGACCAACCCACCAAGGTCAACCCAGCTGTACAAACCACTCCAGCTCTGAGATCACCTCCC 7043
DB 481 TGACCAACCCACCAAGGTCAACCCAGCTGTACAAACCACTCCAGCTCTGAGATCACCTCCC 540
QY 7044 TCTACTACGACTGTGCAAGGACACCTCTTTGCCATGGAGCTGAGAGTGGTGTGATGATTTT 7103
DB 541 TCTACTATGATGTGCAAGGACACCTCTTTGCCATGGAGCTGAGAGTGGTGTGATGATTTT 600
QY 7104 ACATAGCTTGTGCAACATCGGACCCCTCTTCTGCTTTAGTGGAAACAGGTTTGTATGA 7163
DB 601 ACATAGCTTGTGCAACATCGGACCCCTCTTCTGCTTTAGTGGAAACAGGTTTGTATGA 660
QY 7164 TCAAGCAAACTCTGTACACAGCTTATGGGAGATCTACATGGATACCAACCCCAACTTTC 7223
DB 661 TTAAGCAGATCTTATACACGGCTATGGGAGATCTACATGGATACCAACCCCAACTTTC 719
QY 7224 AGATCATATGAGCTACCATGGTCTTATGATCCACTCACAAAGCTTGTCCACATGG 7283
DB 720 AGATCATATGAGCTACCATGGTCTTATGATCCACTCACAAAGCTTGTCCACATGG 775
QY 7284 GCGGCGAGATTATGATGTGCTGGCGGAGCTGGACTAGCC 7325
DB 776 GCGGCGGGA-TATGATGTGCTGGCTGG-CGCTGGCAAGCC 815

RESULT 15

BG036207
LOCUS 602326960F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4428351 5',
DEFINITION mRNA sequence.

ACCESSION BG036207

VERSION BG036207.1 GI:12431132

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 870)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Straubeberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/OTF

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10178 row: h column: 16

High quality sequence stop: 713.

Location/Qualifiers

FEATURES

source

1..870

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:4428351"

/issue_type="adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_91"

/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dr primed.

Average insert size 1.4 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

ORIGIN

Query Match

Best Local Similarity 98.2%; Score 629; DB 2; Length 870;

Matches 700; Conservative 0; Mismatches 5; Indels 8; Gaps 6;

QY 904 AGSCACCTCCCGCTCTTCTTGCAACCATCACCGGGTACCCACTGACGTCACGACAGT 963
DB 1 AGSCACCTCCCGCTCTTCTTGCAACCATCACCA-GGTACCCACTGACGTCACGACAGT 59
QY 964 GTACTCTCTCCCGCCGACCTTGCCTCCGACGACCTTGCCTCCGCGCGCTTTAACT 1023
DB 60 GTACTCTCTCCCGCCGACCTTGCCTCCGACGACCTTGCCTCCGCGCGCTTTAACT 119
QY 1024 CAAGAAGCCCTCCCAAGTACTGTAACTGGAAGTGCAGAGCCCTGAGGCCATCTCATCTC 1083
DB 120 CAAGAAGCCCTCCCAAGTACTGTAACTGGAAGTGCAGAGCCCTGAGGCCATCTCATCTC 179
QY 1084 AGSCACTCTGGTCATCTCTGCTGGCATCTTGTGGCCATGACCTGTTTGGCCCTAACTG 1143
DB 180 AGSCACTCTGGTCATCTCTGCTGGCATCTTGTGGCCATGACCTGTTTGGCCCTAACTG 239
QY 1144 GCACCTGACAGCCGATGGAGGGGAGATGTATGAGATCAAGGAGACACAGCCAGCAGTTG 1203
DB 240 GCACCTGACAGCCGATGGAGGGGAGATGTATGAGATCAAGGAGACACAGCCAGCAGTTG 299
QY 1204 GCCTGTGCCAACCGAGCTCTCCCTATACCCCTCAGGGGACCTGGCTTACAGACCCCTGA 1263
DB 300 GCCTGTGCCAACCGAGCTCTCCCTATACCCCTCAGGGGACCTGGCTTACAGACCCCTGA 359
QY 1264 CAGGAAAGGCACAAAGGAACCAACAGAGGAAAGCCAGTAGTTCTTTCCAGAGGACAGTTT 1323
DB 360 CAGGAAAGGCACAAAGGAACCAACAGAGGAAAGCCAGTAGTTCTTTCCAGAGGACAGTTT 419
QY 1324 CATAGATTCTGGAGAAATTTGATGTGGAGGGGAGAGCTCCAGAGATTCTCTCTGGCAC 1383
DB 420 CATAGATTCTGGAGAAATTTGATGTGGAGGGGAGAGCTTCCAGAGATTCTCTCTGGCAC 479
QY 1384 TTTCTGAGATCTCAAGTGTTCATAGACCATCTGTGCATCTGAAATTCATATGTCTCT 1443
DB 480 TTTCTGAGATCTCAAGTGTTCATAGACCATCTGTGCATCTGAAATTCATATGTCTCT 539
QY 1444 GGGAAAGGCAGCCCT--GGTTGGCATTTATGGCAGAAAGGCTTCCCTCTTCACTACA-TAC 1500
DB 540 GGGAAAGGCAGCCCTGGGGTTGGCATTTATGGCAGAAAGGCTTCCCTCTTCACTACA 599
QY 1501 ACAGTTTGAATTTGTGGAGCTGCTGGATGGCAGAGGCT--CCTAACCCAGAGCGCGGA 1559
DB 600 ACAGTTTGAATTTGTGGAGCTGCTGGATGGCAGAGGCTCCTTAACCCAGAGCGCGGA 659
QY 1560 GCCTAGA-GGGGACCCCGCCAGTCT--CGGGGAACTGTGCCCCCTCCAGC 1609
DB 660 GCCTAGAGGGGGACCCCGCCAGTCTTTCGGGGGAACTGTGCCCCCTCCAGC 712

Search completed: December 10, 2005, 15:29:45

Job time : 29321 secs

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